Supplemental Data

A Robust Toolkit for Functional Profiling of the Yeast Genome

Xuewen Pan, Daniel S. Yuan, Dong Xiang, Xiaoling Wang, Sharon Sookhai-Mahadeo, Joel S. Bader, Philip Hieter, Forrest Spencer, and Jef D. Boeke

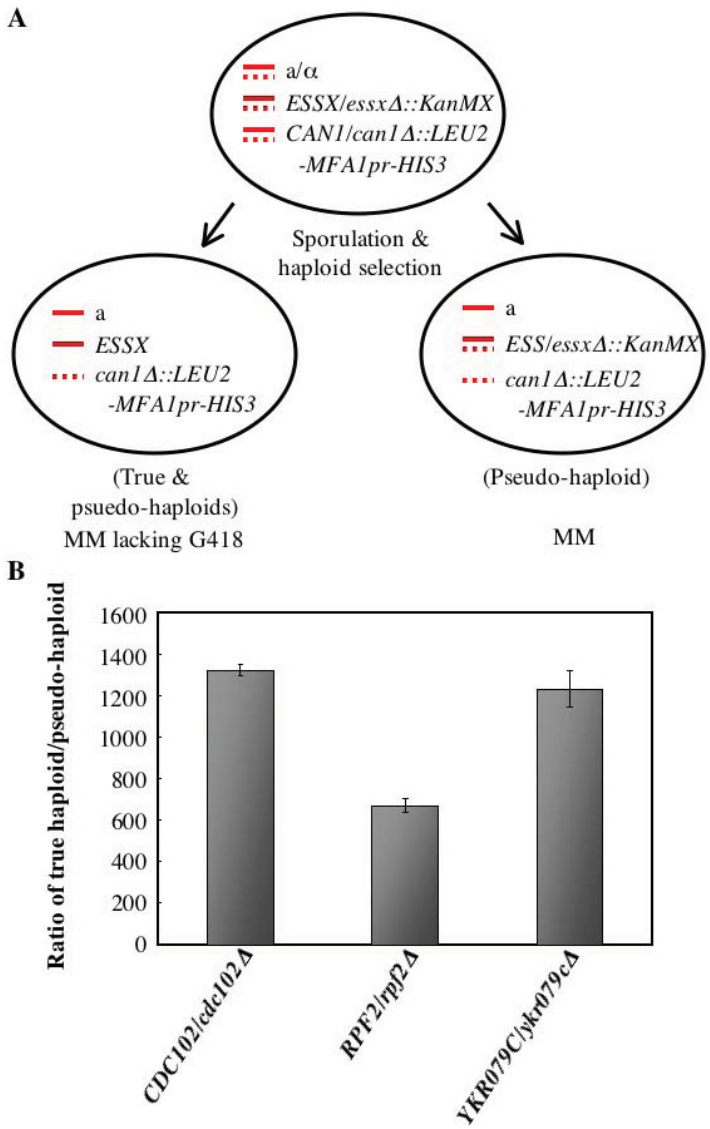

Figure S1. The SGA Reporter Can Be Exploited to Convert Diploid into Haploid Yeast

(A) An experimental design to test the efficiency of haploid selection with the SGA reporter. A heterozygous diploid YKO mutant of an essential gene (*ESSX/essxΔ::kanMX*) containing the SGA reporter is sporulated. Haploid progenies are selected on the magic medium with (MM) or without (MM lackingG418) G418. Cells grown on the MM medium should contain both the wild-type and the *kanMX* alleles of the essential gene. These *kanMX* allele-containing cells likely result from meiotic nondisjunction or more rarely from mitotic homozygosis of both the mating-type and *CAN1* loci. These are not true haploids and we call them pseudo-haploid cells. By comparing the number of wild-type haploid cells and the psuedo-haploid cells generated from the same sporulation one can estimate the power of haploid selection with the SGA reporter.

(B) The haploid-selection power of the SGA reporter is around 10^3. Three "SGA reporter"-containing heterozygous diploid YKO mutants of essential genes (*CDC102/cdc102Δ::kanMX*, **XPY452a/α**; *RPF2/rpf2Δ::kanMX*,. **XPY454a/α**; *YKR079C/ykr079cΔ::kanMX*, **XPY460a/α**) were sporulated. Meiotic progenies were selected on the magic medium with or without G418. The number of colonies from the same amount of sporulation culture generated on both media was compared. A ratio of true haploid (without G418) over pseudo-haploid (with G418) was plotted.

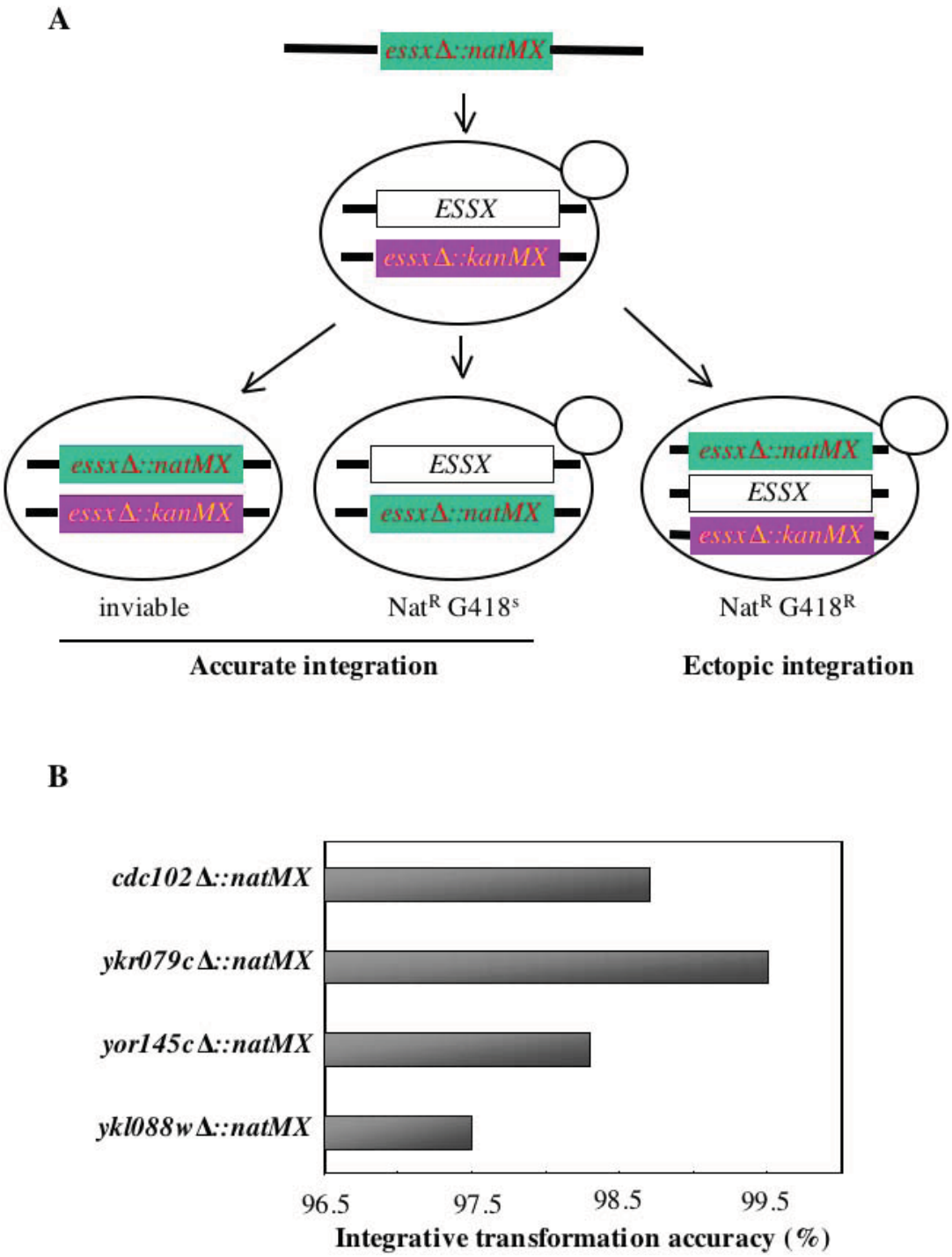

Figure S2. High Accuracy of Integrative Transformation in the Heterozygous Diploid YKOs

(A) A diagram of the test of transformation accuracy in a heterozygous diploid YKO mutant. A gene disruption cassette of an essential locus (*essxΔ::natMX* with ~1.5kb flanking sequence) was transformed into a preexisting heterozygous YKO diploid mutant of the same essential gene (*ESSX/essxΔ::kanMX*). When the *essxΔ::natMX* cassette integrates into the right locus, it either disrupt the wild-type *ESSX* gene and cause lethality or replace the *essxΔ::kanMX* copy and the resultant transformants become resistant to CloNat but sensitive to G418 (Nat^R $G418^s$). When ectopic integration happens, the resultant transformants are resistant to both drugs (Nat^R $G418^R$). By comparing the number of Nat^R $G418^s$ and Nat^R $G418^s$ colonies from the same transformation reaction, one can calculate what portion of the Nat^R transformants are results of accurate integration of the knockout cassette into that essential locus in the heterozygous diploid strain.

(B) Integrative transformation accuracy in heterozygous diploid YKOs. Four different gene-disruption cassettes depicted were individually transformed into the preexisting heterozygous diploid YKO mutants of the corresponding essential genes. Transformation accuracy (in the form of percentage) for each reaction was plotted.

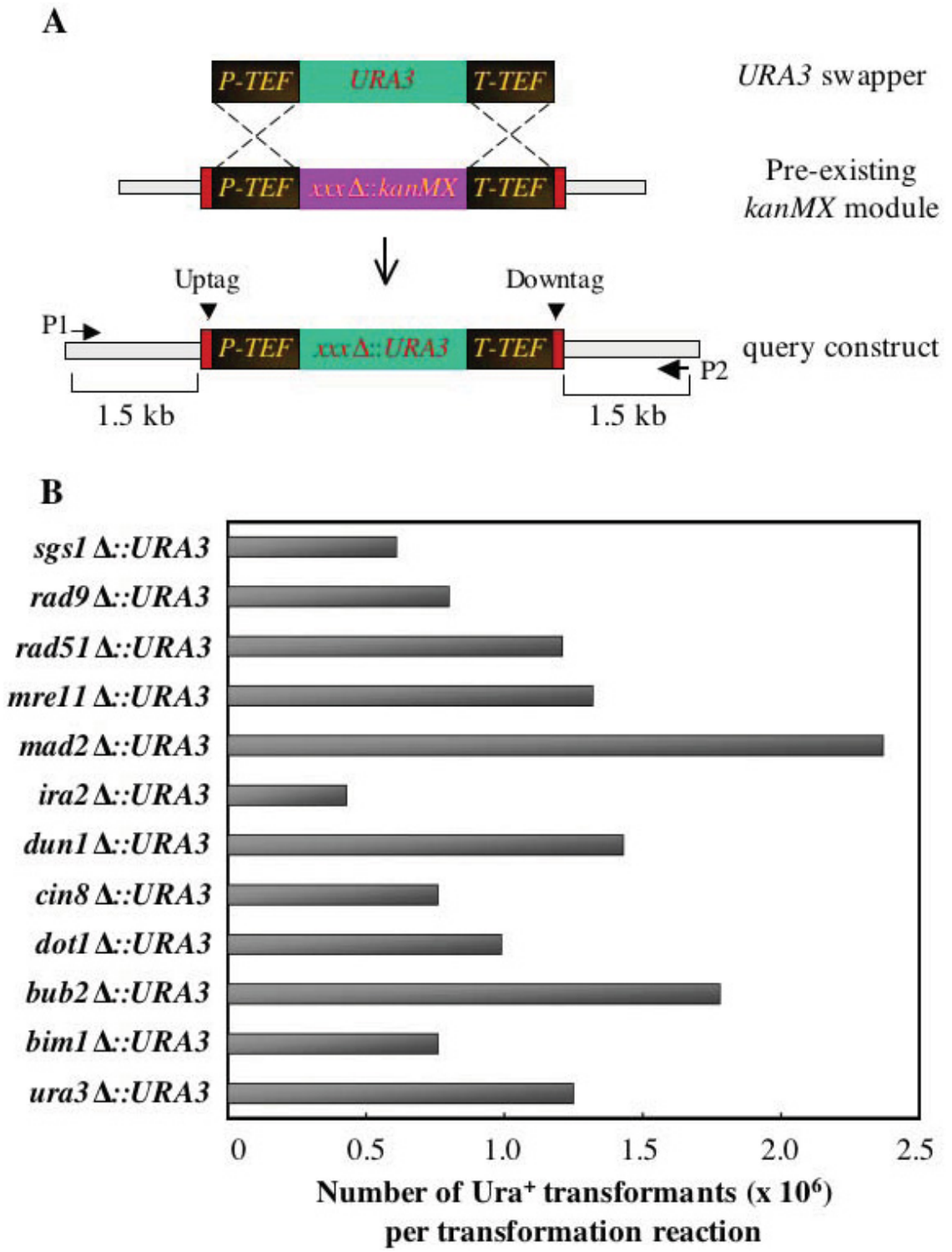

Figure S3. The Heterozygous Diploid Pool Is Easy to Transform

(A) A diagram of making a query construct for the integrative transformation. A *URA3* marker was used to replace the pre-existing *xxxΔ::kanMX* module in each YKO mutant (haploid or diploid) via homologous recombination (*xxx* represents any YKO mutation). The resultant Ura$^+$ G418^s mutant is used as the template in a long-range PCR reaction to amplify the query construct (*xxxΔ::URA3)* for integrative transformation. An *xxxΔ::natMX* cassette can be constructed in a similar manner.

(B) High integrative transformation yields in a heterozygous diploid pool. Twelve randomly chosen gene-disruption cassettes depicted were individually en masse transformed into a pool of 5,896 heterozygous diploid YKO mutants containing the SGA reporter as described in Materials and Methods. The number of Ura$^+$ transformants obtained from each reaction was plotted.

Table S1. Behaviours of DNA damage response YKO mutants in high throughput screens.

Strain genotype	Type of YKOs used								
	*MAT***a**/Δ homozygous diploid YKO[a]			MAT**a** haploid YKO[b]			heterozygous diploid YKO derivatives[c]		
	MMS	HU	UV	MMS	HU	UV	MMS	HU	UV
*ddc1*Δ	NA	NA	NA	S	S	S	S	S	S
*mec3*Δ	**R**	**R**	S	S	S	S	S	S	S
*rad17*Δ	S	**R**	S	S	S	S	S	S	S
*rad24*Δ	NA	NA	NA	S	S	S	S	S	S
*rad9*Δ	**R**	**R**	**R**	S	**R**	S	S	S	S

Notes: **R**- resistant; S-sensitive; NA-no data is available. Data in this table was adopted from: [a] Bennett et al. (2001); [b] Chang et al., (2002); [c] Pan et al., in preparation.

Table S2. Benomyl-sensitivity of YKO mutants studied by microarray analysis

Gene Name	Benomyl concentration (μg/ml)								
	1	**5**	**10**	**15**	**20**	**25**	**30**	**35**	**40**
CIN1	4.28	83.68	100.61	148.13	98.20	371.48	176.94	212.63	169.98
YML094C-A	2.66	18.12	47.09	30.68	26.18	77.70	35.66	28.90	30.00
PAC10	2.63	9.28	51.57	75.01	19.63	75.57	19.73	7.28	32.89
PFD1	2.59	14.63	60.19	71.96	33.03	101.15	110.11	57.04	30.98
GIM3	2.37	7.86	47.91	84.08	26.35	94.88	33.27	39.20	29.48
TUB3	2.28	23.01	80.12	79.25	93.04	110.69	87.58	77.60	107.84
GIM5	2.14	17.88	44.67	28.74	17.25	118.62	21.87	50.97	29.16
YKE2	1.74	8.36	28.07	29.29	7.56	29.18	26.05	25.05	25.05
GIM4	1.58	5.55	25.76	85.44	319.30	407.87	350.77	278.47	421.53
CIN2	1.49	74.87	38.18	56.57	72.59	147.35	121.31	77.04	54.52
NFU1	1.15	5.37	5.09	8.72	17.77	41.56	53.82	31.13	85.97
WHI2	1.10	6.77	10.23	2.66	4.32	67.88	41.75	183.34	60.69
SOD2	1.00	5.84	32.29	19.03	28.67	100.02	47.70	23.45	264.13
ISU1	0.97	8.84	9.65	11.55	13.95	102.81	57.09	43.87	10.39
CIN4	0.86	0.82	5.27	21.26	73.96	83.90	47.97	56.54	129.72
CCR4	0.84	0.90	1.85	1.14	2.47	14.96	18.94	138.82	116.63
PYC1	0.89	6.00	9.64	16.73	15.94	13.29	39.59	31.28	36.72
UBA3	1.09	4.21	7.89	10.10	21.18	31.58	27.70	13.66	14.86
POP2	0.83	0.97	1.26	1.97	6.38	35.36	36.64	31.98	95.14
MIR1	1.15	11.36	47.08	9.26	6.54	9.33	9.70	13.93	12.96
UBI4	1.36	0.28	0.91	7.86	4.65	32.59	16.18	25.94	24.87
DHH1	1.13	0.53	1.10	1.22	3.59	12.79	34.05	30.00	19.85
YBR030W	0.75	1.40	1.14	1.02	1.09	3.02	4.70	67.94	232.45
THR1	0.81	1.95	13.33	17.75	15.90	6.08	10.17	15.00	20.31
RTG1	0.72	2.80	7.55	7.10	13.46	9.03	10.64	28.27	21.12
BRO1	1.47	1.37	1.65	5.59	14.19	34.46	10.14	8.47	25.80
RTG2	1.02	3.15	9.62	9.22	14.19	9.21	12.14	14.16	22.75
MAD2	1.20	1.30	1.26	1.04	2.36	6.86	21.20	36.79	227.73
YJR018W	1.05	2.80	2.58	1.71	3.98	2.96	6.50	49.56	35.45
YGR046W	0.86	6.37	3.04	3.28	9.30	19.82	8.09	19.72	42.06
FYV6	1.43	1.97	7.85	11.27	7.66	16.85	9.87	13.56	10.19
PPZ1	1.03	4.32	4.14	2.77	5.53	12.49	13.07	26.33	28.36
YDR334W	1.19	1.24	1.11	2.24	4.46	8.57	12.84	34.67	24.13
SNT309	0.89	1.92	0.86	1.32	2.41	14.49	18.48	25.79	11.82
YOR073W	1.22	2.64	3.80	5.19	8.17	13.32	6.31	25.39	11.93
PSO2	0.83	0.92	1.34	1.15	1.43	9.09	24.09	27.05	76.23
RMD11	0.95	1.97	2.46	1.59	2.39	7.79	16.67	28.17	60.22
AFG3	1.09	3.42	3.03	1.84	3.13	6.05	8.76	33.99	15.89
GPB2	1.18	1.40	1.26	1.32	1.14	23.95	15.15	14.61	28.27
GLR1	1.05	3.80	3.45	3.62	5.15	20.70	8.31	12.46	20.80

YAL046C	1.19	2.46	4.83	6.24	5.78	13.65	10.19	12.20	20.57
CTK1	1.38	0.67	1.15	1.86	5.85	16.46	12.81	16.12	22.58
YKL134C	0.87	5.25	3.27	2.27	3.61	6.20	16.49	18.30	29.74
GPB1	1.05	1.83	1.25	0.84	1.13	24.01	8.99	16.69	17.32
SKN7	0.84	1.08	2.12	6.86	17.41	15.85	6.38	5.21	3.99
RTG3	1.09	2.32	12.09	9.17	7.83	6.96	8.34	6.99	21.53
YLR294C	1.09	4.87	4.16	1.85	3.16	4.55	7.70	26.79	14.16
EAP1	1.21	1.48	1.21	1.16	2.86	7.95	10.25	27.80	26.53
YME1	1.07	4.44	1.31	1.17	2.82	9.80	11.32	19.83	16.25
RIM15	0.92	0.50	0.73	0.75	0.75	14.62	18.64	13.82	10.16
POR1	1.01	3.13	1.99	1.45	2.41	4.69	7.81	26.57	29.97
DBF2	1.13	11.66	2.90	0.87	3.53	4.85	6.89	16.82	23.98
PAN2	1.08	1.16	1.73	2.18	3.49	4.03	11.10	23.20	71.31
MCT1	0.65	3.70	2.51	1.20	2.14	6.10	15.72	15.10	12.46
CTK3	1.67	4.12	2.38	2.78	7.32	11.42	7.18	9.40	21.29
RPN4	0.81	1.69	1.63	4.28	4.30	5.37	14.47	12.90	12.89
HTZ1	0.87	1.77	1.36	1.92	2.83	4.35	9.85	22.07	42.25
YLR349W	0.80	2.59	4.10	2.81	3.47	5.12	8.47	15.73	16.03
STE50	0.84	3.74	2.35	3.75	2.95	7.85	9.81	11.66	15.86
MAD1	0.88	1.21	1.26	1.44	2.18	5.69	8.87	21.32	24.96
PHO80	1.15	0.89	1.13	1.44	1.51	8.90	8.65	19.05	25.57
ALF1	0.75	0.14	0.27	1.63	4.96	18.95	6.65	8.64	6.84
MAE1	0.85	6.65	7.20	4.34	5.01	3.03	6.59	8.00	23.63
VID21	0.98	3.36	1.92	2.90	6.66	3.11	13.21	8.83	9.35
DIC1	1.15	4.11	5.27	3.97	5.29	3.84	8.76	7.98	8.54
VPS34	0.91	1.77	1.30	1.84	6.30	9.16	4.35	14.52	8.96
MRPS8	0.64	1.32	1.06	1.00	3.35	7.64	8.97	15.85	14.21
MRPL16	0.95	3.58	2.40	1.08	1.98	12.68	8.40	8.23	7.37
GUF1	1.23	4.31	3.93	2.79	2.29	5.01	6.42	12.75	18.83
YCR006C	0.56	1.09	6.30	2.15	1.55	2.87	18.71	5.35	4.26
PIN4	1.03	2.06	1.87	1.31	2.13	4.14	9.95	14.71	21.54
BUB1	1.12	1.58	0.88	5.34	4.96	5.01	8.46	9.81	6.69
TIM18	0.85	2.86	2.68	5.27	10.33	6.18	3.86	5.12	3.07
FZO1	1.13	2.47	2.34	3.36	3.84	5.77	15.03	3.00	46.29
BUB3	1.01	3.22	2.67	3.82	4.24	8.85	5.11	7.87	4.32
UBP6	1.22	0.82	0.58	2.01	4.50	9.70	12.38	5.11	4.74
YML090W	1.21	2.20	2.99	2.18	2.54	5.57	9.46	10.06	16.73
VAC7	0.92	0.47	0.46	2.16	2.22	19.60	5.50	4.70	11.83
ATP12	1.00	3.96	3.58	3.01	3.42	6.26	4.98	9.43	9.68
YLR296W	1.20	4.09	3.26	2.29	1.93	4.13	7.63	10.38	3.60
ADO1	1.77	1.69	0.26	1.38	1.16	17.90	6.18	4.44	8.32
YCR079W	0.88	3.68	3.22	3.26	5.15	8.74	6.03	3.82	2.80
YHR100C	1.10	2.76	2.19	2.23	2.40	5.61	8.13	10.25	40.40
MDM30	1.26	1.92	2.50	3.09	6.99	4.78	6.50	7.58	10.06

MDM38	1.05	1.71	2.30	1.69	1.78	10.78	6.44	8.64	10.96
RPS6B	1.66	1.31	0.99	1.20	1.03	15.76	6.65	5.33	6.75
SIR3	0.80	1.89	1.00	1.21	2.62	4.97	14.43	6.90	23.29
STE20	1.14	1.41	2.01	2.77	2.71	4.49	10.77	8.44	34.24
MIS1	1.01	2.09	5.34	2.64	3.50	5.48	4.89	8.70	18.80
NOT3	1.04	2.46	3.58	3.98	4.86	7.81	4.25	5.57	11.66
YAF9	0.75	2.29	1.47	1.71	1.96	4.95	5.78	14.54	34.00
YER087W	1.10	2.57	1.49	1.17	1.70	3.85	6.19	14.57	16.68
EMI1	1.02	3.96	3.34	3.19	3.86	3.25	6.59	7.25	8.09
MEC3	1.00	3.00	2.95	2.01	2.24	5.54	7.08	8.57	7.98
ARP6	0.97	1.11	1.07	1.65	2.27	3.32	7.61	14.26	30.10
MRP51	1.25	2.92	1.05	1.12	2.18	3.46	7.99	12.16	6.02
YKL030W	1.01	4.05	5.14	5.67	5.83	2.72	3.99	3.67	4.58
YGL196W	1.17	0.89	1.14	0.93	1.21	4.25	6.04	16.44	13.87
SOV1	1.16	2.87	1.91	1.37	3.03	5.43	8.45	7.73	6.38
ATP11	0.97	4.35	3.19	1.69	3.00	2.96	5.38	10.33	9.05
YLR290C	0.99	4.24	2.77	2.51	1.84	5.16	8.51	5.79	5.87
SIR3	0.91	2.10	1.15	1.58	2.06	8.19	9.21	5.73	17.42
YLR257W	1.02	1.51	1.51	1.26	1.37	6.12	9.53	8.53	20.99
CSR2	1.16	1.66	1.00	1.06	1.09	6.16	5.30	13.40	5.29
YOR205C	1.17	2.78	2.04	1.65	2.21	3.78	6.94	10.23	12.84
BUB2	0.95	0.88	1.51	1.16	1.44	2.97	4.77	16.94	10.23
MDH2	0.94	3.52	5.43	4.62	3.08	2.68	4.29	6.01	7.58
RPO41	1.06	3.94	2.92	2.39	2.98	3.20	3.34	10.67	4.85
SLT2	0.86	1.80	1.14	0.91	1.66	8.25	8.43	7.26	3.37
PAN3	1.12	0.76	1.28	1.81	2.25	3.68	5.76	13.64	30.16
YLR280C	1.03	4.19	2.85	2.31	1.79	4.13	7.63	6.30	4.61
MSH2	0.69	2.85	3.33	1.98	2.70	4.63	8.10	5.82	14.11
MSU1	0.78	2.60	1.46	1.23	1.67	3.83	5.05	12.97	7.56
YPR099C	1.09	3.33	1.20	1.33	2.43	4.72	7.43	8.00	6.97
YLR312C	1.06	4.21	3.36	2.13	2.77	4.65	4.88	6.33	10.10
ATP5	0.87	5.45	4.30	1.92	2.73	4.53	4.49	5.03	5.36
ADH3	0.83	1.43	2.00	1.93	3.59	5.59	4.66	8.97	6.86
DEF1	2.91	0.29	0.62	0.48	1.27	4.91	3.19	15.19	4.52
NAT1	1.02	1.32	0.72	1.61	2.67	3.64	6.38	11.35	19.54
IMG1	1.33	3.19	2.71	1.59	1.95	5.15	6.67	6.11	10.21
YJL022W	0.86	2.43	0.78	0.58	1.04	2.19	4.29	16.34	11.76
BCK1	0.82	1.82	1.14	1.26	1.56	7.48	7.30	6.81	2.72
YLR283W	1.16	4.23	3.14	2.71	2.09	4.39	3.70	6.73	3.61
SDH2	1.05	2.40	3.32	1.29	1.66	3.89	4.65	9.73	4.26
MRP1	0.99	3.82	1.19	1.30	2.18	3.56	7.08	7.66	11.28
TCM10	0.82	3.13	2.75	1.95	3.25	2.43	7.28	6.02	3.47
GGA1	1.01	1.18	0.79	0.78	1.07	4.04	12.41	6.23	21.82
PET8	0.66	2.74	1.47	1.26	2.07	2.70	3.73	12.87	7.02

YLR287C	1.14	3.02	2.50	1.44	2.25	3.55	3.36	10.22	2.83
ATP10	0.86	1.84	2.77	1.53	1.86	2.73	6.30	9.52	5.64
YLR279W	1.09	2.83	2.86	2.06	2.09	4.92	3.92	7.61	3.94
MGM101	0.98	4.01	2.02	1.85	2.54	3.22	4.46	8.27	13.22
ATP7	1.09	4.06	2.87	2.94	2.70	4.17	5.20	4.28	4.54
SHP1	1.14	1.25	1.25	0.88	1.07	4.57	4.02	13.10	3.39
SNF8	1.09	1.76	1.14	4.39	4.65	7.92	3.03	3.12	6.06
SLS1	0.88	1.04	1.06	1.64	2.39	2.33	12.01	5.65	19.27
DIA4	1.41	2.03	2.77	1.70	2.01	2.64	5.13	9.24	4.34
MSE1	1.26	1.36	2.46	1.02	1.55	2.70	9.16	7.17	5.09
MDM12	1.22	1.50	1.19	0.72	0.93	3.05	3.31	14.76	5.68
EXG1	1.15	2.26	2.47	1.46	1.80	4.02	3.74	9.67	8.89
POS5	1.05	2.76	4.96	1.86	0.64	6.85	3.72	4.72	13.02
PDC1	0.92	1.27	2.17	1.79	1.94	8.18	6.60	3.67	5.37
YLR358C	1.13	2.11	2.83	1.78	3.77	5.24	3.57	5.95	8.60
ECM38	1.22	3.51	3.21	1.67	1.69	4.01	7.18	3.86	2.44
MTF1	0.75	1.72	1.53	1.51	2.26	4.45	6.78	7.25	18.05
GRX5	0.97	1.28	0.98	0.92	1.61	7.12	5.59	7.67	5.21
YPL005W	0.67	3.79	2.52	1.72	2.24	2.59	4.66	7.96	3.75
LPE10	1.16	1.89	1.87	1.95	2.17	4.26	4.55	8.27	5.99
TOM70	0.78	1.55	1.83	1.85	2.93	4.42	5.93	6.83	15.25
WSC3	0.99	2.25	4.13	1.95	1.59	3.83	7.63	3.73	7.77
URE2	0.76	1.16	3.94	2.35	3.47	3.29	4.48	6.58	8.59
MRP2	0.80	2.36	1.77	0.66	2.18	2.22	6.94	9.03	8.37
YJR120W	1.05	3.75	3.24	2.54	2.26	3.79	3.74	5.55	4.24
YHR039C-B	2.01	0.21	0.44	1.45	1.03	11.14	2.71	6.91	6.81
MRPL32	0.78	4.06	1.40	1.10	2.49	2.39	4.36	9.28	8.81
MRPL22	1.01	2.67	0.99	1.03	1.63	2.06	4.35	12.09	5.31
YDL033C	1.15	1.58	1.55	1.78	2.21	3.64	5.62	8.19	9.83
MSM1	1.30	3.64	1.75	1.85	3.03	3.57	4.57	5.86	9.66
YER077C	0.97	1.99	1.14	0.98	2.34	1.88	5.26	10.97	13.66
BIK1	0.90	1.54	1.61	1.62	2.03	4.72	7.68	5.42	18.38
BFA1	1.22	0.88	1.12	1.11	1.23	3.17	5.58	11.22	11.48
VMA5	0.89	0.12	0.31	0.89	1.22	13.27	5.31	3.37	10.25
MRPL33	0.94	3.55	1.43	1.26	1.84	2.92	8.43	4.87	3.33
NPR2	0.88	1.18	1.79	2.07	3.24	2.80	6.11	7.13	11.25
YCL003W	1.05	1.63	1.41	1.24	1.61	3.81	2.61	11.77	7.32
CDA2	1.22	3.32	3.94	1.88	1.75	3.91	3.71	5.30	10.27
NKP2	0.97	3.42	2.84	1.73	2.17	5.98	4.12	3.76	2.31
YJL169W	0.95	3.08	1.28	1.50	1.90	2.26	7.75	6.24	5.92
YPL107W	1.13	3.19	2.69	2.13	1.45	3.70	4.60	6.05	4.31
ATP11	0.67	2.89	1.76	1.31	1.67	2.39	4.33	9.91	8.90
YPL105C	0.90	1.36	1.07	1.57	1.45	3.21	3.88	11.42	6.63
KAP123	1.01	1.60	4.65	1.67	3.80	2.55	5.09	4.47	4.94

RSM22	1.12	3.07	2.31	1.62	1.85	3.75	5.11	5.99	7.21
YDL025C	1.02	1.78	3.01	3.52	5.58	3.34	3.04	3.52	6.48
AEP2	0.94	3.19	2.54	1.99	2.00	3.25	4.51	6.32	9.48
HCM1	0.79	2.19	1.41	1.37	1.87	3.37	4.37	9.35	25.53
MRPL4	1.18	2.56	2.14	1.10	2.93	3.77	5.16	5.80	6.43
PET56	0.72	2.06	1.18	1.11	1.38	2.38	5.07	10.72	11.61
PET130	1.20	2.95	1.80	1.06	1.81	3.59	2.66	9.45	9.48
MRPL9	1.03	2.21	1.12	1.18	1.61	2.43	3.50	11.22	7.12
SET2	1.20	2.21	1.76	1.36	1.65	3.13	5.59	7.37	20.93
NPR1	1.30	3.95	3.27	2.01	2.65	2.53	3.37	5.17	8.09
MAD3	2.14	1.96	2.55	2.06	2.99	1.42	4.39	6.73	10.81
MSK1	0.90	2.12	0.99	0.51	1.59	2.32	7.35	8.42	8.32
EMI1	0.74	2.64	2.76	2.86	2.78	3.32	3.25	5.75	3.34
YIL064W	1.09	2.91	2.73	2.20	2.41	3.85	3.27	5.59	2.81
RSM19	0.65	3.03	0.79	1.63	3.26	2.29	3.02	9.34	3.74
ISM1	1.22	2.44	2.25	1.28	1.35	2.50	4.27	8.69	6.09
GLC8	0.96	1.63	1.40	2.10	2.31	4.56	5.60	5.39	8.92
CDA1	1.06	1.92	2.29	1.41	1.25	3.11	5.91	6.99	7.78
YLR281C	0.86	3.80	2.98	1.84	1.60	3.65	5.94	3.20	14.11
YGR150C	0.75	2.17	1.71	0.95	2.02	4.13	5.38	6.72	4.22
MSC1	0.80	3.52	2.75	1.72	1.75	4.65	2.86	5.73	22.98
AOR1	0.67	1.11	0.86	1.11	2.26	2.45	2.76	12.49	20.07
RMD12	1.25	1.64	1.18	1.12	2.43	5.14	5.65	5.30	5.66
MCK1	1.02	1.72	1.79	1.24	1.79	4.57	5.08	6.15	4.06
PDR15	1.00	0.62	0.61	0.61	0.68	7.79	6.73	5.29	6.62
YDR065W	1.28	2.54	2.02	1.21	1.78	3.75	3.43	7.33	8.27
MRPL49	0.90	1.87	0.79	0.75	1.58	1.96	6.14	9.10	10.35
YPL098C	1.15	2.65	1.62	1.57	2.09	3.38	4.63	6.01	3.97
YNL213C	0.86	2.93	1.76	1.03	1.47	2.90	5.95	6.19	13.59
YMR293C	0.74	2.46	1.04	1.20	1.60	4.10	3.59	8.18	10.58
SPH1	1.34	3.49	3.42	2.29	1.85	3.10	3.98	3.27	6.23
SWC1	1.15	1.41	1.26	3.52	2.40	3.76	4.55	4.58	12.18
MRH4	0.94	1.73	1.29	1.33	1.61	2.66	4.93	8.13	79.01
RSC1	0.81	1.68	3.24	3.28	4.85	2.76	2.80	3.13	4.13
ATP4	0.97	3.08	2.79	2.26	1.59	3.76	2.35	5.74	4.80
UBC12	1.09	2.79	3.45	1.59	1.99	2.81	4.11	4.66	8.71
YPL183W-A	1.15	2.87	1.93	1.51	1.82	2.79	4.29	6.08	3.13
YDR532C	0.98	1.88	0.60	0.88	2.00	3.65	7.78	4.65	3.31
MRPL23	1.19	3.37	1.44	1.27	1.09	3.31	4.53	6.19	13.00
HOS2	0.96	1.84	0.93	1.61	2.39	2.23	2.60	9.80	5.36
YKL169C	0.73	2.43	1.37	1.38	1.17	5.79	3.76	5.72	5.57
MDM10	0.82	2.44	0.74	1.11	1.00	1.08	2.37	12.72	10.66
STP1	0.87	2.63	4.45	2.64	2.47	2.28	3.17	3.77	2.40
YLL033W	0.94	1.80	1.52	1.31	2.06	3.72	3.24	7.68	23.79

MRPS9	0.81	1.25	0.97	1.01	2.21	3.31	4.91	7.64	4.91
YPR116W	0.48	1.37	1.14	1.14	1.75	2.69	3.41	10.13	6.13
PSR1	0.72	2.58	1.79	1.23	1.51	3.88	2.46	7.93	8.94
VIP1	1.18	2.36	2.65	1.71	1.93	4.33	4.63	3.29	4.85
MIP1	1.26	1.65	1.76	1.38	3.33	3.73	5.64	3.33	9.34
ARG80	0.65	2.94	1.10	1.05	1.83	4.40	3.61	6.49	7.85
MRPS16	1.05	2.37	1.37	1.16	2.09	2.64	6.23	5.12	5.44
RSM18	0.73	3.92	1.25	0.95	2.06	4.63	2.87	5.62	11.55
MRPS17	1.01	2.49	1.93	1.10	1.30	3.07	4.12	6.97	4.93
YOR200W	0.85	3.33	1.57	1.15	1.87	2.23	4.39	6.53	10.81
VPS36	1.21	1.07	1.41	3.27	4.71	3.72	3.75	2.66	5.68
GCV1	1.07	1.55	1.77	1.81	2.51	2.92	3.66	6.45	3.47
VMA8	0.90	0.16	0.26	0.84	1.61	3.15	2.11	12.65	7.30
IMG2	0.69	0.95	0.80	0.72	1.45	5.35	6.20	5.45	5.47
MRF1	0.70	2.37	1.72	1.34	1.75	2.50	2.96	8.21	7.64
STP22	1.37	1.43	0.60	2.76	3.73	4.66	4.30	2.67	4.45
MRPL19	0.70	1.76	3.40	1.01	1.40	5.02	3.11	5.11	16.12
QRI5	1.16	2.65	1.93	1.57	3.11	3.79	3.48	3.77	12.59
MSY1	0.84	1.43	0.84	0.98	1.48	2.86	7.17	5.87	12.53
VPS25	1.26	1.37	1.27	2.70	3.80	4.39	3.78	2.88	3.70
IFM1	0.65	2.95	1.52	1.31	2.82	3.80	2.83	5.54	10.14
YGR102C	0.88	2.66	1.68	0.89	1.50	3.78	3.65	6.28	10.85
MRP13	1.16	2.40	1.79	1.53	2.15	3.16	5.74	3.37	10.38
ARD1	1.26	1.72	0.69	1.18	1.89	2.38	3.16	8.93	18.94
BUD6	0.85	2.56	2.40	1.70	1.45	3.71	4.04	4.40	1.67
YDR479C	1.00	1.92	1.89	2.67	2.89	2.99	3.57	4.14	5.53
MTG1	0.90	2.02	0.94	0.94	1.29	2.90	4.15	7.91	14.68
YDR248C	0.87	1.05	0.99	0.95	0.69	5.45	6.72	4.19	94.77
PDE2	0.95	1.89	1.37	0.85	1.34	7.37	4.28	2.84	6.37
YIL077C	1.20	3.16	2.70	1.96	2.22	3.40	2.52	3.57	5.02
PUS2	0.96	1.69	2.36	1.87	1.90	2.63	2.78	6.48	4.92
AEP1	0.85	2.46	1.77	1.24	1.76	2.20	4.65	5.70	5.94
YLR282C	0.92	3.02	2.50	1.83	1.99	4.15	3.66	2.51	3.86
CAJ1	1.00	2.28	1.53	1.72	2.24	2.81	3.85	5.15	5.60
YDL032W	1.12	1.96	1.70	1.16	1.50	2.73	4.29	6.10	6.40
MRP20	1.03	3.01	0.87	1.44	1.74	3.39	3.04	6.03	7.42
YPL099C	1.12	1.88	2.26	1.65	2.12	2.48	2.81	6.14	4.12
MON2	0.86	1.86	2.05	1.26	1.24	2.58	4.33	6.24	19.23
PET123	1.29	1.93	1.77	1.37	1.75	3.53	3.23	5.50	5.04
YML100W-A	0.76	2.47	1.40	1.20	1.85	4.06	4.33	3.99	19.45
THR4	1.15	1.11	2.49	3.22	2.38	3.13	3.55	3.01	5.01
SUV3	0.97	2.22	1.35	1.00	1.19	2.89	4.75	5.63	8.92
PIF1	1.05	2.19	2.81	1.94	3.45	1.77	2.21	4.55	8.27
YBR004C	0.96	1.71	0.89	0.84	1.45	1.71	2.43	9.94	15.60

YDR114C	1.09	1.27	1.93	1.14	2.14	3.00	3.67	5.66	10.17
YLR091W	1.04	2.58	1.47	1.12	1.40	2.74	3.00	6.49	5.54
SET3	0.78	1.81	0.63	1.47	1.91	3.35	2.98	6.86	11.36
SNQ2	1.08	0.78	0.56	0.88	1.02	2.61	5.13	7.67	25.47
YLR311C	0.78	3.21	2.76	1.55	1.68	1.90	3.17	4.68	7.73
MRPL8	1.22	1.96	1.22	1.17	1.99	2.12	5.02	4.98	4.45
EAF3	1.01	2.31	1.61	1.33	1.41	1.81	4.54	5.47	12.94
ATP2	1.00	2.54	3.50	1.94	2.02	3.10	2.00	3.38	7.85
NNT1	1.27	2.66	2.60	1.39	1.66	3.61	2.58	3.68	5.31
AQR1	0.91	1.74	2.22	2.89	2.54	1.82	3.15	4.14	3.55
YLF2	0.70	3.15	0.95	0.81	2.03	3.02	4.06	4.62	3.33
RML2	1.27	2.24	1.30	0.98	1.68	3.33	4.93	3.60	7.78
YJL045W	0.91	1.46	2.94	1.76	2.04	2.74	3.38	4.08	3.28
LTE1	0.96	1.29	3.01	3.56	3.46	1.67	2.00	3.31	6.52
YPL184C	1.09	1.98	1.08	1.05	1.26	2.14	4.97	5.69	9.30
PRP12	1.52	1.03	0.04	0.71	1.00	5.93	5.14	3.82	3.93
REF2	0.97	0.82	1.55	1.94	1.80	5.45	3.85	2.81	7.50
ECI1	0.90	2.32	2.58	1.69	1.47	3.50	2.89	3.84	13.29
MGM1	1.13	1.36	1.82	1.43	2.56	4.41	2.61	3.81	5.30
OAR1	1.29	1.03	1.36	1.55	1.79	3.12	4.29	4.69	8.11
MRPL24	1.31	1.65	1.65	1.35	2.05	2.46	3.60	5.00	7.93
PET112	0.63	1.30	0.82	1.04	1.08	3.95	4.88	5.33	11.12
YBR219C	0.74	2.52	2.14	2.23	2.97	2.19	2.61	3.60	6.87
MAK10	1.07	1.85	1.76	1.25	1.18	1.82	2.83	7.23	7.21
YBR281C	1.19	3.21	1.68	1.65	1.92	3.64	1.71	3.94	3.78
MDM20	0.79	1.31	0.80	1.43	2.06	2.08	4.22	6.04	16.78
BUD26	1.13	0.77	0.51	0.83	1.06	1.93	4.42	8.06	34.76
AHP1	0.82	0.89	0.91	0.92	1.07	3.43	2.89	7.69	39.28
SUM1	1.32	1.27	2.34	2.18	3.06	2.04	2.49	3.78	4.98
MSN1	0.97	2.21	1.65	1.69	2.46	2.37	3.06	4.00	3.05
RSM27	1.07	2.44	1.29	1.10	2.36	2.61	4.54	2.82	2.36
MRPL38	1.11	2.33	1.53	0.87	1.11	2.36	3.46	5.35	3.09
MRS4	1.17	1.65	1.47	1.18	1.32	2.59	3.15	5.53	1.75
MST1	0.74	2.98	1.56	1.00	1.39	1.74	4.27	4.31	4.45
YCR050C	1.17	2.10	1.97	1.01	1.24	4.57	1.75	4.17	7.96
SPC72	1.13	1.62	0.78	1.85	2.69	3.33	2.71	3.73	12.37
YJL149W	0.85	1.82	2.14	1.84	1.84	2.12	2.94	4.21	4.99
BUD25	1.04	1.55	1.28	1.36	1.66	2.51	3.24	4.98	0.86
MIG1	0.56	1.56	2.60	1.03	1.62	3.97	2.93	3.35	6.36
MRPL35	0.92	2.27	0.98	0.98	2.15	2.82	2.84	4.65	3.78
YLR252W	1.16	1.67	1.43	1.48	2.23	2.48	4.29	2.81	2.90
MHR1	0.77	3.30	0.98	1.04	1.30	2.59	2.27	5.28	4.91
NGR1	0.92	2.03	1.78	1.45	1.19	2.23	2.74	5.17	5.79
PAK1	0.92	2.14	1.69	1.10	1.12	3.21	3.65	3.63	3.82

MRPL40	0.86	3.20	1.36	1.32	1.60	2.77	3.00	3.31	6.81
MTF2	0.78	2.60	0.66	0.72	1.43	2.23	4.52	4.49	11.52
NAM2	0.87	2.04	1.46	1.16	1.38	2.04	4.44	4.02	7.76
HOG1	1.00	1.40	1.92	2.03	2.58	2.11	3.69	2.65	3.34
KTR2	0.64	1.59	0.87	0.76	1.12	2.34	3.75	6.24	14.79
SIR1	0.84	1.42	0.75	1.18	1.24	3.01	5.06	3.75	3.38
RRN10	1.23	1.44	1.23	0.79	1.28	2.85	2.13	6.27	10.21
HEM14	0.76	2.08	1.55	1.38	2.16	3.35	2.63	3.28	5.25
RIM1	1.23	1.64	1.43	1.23	1.87	1.82	3.81	4.16	6.87
SMY2	0.89	1.34	1.44	1.54	2.08	1.68	2.40	5.77	4.70
YNL157W	0.74	0.78	0.65	0.66	0.82	6.45	3.00	3.99	7.19
YOR199W	0.84	2.18	1.72	1.35	1.16	1.91	3.08	4.79	7.79
SEC22	0.75	1.68	1.34	1.47	1.20	3.68	3.22	3.67	5.99
RTN1	1.01	0.77	0.91	0.69	0.96	1.74	1.10	9.70	58.30
SAM1	0.90	1.37	1.96	1.72	2.10	1.30	2.76	4.70	5.34
VPS15	1.07	0.59	0.88	1.53	1.19	2.12	4.62	4.79	10.08
YPL114W	1.08	2.35	2.13	1.47	1.57	2.69	2.89	2.57	2.27
YLR235C	1.28	2.05	1.73	1.43	1.64	2.30	2.76	3.54	7.81
SHM1	0.87	0.89	1.66	1.21	1.17	4.23	4.02	2.62	4.68
NCL1	0.92	1.30	0.75	1.00	1.28	3.00	4.25	4.11	4.89
HOS3	0.90	1.36	1.24	1.21	1.19	2.09	3.31	5.31	3.58
YPL183W-A	1.09	2.00	1.93	1.50	1.13	2.67	3.43	2.82	1.98
LRS4	1.20	1.16	0.92	0.92	0.79	2.06	2.67	6.81	6.15
YGL072C	1.02	3.53	0.86	0.75	1.58	1.74	3.41	3.54	12.68
YNL296W	0.99	1.31	1.46	1.34	1.87	2.98	3.13	3.34	9.14
ICY2	0.94	0.95	1.05	1.06	1.57	3.22	3.56	4.07	3.58
TSA1	1.07	0.90	0.74	0.90	1.10	4.82	3.05	3.75	5.09
MKK1	0.80	1.14	0.97	1.14	1.05	2.61	2.12	6.42	15.96
SHE9	1.32	0.91	1.13	0.76	1.03	3.10	2.55	5.41	3.68
YER093C-A	0.83	2.49	1.99	1.95	1.72	2.13	2.18	2.88	3.83
TTR1	0.83	1.34	1.45	1.60	1.93	2.82	2.37	3.77	7.67
HMI1	0.88	1.47	1.85	1.31	1.27	2.30	3.27	3.71	11.60
YLL029W	1.06	1.50	1.73	1.32	1.47	2.71	3.16	2.99	5.01
YPL113C	1.07	2.12	1.51	1.24	1.47	1.98	3.25	3.30	2.79
THI4	0.79	2.17	1.60	1.22	1.66	2.35	2.31	3.81	11.50
SCD6	0.96	1.25	1.73	1.16	1.17	2.32	2.50	4.74	4.38
YCR087C-A	0.84	2.01	1.25	1.15	1.17	1.30	2.63	5.46	2.04
MRPL11	0.94	2.51	1.20	1.41	0.78	2.52	2.96	3.48	3.73
DEM1	1.15	2.37	1.34	1.51	1.46	1.87	1.98	4.04	5.55
YMR075C-A	1.11	2.06	2.07	1.09	1.20	1.74	2.51	3.93	9.65
SWF5	1.44	1.19	1.32	1.18	1.24	3.11	2.50	3.69	6.28
SMF1	0.73	1.54	1.61	1.12	1.30	2.11	3.42	3.81	3.43
CCE1	1.28	0.93	1.64	1.41	1.74	2.29	3.52	2.80	2.36
ETR1	0.78	1.39	1.17	1.12	1.25	2.61	3.30	3.86	3.00

ICL1	1.23	2.84	0.75	1.33	1.85	2.13	1.82	3.53	5.50
SSU1	1.01	1.24	1.42	1.32	1.71	1.82	2.69	4.27	4.45
MRPL25	0.83	1.78	1.29	0.45	1.56	2.32	2.15	5.08	6.44
SAS2	0.93	0.71	0.74	0.71	0.79	1.78	3.43	6.35	27.69
MRPL37	1.02	2.49	0.89	0.85	1.80	2.24	3.38	2.74	5.01
PMP3	1.07	0.72	0.52	0.99	0.75	2.71	2.08	6.56	8.20
YPR050C	0.89	1.45	1.33	1.14	1.11	1.71	2.62	5.07	7.42
SEF1	1.13	2.05	1.27	1.16	1.21	1.49	2.14	4.88	4.39
MAK31	0.66	1.90	1.23	1.45	1.10	1.38	2.80	4.77	4.16
YLR199C	0.67	0.64	0.60	0.74	0.97	2.44	5.91	3.28	14.74
MSR1	1.09	1.93	0.93	0.98	1.57	1.21	3.35	4.15	17.47
COX6	1.00	2.72	1.79	1.26	1.09	1.65	3.15	2.52	2.58
HHO1	0.78	1.71	1.29	1.39	1.80	1.41	2.97	3.78	4.14
COX19	1.12	1.49	1.30	1.33	1.32	1.99	3.02	3.40	4.34
BUR2	0.50	0.53	0.77	1.83	0.98	2.76	2.69	4.70	2.66
COX10	1.05	1.64	1.10	1.24	1.47	2.40	3.03	2.65	2.48
CSM1	1.03	1.00	1.04	1.09	1.30	2.84	3.51	2.67	5.18
YGK3	0.78	1.52	1.74	1.48	1.74	1.58	2.98	2.61	2.37
YPL017C	1.29	1.39	1.00	0.92	1.25	1.22	3.37	3.95	9.92
IES6	1.01	1.41	0.97	1.23	1.20	1.97	3.78	2.77	6.88
RBL2	0.90	0.73	1.10	1.51	2.04	1.94	2.65	3.46	33.40
YOR052C	1.01	1.44	0.95	1.11	1.34	1.85	2.37	4.07	4.55
DCC1	0.95	1.48	1.34	0.92	1.28	1.78	3.06	3.34	16.03
PET100	1.24	1.61	1.45	1.55	1.25	2.37	2.42	2.17	3.65
ATE1	1.17	1.26	1.24	1.78	1.69	1.71	2.34	2.82	4.13
STM1	1.09	1.34	0.66	1.17	1.38	2.58	2.48	3.27	11.56
MRP49	1.05	1.70	1.52	1.45	1.25	1.63	2.40	2.91	4.33
TRP1	1.10	1.60	0.83	1.69	1.47	1.75	1.58	3.87	5.55
ACA1	1.14	1.38	1.18	1.08	1.09	2.03	1.87	4.08	4.23
YOR084W	1.01	1.49	1.25	1.00	1.35	2.11	2.24	3.40	15.54
SHO1	1.39	2.60	1.72	0.81	0.67	1.75	0.96	3.91	8.85
GNP1	1.13	1.55	1.67	0.94	0.99	1.76	2.72	3.05	4.49
YNL081C	0.99	0.92	0.88	0.55	0.58	3.08	2.35	4.45	12.04
YKL161C	1.01	1.56	1.56	1.23	1.18	2.24	2.16	2.85	6.02
ISY1	1.05	0.97	1.21	1.13	1.33	2.01	2.89	3.17	9.46
BEM2	0.67	1.14	0.49	0.73	1.12	2.07	2.34	5.19	14.32
PCP1	1.05	1.27	1.24	1.40	1.71	1.51	2.04	3.51	5.83
CTF19	1.25	1.25	0.99	1.01	1.01	1.36	3.54	3.28	6.82
ACF2	1.17	1.33	1.49	1.63	1.43	1.59	1.38	3.66	4.66
MCM21	0.81	1.40	1.28	0.88	1.28	1.67	2.12	4.16	13.63
BUD13	0.97	1.34	0.45	0.93	1.25	3.07	2.35	3.24	11.70
YPR097W	0.98	0.85	0.98	0.87	1.01	1.95	4.35	2.60	4.74
YCR025C	1.05	3.71	0.81	1.05	2.82	0.81	1.05	2.27	3.81
MDM31	0.74	1.14	0.64	1.02	1.31	1.35	1.94	5.41	6.32

TOM5	1.68	0.60	0.62	0.93	1.65	1.13	3.04	3.84	12.12
IBD2	0.76	1.16	0.72	0.67	0.80	2.51	2.34	4.53	26.35
YHR132W-A	0.95	0.71	1.09	1.18	0.97	1.45	1.57	5.55	11.24
PHO2	1.02	1.15	1.06	1.01	1.11	1.86	3.90	2.33	4.45
SHE4	0.81	1.25	0.89	0.85	1.58	2.35	1.89	3.61	9.21
JIP3	0.77	1.63	0.89	1.20	1.16	1.97	3.05	2.51	3.72
CLB4	0.98	0.98	1.01	1.03	1.13	1.17	2.20	4.63	19.30
YDR010C	0.84	0.96	0.67	0.81	0.69	1.57	3.10	4.44	8.40
YPR045C	1.17	1.01	0.87	0.92	0.83	1.25	1.50	5.50	10.78
HST1	1.30	0.96	1.09	1.15	1.57	1.25	1.91	3.73	3.72
DPH2	1.20	0.94	1.27	0.81	0.96	1.48	1.76	4.50	5.77
PRY2	0.85	1.52	1.15	1.32	1.66	1.77	1.53	2.97	4.95
LIP5	0.75	1.50	1.10	0.30	1.42	1.96	1.10	4.51	13.22
SSP1	1.20	1.30	1.16	1.26	1.39	1.65	2.09	2.58	5.82
YDR133C	0.57	1.29	1.36	1.23	1.23	2.44	1.28	3.20	7.46
MCM16	0.97	1.17	0.90	0.86	1.24	1.45	1.71	4.22	9.91
YBR042C	1.28	1.46	1.28	1.24	1.49	1.35	1.48	2.91	4.24
YMR041C	0.94	1.16	1.23	0.93	0.91	2.24	2.34	2.75	4.74
MAK3	0.99	1.17	1.46	1.09	1.40	1.35	2.34	2.67	3.66
MEU1	0.91	1.77	0.93	0.91	1.20	1.65	1.61	3.41	5.58
ALK1	0.93	1.15	0.93	1.11	1.09	1.76	1.60	3.81	4.57
YJL046W	0.76	0.79	1.13	0.61	0.92	2.26	2.74	2.93	2.63
MBF1	0.73	1.28	1.11	0.79	1.12	1.64	2.95	2.49	2.44
TES1	1.12	1.35	1.42	0.93	1.09	2.30	1.34	2.49	4.82
MRS2	0.74	1.08	0.60	0.71	0.77	1.92	2.61	3.60	5.41
YEL014C	0.97	0.85	1.25	1.07	0.87	1.45	1.47	4.08	3.93
PBP2	1.10	0.64	0.77	0.77	0.86	0.80	1.06	5.99	4.77
YPR076W	0.77	1.26	1.64	0.70	0.96	1.64	1.61	3.41	3.65
YDR219C	1.08	0.63	0.99	1.05	1.38	1.78	2.08	2.74	6.57
BMH1	0.92	1.28	1.30	0.88	0.95	1.18	1.53	3.66	11.63
CEM1	0.83	0.72	0.54	0.78	0.73	1.86	2.17	3.99	7.81
YBR269C	0.64	0.93	1.02	1.15	0.93	2.10	2.45	2.35	4.01
RRD2	0.82	0.73	0.55	0.66	0.90	0.99	2.24	4.63	4.07
YDR134C	0.83	1.20	0.96	1.16	1.37	1.52	2.07	2.34	7.58
OM45	1.09	1.07	1.25	0.92	1.22	1.27	2.05	2.54	5.04
YMR160W	0.95	1.34	1.07	0.96	1.28	1.40	1.62	2.74	4.26
PPT2	1.14	1.06	1.38	0.83	0.94	1.49	1.90	2.60	3.64
YPL017C	1.36	1.12	0.87	0.83	1.13	1.03	1.87	3.07	6.40
INP54	0.54	1.32	1.62	1.00	0.93	1.36	1.92	2.61	6.83
FIL1	1.08	0.81	0.60	0.67	1.03	1.29	1.37	4.35	11.01
ASP1	0.99	1.05	1.48	1.03	0.96	1.80	1.60	2.26	5.31
EAF5	1.10	1.09	0.95	0.84	0.66	1.54	1.24	3.71	10.68
PNP1	1.07	0.79	0.84	0.92	0.91	1.59	2.08	2.92	6.37
LCB5	1.34	1.05	1.23	1.06	1.23	1.38	1.44	2.38	6.27

YIL028W	1.35	1.28	0.92	0.88	1.09	1.61	1.37	2.61	4.04
BRR1	0.95	1.03	0.52	0.64	0.63	1.24	1.95	3.98	6.87
TRM1	1.06	1.88	0.97	0.84	0.75	1.21	1.41	2.80	8.33
ISW2	1.12	0.98	0.72	0.95	0.62	2.05	1.02	3.34	3.99
RPN10	0.82	0.66	0.63	0.79	0.93	0.52	0.56	5.88	7.40
KSS1	1.01	1.23	1.15	0.90	0.96	0.86	1.08	3.60	5.78
YKR032W	0.85	1.90	0.99	1.11	1.20	1.25	1.22	2.25	4.56
CTF8	0.85	1.24	1.07	1.01	1.03	1.12	1.36	3.08	5.56
CSN12	0.86	1.86	0.80	1.02	0.82	1.02	1.57	2.75	4.37
SYF2	0.81	1.09	1.33	1.04	1.42	1.55	1.17	2.22	3.65
DOG2	0.89	1.22	1.20	0.94	0.94	1.17	1.57	2.58	3.22
ELM1	1.00	0.84	0.71	0.76	0.72	1.22	1.33	3.35	18.98
LEA1	1.10	0.57	0.36	0.50	0.43	1.26	1.25	4.28	4.87
DSE4	0.91	0.90	0.90	1.16	0.97	0.86	1.58	2.35	4.04
YCK3	1.07	0.45	0.48	0.62	0.68	1.14	2.03	2.88	4.50
SPO1	0.77	1.27	1.13	0.90	0.60	0.92	0.77	2.94	4.22

Notes: Benomyl-sensitivity of each freshly generated *MAT***a** haploid YKO mutant was measured by microarray analysis of the representing TAGs in the experimental pool (treated with drug of the indicated concentrations) as compared to a control (drug-untreated) pool. A high C/E ratio indicates that the mutant is benomyl-sensitive and was shaded in gray.

Table S3. Heterozygous diploid YKO strains excluded from the pool

ORF name	plate	His+[a]	Mates as *MAT*a[b]	Papillates as *MAT*a[b]	Mates as *MAT*a[b]	Papillates as *MAT*a[b]
YAL051W	201	1	0	0	0	0
YAL035W	201	1	0	0	0	0
YAL017W	201	1	0	0	0	0
YAL005C	201	0	1	0	0	0
YAR002W	201	0	0	0	1	0
YAR018C	201	0	1	0	0	0
YML089C	203	1	0	0	0	0
YML088W	203	1	0	0	0	0
YML087C	203	1	0	0	0	0
YML086C	203	1	0	0	0	0
YML084W	203	1	0	0	0	0
YML083C	203	1	0	0	0	0
YML082W	203	1	0	0	0	0
YML081W	203	1	0	0	0	0
YML080W	203	1	0	0	0	0
YML079W	203	1	0	0	0	0
YML078W	203	1	0	0	0	0
YMR223W	205	1	0	0	0	0
YPL273W	209	0	1	0	0	0
YPL202C	210	0	0	0	1	0
YER068W	215	0	0	1	0	0
YHR080C	217	0	0	0	0	1
YHR094C	217	0	0	0	0	1
YCL014W	218	0	0	0	0	1
YCL044C	219	0	0	1	0	0
YLR151C	219	0	0	0	0	1
YGR051C	221	0	0	0	0	1
YGR065C	221	0	0	0	0	1
YOR138C	223	0	0	1	0	0
YOR143C	223	0	0	0	0	1
YGL215W	228	0	0	0	1	0
YIL046W	237	0	0	1	0	0
YFL030W	237	0	0	0	0	1
YJL111W	242	0	1	0	0	1
YJR148W	246	0	0	0	0	1
YLR343W	246	0	0	0	0	1
YML031W	246	0	0	0	0	1
YML046W	246	0	0	0	0	1
YML067C	246	0	0	0	0	1
YDL217C	246	0	0	1	0	0

YDR004W	246	0	0	1	0	0
YDR006C	246	0	0	0	0	1
YNR017W	252	0	0	0	0	1
YBR159W	258	0	0	1	0	0
YBR161W	258	0	0	0	0	1
YIL102C	262	0	0	0	1	0
YIL051C	262	0	1	0	0	0
YJL166W	280	0	1	0	0	0
YLR069C	280	0	0	0	0	1
YML060W	280	0	0	0	0	1
YML052W	280	0	0	0	0	1
YMR266W	280	0	1	0	0	0
YNL331C	280	0	1	0	0	0
YNL262W	280	0	0	0	1	0
YNL251C	280	0	0	0	0	0
YOR014W	280	0	0	0	0	1
YOR078W	280	0	0	0	0	1
YOR089C	280	0	0	1	0	0
YOR093C	280	0	0	1	0	0
YOR095C	280	0	0	1	0	1
YOR097C	280	0	0	1	0	1
YOR106W	280	0	0	1	0	1
YOR132W	280	0	0	1	0	0
YOR149C	280	0	0	1	0	0
YOR202W	280	0	0	1	0	0
YOR204W	280	0	0	1	0	1
YOR278W	280	0	1	0	0	1
YOR279C	280	0	0	1	0	1
YOR281C	280	0	0	1	0	1
YDR077W	280	0	1	0	0	0
YEL065W	280	0	0	1	0	1
YER007W	280	0	0	0	0	0
YER058W	280	0	0	0	0	0
YER086W	280	0	0	0	0	0
YGR096W	280	0	0	0	0	0
YGR111W	280	0	0	0	0	0
YGR186W	280	0	0	0	0	0
YGR198W	280	0	0	0	0	0
YGR199W	280	0	0	0	0	0
YGR206W	280	0	0	0	0	0
YHR148W	280	0	0	0	0	0
YHR160C	280	0	0	0	0	0
YHR195W	280	0	0	0	0	0
YHR207C	280	0	0	1	0	1

YBL023C	281	0	1	0	0	1
YBL091C	281	0	1	0	0	0
YBR023C	281	0	0	1	0	1
YFL008W	281	0	1	0	0	0
YER157W	281	0	1	0	0	0
YMR075W	281	0	1	0	0	1
YNL004W	281	0	0	0	1	0
YNL169C	281	0	0	0	1	0
YIL102C	281	0	0	1	0	1
YOR162C	281	0	0	1	0	1
YBL021C	281	0	0	0	1	0
YDR501W	281	0	0	0	1	0
YKR078W	281	0	0	1	1	0
YBR272C	281	0	0	1	0	1
YFL039C	281	0	1	0	1	0
YCL026C	281	0	0	1	0	1

Notes: "1" means "yes", whereas "0" means "no" as results of strain quality control. "*a*" His^+ was defined by the growth of the strain in synthetic medium lacking L-Histidine. "*b*" mating phenotypes were tested with wild-type strains BY4741**a**, BY4742□, and BY4743**a**/□ as control. His^+ strains and mutants behaved like haploid in mating type tests were excluded from the pool used in this study. All strains on plates 280 and 281 were excluded because most strains on these two plates failed in the quality tests. In total, 100 of the 5,996 strains were not included in the heterozygous diploid mutant pool used in this study. The identity of all other 5,896 strains used in this study can be obtained from Research genetics.

Table S4. Internal controls of the *cin8Δ* dSLAM screens

ORF	Gene Name	Gene description	single/double hybridization			
			ratio #1	ratio #2	ratio #3	mean ratio
YKL216W	URA1	Uracil synthesis	22.17	39.85	22.69	28.24
YJL130C	URA2	Uracil synthesis	10.68	6.27	6.35	7.77
YLR420W	URA4	Uracil synthesis	132.08	45.14	141.79	106.34
YML106W	URA5	Uracil synthesis	27.89	44.94	51.26	41.36
YLR014C	PPR1	Uracil synthesis	6.98	7.87	4.95	6.60
YEL060C	PRB1	right to *CIN8* ORF	10.52	8.68	9.10	9.43
YEL061C	CIN8	query gene	0.19	0.20	0.16	0.18
YEL062W	NPR2	left to *CIN8* ORF	13.73	12.81	7.81	11.45

Notes: In each *cin8Δ* dSLAM experiment, useful UPTAG and DOWNTAG ratios were averaged to obtain a single/double (C/E) hybridization ratio for each YKO. A mean ratio was taken among all three experiments.

Table S5. A summary of the *cin8*Δ dSLAM screen.

ORF	Gene Name	single/double hybridization				confirmation	
		ratio #1	ratio #2	ratio #3	mean ratio	RSA	Tetrad
YJL013C	MAD3	52.95	120.19	37.11	70.08	SL	SL
YER177W	BMH1	5.49	95.83	9.50	36.94	SL	SL
YBL063W	KIP1	46.98	31.25	20.40	32.88	SL	SL
YPR119W	CLB2	20.58	20.23	31.28	24.03	SL	SL
YCR076C	□	3.27	61.16	5.27	23.23	NO	undecisive
YER135C	□	31.68	20.60	17.22	23.17	SL	undecisive
YMR055C	BUB2	23.63	15.68	20.15	19.82	SL	SL
YHR013C	ARD1	22.28	18.73	14.12	18.38	SL	SL
YEL003W	GIM4	21.06	19.10	13.81	17.99	SF	SL
YOR073W	SGO1	10.62	10.47	31.89	17.66	SL	SL
YDR149C	□	21.66	21.16	9.67	17.50	SL	SL
YJL179W	PFD1	13.61	12.27	14.54	13.47	SL	SL
YMR299C	DYN3	8.12	16.52	11.67	12.10	SL	SL
YMR294W	JNM1	15.54	11.12	7.41	11.36	SL	SL
YMR078C	CTF18	11.35	12.24	10.35	11.32	SL	SL
YLR226W	BUR2	16.13	5.39	12.41	11.31	SL	SL
YNL016W	PUB1	3.99	2.97	25.93	10.96	SF	SF
YKR061W	KTR2	8.67	5.80	15.83	10.10	SF	SL
YDR488C	PAC11	5.66	13.34	11.00	10.00	SL	SL
YPL174C	NIP100	10.44	7.93	10.55	9.64	SL	SL
YHR191C	CTF8	8.61	11.27	8.58	9.49	SL	SL
YML010W-A	□	3.06	7.86	17.45	9.46	SL	SL
YDR150W	NUM1	7.85	10.51	9.05	9.14	SL	SL
YOR269W	PAC1	10.41	7.53	7.90	8.61	SL	SL
YBR194W	SOY1	3.52	10.73	11.56	8.60	SF	SF
YLR418C	CDC73	8.16	9.40	7.50	8.35	SL	SL
YDR432W	NPL3	16.21	3.81	3.15	7.72	SL	SL
YLL049W	□	8.96	7.84	5.38	7.39	SL	SL
YCR086W	CSM1	7.47	10.16	4.23	7.29	SL	SL
YDR435C	PPM1	7.55	7.05	6.68	7.09	SF	SF
YLR210W	CLB4	6.69	7.92	6.41	7.01	SL	SL
YBL058W	SHP1	6.30	10.21	4.27	6.93	SL	SL
YNL147W	LSM7	6.54	5.87	8.35	6.92	SL	SL
YOR195W	SLK19	7.01	6.44	7.11	6.85	SL	SL
YPL008W	CHL1	7.16	6.63	5.81	6.53	SL	SL
YBR140C	IRA1	7.86	6.42	5.19	6.49	SF	SL
YCL016C	DCC1	5.22	8.20	5.86	6.43	SL	SL
YGL086W	MAD1	7.16	5.52	6.43	6.37	SL	SL
YGL003C	CDH1	4.64	5.09	9.20	6.31	SL	SL

YGR188C	BUB1	5.91	4.12	8.88	6.30	SL	SL
YJL030W	MAD2	6.95	5.02	6.78	6.25	SL	SL
YOR349W	CIN1	5.00	6.99	6.21	6.07	SL	SL
YJL124C	LSM1	5.79	5.43	6.55	5.92	SL	SL
YNL153C	GIM3	6.87	4.50	5.59	5.65	SL	SL
YML094W	GIM5	5.71	6.51	4.60	5.61	SL	SL
YKL057C	NUP120	6.82	4.30	5.57	5.56	SL	SL
YNR052C	POP2	6.15	4.98	5.10	5.41	SL	SL
YIL125W	KGD1	6.59	4.40	5.17	5.39	NO	NO
YGL031C	RPL24A	9.72	2.68	3.55	5.32	NO	NO
YAL024C	LTE1	5.01	4.93	5.94	5.29	SL	SL
YHR041C	SRB2	3.48	5.48	6.72	5.22	SL	SL
YJR053W	BFA1	4.04	5.30	6.33	5.22	SL	SL
YBR171W	SEC66	7.43	4.14	3.88	5.15	SF	SL
YDL040C	NAT1	4.97	5.58	4.76	5.10	SL	SL
YKR010C	TOF2	4.85	5.58	4.83	5.09	SF	SF
YHL019C	APM2	5.20	5.13	4.76	5.03	NO	NO
YMR116C	ASC1	6.63	5.00	2.83	4.82	NO	NO
YDL134C	PPH21	5.47	4.90	4.03	4.80	SF	SF
YDR424C	DYN2	5.91	3.83	4.37	4.70	SF	SL
YGR078C	PAC10	6.17	4.45	3.45	4.69	SL	SL
YHR129C	ARP1	4.83	3.73	5.49	4.68	SF	SL
YLR268W	SEC22	4.97	4.85	4.11	4.64	SL	SL
YNL269W	□	4.38	4.73	4.75	4.62	NO	undecisive
YDL229W	SFB1	3.39	4.85	5.45	4.56	NO	NO
YKL191W	DPH2	2.65	7.85	2.99	4.50	NO	NO
YLR200W	YKE2	4.79	4.70	3.84	4.44	SF	SL
YNL171C	□	7.14	3.71	2.31	4.39	SL	SL
YNL225C	CNM67	7.32	2.66	3.07	4.35	SL	SL
YLR338W	□	4.71	4.56	3.56	4.28	SF	SF
YER019W	ISC1	3.36	4.57	4.78	4.24	SF	SF
YIL137C	□	3.59	4.34	4.67	4.20	NO	NO
YBR282W	MRPL27	6.32	4.02	2.25	4.20	NO	NO
YOR360C	PDE2	4.85	4.05	3.65	4.18	SF	SF
YKL048C	ELM1	3.95	4.03	4.51	4.17	SF	SL
YOR058C	ASE1	3.63	4.02	4.83	4.16	SL	SL
YEL044W	IES6	5.32	3.86	3.22	4.14	SF	SF
YNL273W	TOF1	4.33	4.19	3.41	3.98	SF	SL
YKL176C	LST4	5.91	3.18	2.80	3.96	SF	SF
YGL167C	PMR1	3.53	3.89	4.26	3.89	SF	SL
YLR315W	NKP2	4.15	3.26	4.26	3.89	SF	SF
YLR254C	□	3.66	4.14	3.82	3.87	SF	SL
YIL114C	POR2	4.52	3.33	3.65	3.83	NO	NO

YIL039W	□	2.56	3.43	5.32	3.77	NO	NO
YDL234C	GYP7	4.61	2.92	3.78	3.77	NO	NO
YPR135W	CTF4	3.56	3.34	4.35	3.75	SL	SL
YGR165W	MRPS35	3.27	4.96	3.00	3.74	NO	NO
YIL153W	RRD1	5.53	3.21	2.39	3.71	SF	SL
YGR285C	ZUO1	3.33	3.34	4.39	3.69	SF	SL
YOR026W	BUB3	4.18	2.58	4.28	3.68	SL	SL
YFR055W	□	2.27	3.03	5.70	3.67	NO	□
YGL219C	MDM34	5.01	3.53	2.17	3.57	SF	SF
YGL153W	PEX14	2.58	4.14	3.89	3.54	SF	NO
YPL241C	CIN2	3.03	4.07	3.33	3.48	SL	SL
YNL307C	MCK1	2.69	3.54	4.00	3.41	SF	SL
YDR532C	□	3.26	2.53	4.39	3.40	SL	□
YGR104C	SRB5	4.31	3.40	2.44	3.38	SF	SL
YIL165C	□	3.31	4.10	2.72	3.38	NO	□
YEL017W	GTT3	2.45	5.41	2.25	3.37	NO	□
YKL204W	EAP1	3.60	2.42	3.93	3.32	SF	SF
YML016C	PPZ1	3.42	2.84	3.62	3.29	SF	SF
YKR047W	□	3.63	3.30	2.94	3.29	NO	□
YKR059W	TIF1	2.79	3.70	3.31	3.27	SF	SF
YMR048W	CSM3	2.64	3.30	3.79	3.24	SL	SL
YOL076W	MDM20	3.45	3.25	3.00	3.23	SF	SF
YIL055C	□	3.02	3.53	3.12	3.23	NO	□
YPR141C	KAR3	2.48	4.33	2.85	3.22	SF	SL
YIL154C	IMP2	3.49	3.37	2.76	3.21	NO	□
YJL169W	□	3.16	3.35	3.08	3.20	SF	SF
YOL081W	IRA2	4.18	2.89	2.46	3.17	SF	SF
YGR238C	KEL2	3.03	2.87	3.62	3.17	NO	□
YIL141W	□	2.88	3.93	2.64	3.15	NO	□
YPL018W	CTF19	3.16	3.01	3.23	3.14	SL	SL
YJR102C	VPS25	3.62	2.85	2.88	3.12	SF	SF
YHR064C	SFZ1	2.79	2.98	3.53	3.10	SF	SF
YLR417W	VPS36	2.91	2.97	3.32	3.07	NO	□
YGR229C	SMI1	3.80	3.02	2.14	2.98	SF	SL
YIL073C	SPO22	2.81	3.07	3.05	2.97	NO	□
YBR258C	SHG1	2.91	3.54	2.46	2.97	NO	□
YKR054C	DYN1	2.86	3.23	2.80	2.97	SF	SL
YIL160C	POT1	2.59	3.00	3.28	2.95	NO	□
YML094C-A	□	3.62	2.83	2.34	2.93	NO	SL
YNL332W	THI12	2.66	2.77	3.34	2.92	NO	□
YLR388W	RPS29A	3.57	2.45	2.72	2.91	SF	SF
YOR288C	MPD1	2.82	3.11	2.78	2.90	NO	□
YIL159W	BNR1	2.93	2.63	3.13	2.90	NO	□

YGL127C	SOH1	2.22	3.91	2.45	2.86	NO	□
YLL033W	□	3.14	2.58	2.85	2.85	NO	□
YGL216W	KIP3	2.41	3.08	3.06	2.85	SF	SL
YER095W	RAD51	2.01	3.27	3.27	2.85	NO	NO
YNL136W	□	2.84	2.51	3.17	2.84	SF	SF
YDR334W	SWR1	2.51	3.28	2.61	2.80	SF	SF
YNL298W	CLA4	2.92	3.20	2.25	2.79	SF	SL
YLR084C	RAX2	3.09	2.20	3.05	2.78	NO	□
YGR237C	□	2.71	2.85	2.67	2.74	NO	□
YIL097W	FYV10	2.40	2.78	2.93	2.70	NO	□
YGR077C	PEX8	2.65	2.64	2.83	2.70	SF	NO
YOL012C	HTZ1	2.44	2.43	3.20	2.69	SF	SF
YJL168C	SET2	2.82	2.92	2.33	2.69	SF	SF
YFR039C	□	2.58	2.82	2.56	2.66	NO	□
YHR200W	RPN10	2.22	2.87	2.86	2.65	NO	□
YER040W	GLN3	2.41	2.76	2.77	2.65	NO	□
YOR358W	HAP5	2.24	2.85	2.84	2.64	NO	□
YOR243C	PUS7	2.78	2.67	2.46	2.64	SF	SF
YOL159C	□	2.52	2.77	2.62	2.64	NO	□
YDL115C	IWR1	2.24	3.52	2.14	2.63	SF	SL
YHL023C	RMD11	2.72	3.11	2.05	2.63	NO	□
YPL079W	RPL21B	2.75	2.98	2.15	2.62	NO	□
YNL314W	DAL82	2.60	2.54	2.72	2.62	NO	□
YAL010C	MDM10	2.86	2.53	2.40	2.60	SF	□
YGR286C	BIO2	2.60	2.93	2.24	2.59	NO	□
YJL197W	UBP12	2.39	3.16	2.12	2.56	NO	□
YJR070C	□	2.36	2.45	2.80	2.54	NO	□
YDL188C	PPH22	2.59	2.73	2.25	2.53	SF	SF
YDR014W	RAD61	2.65	2.82	2.06	2.51	SF	SF
YDR431W	□	2.80	2.14	2.59	2.51	SF	SF
YGL249W	ZIP2	2.42	3.01	2.09	2.51	NO	□
YIL049W	DFG10	2.30	2.91	2.30	2.50	NO	□
YKR013W	PRY2	2.93	2.15	2.39	2.49	NO	□
YMR129W	POM152	2.39	2.63	2.46	2.49	NO	□
YJL141C	YAK1	2.35	2.32	2.79	2.48	SF	SF
YIL161W	□	2.08	2.38	2.94	2.47	NO	□
YMR127C	SAS2	3.08	2.17	2.04	2.43	NO	□
YKL174C	□	3.05	2.11	2.13	2.43	NO	□
YML028W	TSA1	2.41	2.48	2.39	2.43	NO	□
YIL017C	VID28	2.22	3.02	2.02	2.42	SF	SL
YPL155C	KIP2	2.44	2.50	2.32	2.42	SF	SL
YGL121C	GPG1	2.57	2.26	2.41	2.41	SF	SF
YNL094W	APP1	2.14	2.74	2.34	2.41	NO	□

YIL136W	OM45	2.73	2.18	2.26	2.39	NO	□
YOR314W	□	2.07	2.55	2.49	2.37	NO	□
YNR073C	□	2.45	2.04	2.62	2.37	NO	□
YPL055C	LGE1	2.68	2.31	2.07	2.35	SF	SF
YDR521W	□	2.37	2.44	2.24	2.35	NO	□
YFR013W	IOC3	2.61	2.21	2.23	2.35	NO	□
YGL138C	□	2.03	2.23	2.77	2.34	NO	□
YIL101C	XBP1	2.12	2.18	2.69	2.33	NO	□
YGR208W	SER2	2.23	2.51	2.20	2.31	NO	□
YER169W	RPH1	2.14	2.33	2.35	2.27	NO	□
YIL167W	□	2.02	2.44	2.36	2.27	NO	□
YIR005W	IST3	2.35	2.37	2.06	2.26	NO	□
YLR433C	CNA1	2.02	2.35	2.40	2.26	NO	□
YIL135C	VHS2	2.20	2.26	2.28	2.25	NO	□
YDR318W	MCM21	2.07	2.21	2.44	2.24	SF	SF
YIL124W	AYR1	2.01	2.26	2.44	2.24	NO	□
YMR297W	PRC1	2.21	2.21	2.30	2.24	NO	□
YPL064C	CWC27	2.24	2.41	2.04	2.23	NO	□
YIL140W	AXL2	2.00	2.29	2.23	2.17	NO	□
YJR095W	SFC1	2.13	2.17	2.16	2.15	NO	□
YLR085C	ARP6	2.09	2.16	2.18	2.15	SF	SF
YBR273C	□	2.09	2.07	2.26	2.14	NO	□
YPL267W	□	2.08	2.09	2.18	2.12	NO	□
YPL260W	□	2.02	2.11	2.15	2.10	NO	□
YKL053W	□	2.00	2.02	2.20	2.07	NO	□
YPL152W	RRD2	2.13	1.92	3.16	2.40	SF	SL
YML124C	TUB3	2.06	1.64	1.90	1.87	SF	SF
YJR135C	MCM22	1.82	1.62	2.04	1.82	SF	SF
YER016W	BIM1	1.52	3.05	0.77	1.78	□	□
YCL029C	BIK1	1.57	1.75	1.95	1.76	SF	SL
YMR138W	CIN4	1.87	1.67	1.72	1.75	SF	□
YDR254W	CHL4	1.38	1.54	2.06	1.66	SF	SF
YGL168W	HUR1	1.76	1.79	1.42	1.66	SF	SF
YOR265W	RBL2	1.78	1.46	1.67	1.64	□	□
YLR381W	CTF3	1.45	1.22	1.56	1.41	□	□
YER155C	BEM2	1.42	1.32	1.05	1.26	SF	SF
YPR046W	MCM16	1.31	1.07	1.31	1.23	□	SF
YBR107C	IML3	0.99	1.11	1.12	1.07	□	□
YER007W	PAC2	□	□	□	□	□	□
YOR014W	RTS1	□	□	□	□	□	□
YBR122C	MRPL36	□	□	□	□	□	□

Notes: In each *cin8Δ* dSLAM experiment, useful UPTAG and DOWNTAG ratios were averaged to obtain a single/double (C/E) hybridization ratio for each YKO. A mean ratio was taken among all three experiments and ranked. Confirmation results were obtained by random spore analysis (on synthetic haploid slection media) or tetrad dissection (on YPD) of heterozygous diploid double YKOs or both: SL-synthetic lethal; SF-synthetic fitness defect or synthetic sick; NO-no synthetic interaction; Blank-not individually tested here. Genes colored in blue are unique to dSLAM; genes in red are unique to SGA; genes identified by both screens are in black.

Table S6. A summary of the *bim1*□ dSLAM screen.

ORF	Gene Name	single/double			confirmation	
		ratio 1#	ratio 2#	mean ratio	RSA	tetrad
YJL030W	MAD2	19.57	33.10	26.34	SL	SL
YDR318W	MCM21	28.19	17.77	22.98	SL	SL
YOR058C	ASE1	22.82	20.46	21.64	SL	SL
YJL124C	LSM1	17.42	21.65	19.53	SL	SL
YDR254W	CHL4	13.66	20.88	17.27	SL	SL
YKR061W	KTR2	19.74	13.59	16.67	SL	SL
YMR078C	CTF18	9.47	22.02	15.74	SL	SL
YHR191C	CTF8	18.38	12.78	15.58	SL	SL
YCL029C	BIK1	13.97	15.82	14.90	SL	SL
YPL018W	CTF19	16.00	13.14	14.57	SL	SL
YDR378C	LSM6	10.20	16.29	13.25	SL	SL
YOR073W	SGO1	13.42	12.88	13.15	SL	SL
YOR195W	SLK19	14.35	11.49	12.92	SL	SL
YCL016C	DCC1	11.79	13.76	12.78	SL	SL
YJR135C	MCM22	10.79	14.62	12.71	SL	SL
YDR150W	NUM1	18.07	6.56	12.32	SL	SL
YGL086W	MAD1	9.58	14.75	12.17	SL	SL
YNL273W	TOF1	11.88	10.82	11.35	SL	SL
YOR026W	BUB3	11.95	8.81	10.38	SL	SL
YML094C-A	□	10.08	10.62	10.35	SL	SL
YJL013C	MAD3	9.44	9.21	9.32	SL	SL
YBR107C	IML3	9.93	8.65	9.29	SL	SL
YPL174C	NIP100	10.73	7.45	9.09	SL	SL
YLR200W	YKE2	9.09	8.77	8.93	SL	SL
YML094W	GIM5	7.86	9.80	8.83	SL	SL
YMR299C	DYN3	10.31	6.88	8.60	SL	SL
YPL017C	□	5.38	11.61	8.50	SL	SL
YPR135W	CTF4	7.19	8.96	8.08	SL	SL
YGL216W	KIP3	7.49	8.62	8.05	SL	SL
YLR381W	CTF3	8.75	7.28	8.02	SL	SL
YDR149C	□	8.27	7.05	7.66	SL	SL
YGR078C	PAC10	8.59	6.39	7.49	SL	SL
YOL072W	THP1	7.16	7.01	7.09	SL	SL
YLR410W	VIP1	8.81	5.16	6.98	SL	SL
YPL155C	KIP2	6.66	6.94	6.80	SL	SL
YDR159W	SAC3	9.79	3.78	6.79	SL	SF
YDR014W	RAD61	5.43	8.12	6.78	SL	SL
YOR269W	PAC1	9.30	3.83	6.56	SL	SL
YPR046W	MCM16	6.87	5.87	6.37	SL	SL

YMR048W	CSM3	5.35	7.07	6.21	SL	SL
YPL008W	CHL1	5.21	7.03	6.12	SL	SL
YLL049W	□	6.41	5.83	6.12	SL	SL
YGL217C	□	5.44	6.73	6.08	SL	SL
YAL021C	CCR4	6.12	6.00	6.06	SF	SF
YKR082W	NUP133	3.00	8.90	5.95	SL	SL
YKR054C	DYN1	6.03	5.64	5.83	SL	SL
YNL153C	GIM3	5.76	5.90	5.83	SL	SL
YCR086W	CSM1	4.10	6.63	5.36	SL	SL
YCR077C	PAT1	6.79	3.69	5.24	SL	SL
YDR532C	KRE28	4.41	5.95	5.18	SL	SL
YAL024C	LTE1	4.40	5.40	4.90	SL	SL
YDR359C	VID21	7.47	1.83	4.65	SL	SL
YEL003W	GIM4	5.45	3.65	4.55	SL	SL
YOL076W	MDM20	5.05	3.58	4.32	SF	SL
YGR180C	RNR4	2.26	6.26	4.26	SL	SL
YNL107W	YAF9	4.54	3.72	4.13	SL	SL
YHR129C	ARP1	5.14	2.86	4.00	SL	SL
YOL012C	HTZ1	4.74	3.23	3.98	SL	SL
YCR079W	□	4.14	3.74	3.94	SF	SF
YDL116W	NUP84	2.91	4.86	3.88	SF	SL
YJR053W	BFA1	3.51	4.15	3.83	SL	SL
YJL148W	RPA34	3.75	3.88	3.81	SL	SF
YDR488C	PAC11	3.25	4.26	3.76	SL	SL
YLR268W	SEC22	3.88	3.46	3.67	SF	SF
YDR439W	LRS4	3.27	4.05	3.66	SL	SL
YDR432W	NPL3	3.84	3.39	3.62	SL	SL
YGR188C	BUB1	2.22	4.94	3.58	SL	SL
YML041C	□	3.61	3.14	3.37	SF	SF
YIL153W	RRD1	2.09	4.56	3.33	SF	SL
YNL171C	□	3.12	3.44	3.28	SL	□
YML112W	CTK3	2.14	4.39	3.26	SF	SL
YOR295W	UAF30	4.52	1.77	3.14	SF	SL
YPL253C	VIK1	3.39	2.82	3.11	SF	SL
YDR156W	RPA14	3.07	3.08	3.07	SF	SF
YER164W	CHD1	3.01	3.11	3.06	SF	SF
YCR024C	□	4.37	1.58	2.97	SF	SF
YER014C-A	BUD25	3.22	2.68	2.95	SF	SL
YMR055C	BUB2	3.05	2.73	2.89	SL	SL
YNR051C	BRE5	2.25	3.48	2.86	SF	SL
YOL054W	□	3.73	1.96	2.85	SF	SF
YEL018W	□	3.61	2.06	2.83	SF	SF
YLR254C	□	2.72	2.80	2.76	SL	SL

YGL003C	CDH1	2.63	2.87	2.75	SL	SL
YBR284W	□	3.82	1.66	2.74	SF	SF
YIR005W	IST3	2.47	2.99	2.73	SF	SF
YDR424C	DYN2	2.37	2.99	2.68	SL	SL
YJL179W	PFD1	2.77	2.55	2.66	SL	SL
YFR030W	MET10	1.97	3.32	2.64	SF	SL
YGR270W	YTA7	1.59	3.70	2.64	SF	SL
YDR383C	NKP1	2.60	2.57	2.58	SF	SF
YNL054W	VAC7	2.85	2.27	2.56	SF	SL
YMR293C	□	2.58	2.52	2.55	SL	SL
YJR060W	CBF1	3.19	1.82	2.51	SL	SL
YPR023C	EAF3	2.89	2.10	2.49	SF	SF
YBR231C	AOR1	2.32	2.63	2.47	SF	SL
YER177W	BMH1	1.56	3.38	2.47	SF	SF
YDR334W	SWR1	2.64	2.30	2.47	SF	SF
YKL048C	ELM1	2.56	2.32	2.44	SF	SF
YDL234C	GYP7	1.84	2.94	2.39	SF	SF
YML016C	PPZ1	2.05	2.66	2.36	SF	SF
YKL205W	LOS1	1.62	3.07	2.34	SF	SF
YPL205C	□	1.60	3.04	2.32	SF	SL
YMR294W	JNM1	2.12	2.49	2.30	SF	SF
YOR349W	CIN1	2.10	2.51	2.30	SF	SF
YCR064C	□	2.12	2.45	2.28	SF	SL
YNL225C	CNM67	2.33	2.14	2.23	SL	SL
YKR010C	TOF2	2.25	2.13	2.19	SF	SF
YML103C	NUP188	1.77	2.60	2.18	SF	SF
YPL152W	RRD2	2.43	1.84	2.13	SF	SL
YJL006C	CTK2	2.16	2.11	2.13	SF	SL
YDR360W	□	2.54	1.68	2.11	SF	SF
YNL248C	RPA49	1.76	2.44	2.10	SF	SF
YAR014C	BUD14	1.67	2.46	2.06	SF	SF
YHR013C	ARD1	1.90	2.17	2.03	SF	SF
YIL017C	VID28	2.18	1.88	2.03	SF	SL
YDR174W	HMO1	2.48	1.59	2.03	SF	SF
YNR052C	POP2	2.44	1.52	1.98	SF	SF
YLR079W	SIC1	2.20	1.74	1.97	SF	SF
YLR085C	ARP6	2.00	1.90	1.95	SF	SL
YNL201C	□	2.13	1.76	1.95	SF	SF
YNL136W	□	2.22	1.65	1.93	SF	SF
YGL240W	DOC1	2.12	1.74	1.93	SF	SL
YNL307C	MCK1	1.97	1.73	1.85	SF	SF
YIL040W	□	1.78	1.90	1.84	SF	SL
YIL103W	□	1.66	1.98	1.82	SF	SF

YKL139W	CTK1	2.03	1.55	1.79	SF	SL
YER095W	RAD51	2.03	1.53	1.78	SF	SF
YDR183W	PLP1	1.93	1.55	1.74	SF	SF
YCL061C	MRC1	1.51	1.96	1.74	SF	SL
YLR399C	BDF1	1.86	1.56	1.71	SF	SL
YCL060C	□	1.37	6.59	3.98	SF	SL
YJR063W	RPA12	3.63	□	3.63	SF	SF
YLR315W	NKP2	1.24	3.14	2.19	SF	SL
YIL036W	CST6	0.74	3.64	2.19	SF	SF
YPL200W	CSM4	1.09	3.13	2.11	SF	SF
YGR200C	ELP2	3.01	1.12	2.06	SF	SF
YFR036W	CDC26	1.13	2.90	2.01	SF	SL
YDR289C	RTT103	2.57	1.41	1.99	SF	SF
YOL081W	IRA2	0.76	3.08	1.92	NO	SF
YLR204W	QRI5	2.51	1.16	1.83	SF	SF
YLR182W	SWI6	2.64	1.00	1.82	SF	SL
YNL298W	CLA4	2.16	1.46	1.81	SF	SF
YPL241C	CIN2	2.06	1.48	1.77	SF	SF
YDR315C	IPK1	2.28	1.20	1.74	SF	SL
YFR019W	FAB1	2.49	0.98	1.74	SF	SL
YOL004W	SIN3	2.47	0.94	1.70	SF	SF
YMR267W	PPA2	1.92	1.47	1.70	SF	SL
YEL061C	CIN8	0.70	2.69	1.70	NO	SF
YNL170W	□	1.98	1.39	1.68	SF	SF
YMR073C	□	2.12	1.14	1.63	SF	SF
YNL330C	RPD3	1.86	1.34	1.60	SF	SL
YGL252C	RTG2	1.07	2.06	1.56	NO	SF
YAL010C	MDM10	0.93	2.15	1.54	NO	SF
YJR104C	SOD1	1.03	2.04	1.53	SF	SL
YOR141C	ARP8	2.06	0.96	1.51	SF	SF
YDL040C	NAT1	1.63	1.29	1.46	SF	SL
YPR120C	CLB5	1.68	1.17	1.42	SF	SF
YDL115C	IWR1	0.72	2.05	1.39	SF	SL
YNL296W	KRE25	2.14	0.24	1.19	SF	SF
YML124C	TUB3	1.49	1.90	1.70	NO	SF
YDL117W	CYK3	1.25	1.48	1.36	□	□
YLR190W	MMR1	1.28	1.35	1.32	□	□
YNL106C	INP52	1.11	1.27	1.19	NO	NO
YPR164W	MMS1	1.46	1.18	1.32	□	□
YDL225W	SHS1	1.38	1.16	1.27	□	□
YGL163C	RAD54	1.15	1.13	1.14	NO	SF
YMR224C	MRE11	0.73	1.10	0.91	NO	SF
YGR229C	SMI1	1.11	1.10	1.11	□	□

YML032C	RAD52	1.12	1.08	1.10	NO	SF
YGR228W	□	0.98	1.07	1.02	□	□
YLR386W	VAC14	1.02	1.04	1.03	NO	SF
YLR373C	VID22	1.23	1.01	1.12	NO	SF
YAL013W	DEP1	0.87	0.97	0.92	□	□
YNL215W	IES2	0.83	0.91	0.87	□	□
YDR162C	NBP2	1.18	0.88	1.03	NO	NO
YMR263W	SAP30	0.94	0.82	0.88	NO	SF
YBR095C	RXT2	1.33	0.74	1.04	□	□
YGL173C	KEM1	1.15	0.69	0.92	NO	SF
YBR200W	BEM1	0.74	0.69	0.71	NO	SF
YGL211W	□	0.87	0.67	0.77	□	□
YLR262C	YPT6	0.78	0.60	0.69	□	□
YMR312W	ELP6	0.82	0.59	0.70	NO	SF
YKL110C	KTI12	1.30	0.59	0.94	□	□
YPL086C	ELP3	1.07	0.53	0.80	NO	SF
YNL097C	PHO23	0.69	0.49	0.59	NO	SF
YLR384C	IKI3	1.01	0.38	0.69	□	□
YHR111W	UBA4	1.13	0.37	0.75	□	□
YPL102C	KRE24	1.04	0.35	0.70	□	□
YDR335W	MSN5	1.26	□	1.26	□	□
YPL101W	ELP4	0.80	□	0.80	NO	SF

Notes: In each *bim1*□ dSLAM experiment, useful UPTAG and DOWNTAG ratios were averaged to obtain a single/double (C/E) hybridization ratio for each YKO. A mean ratio was taken between both experiments and ranked. For YKOs with only one data, that data was used without averaging. Confirmation results were obtained by random spore analysis (on synthetic haploid selection media) or tetrad dissection (on YPD) of heterozygous diploid double YKOs or both: SL-synthetic lethal; SF-synthetic fitness defect or synthetic sick; NO-no synthetic interaction; blank-not individually tested here. Genes colored in blue are unique to dSLAM; genes colored in red are unique to SGA; genes identified by both screens are in black.

Table S7. *sgs1*Δ synthetic interactions identified by dSLAM

Gene Name	C/ E mean ratio[a]	RSA confirmation	SGA	Haploid SLAM	Biological process
SLX4	39.33	SL	Yes[b]	Yes	DNA replication
YBR100W	28.81	SL	Yes	Yes	overlaps with MMS4 ORF
MMS4	24.26	SL	Yes	Yes	DNA repair
YBR099C	17.63	SL	Yes	Yes	overlaps with MMS4 ORF
SLX1	11.49	SL	Yes	Yes	DNA repair
RTT107	9.76	SF	Yes	Yes	DNA transposition
WSS1	5.49	SL	Yes	Yes	protein sumoylation
RAD27	2.38	SL	Yes	Yes	DNA replication and repair
HPR5	8.03	SL	Yes	No	DNA repair
RRM3	5.72	SF	Yes	No	DNA replication
MUS81	4.67	SL	Yes	No	DNA repair
CSM3	3.95	SF	Yes	No	meiosis
POL32	2.85	SF	Yes	No	DNA replication and repair
SOD1	2.63	SL	Yes	No	superoxide metabolism
ASF1	2.53	SF	Yes	No	DNA damage response
ESC2	2.42	SF	Yes	No	chromatin silencing
SAE2	2.10	SL	Yes	No	DNA damage response
YBR094W	2.02	SF	Yes	No	unknown
RAD50	1.93	SF	Yes	No	DNA repair
MGS1	2.26	SF	Yes	No	DNA replication
SLX8	14.30	SL	No[c]	Yes	DNA recombination
RNH35	4.55	SF	No	Yes	DNA replication
LYS7	3.51	SL	No	Yes	copper ion transport
RNH203	2.45	SF	No	Yes	unknown
HST3	2.14	SF	No	Yes	chromatin silencing
HEX3	10.45	SL	No	No	DNA recombination
NUP84	6.33	SF	No	No	Nuclear transportation
NUP133	5.56	SF	No	No	Nuclear transportation
DIA2	4.61	SF	No	No	invasive growth
RAD26	4.44	SF	No	No	DNA repair
YDL162C	4.24	SF	No	No	unknown
VID22	3.72	SF	No	No	vacuolar protein catabolism
MRC1	3.65	SF	No	No	DNA replication checkpoint
TOF1	3.36	SF	No	No	DNA replication checkpoint
POP2	3.03	SF	No	No	transcriptional regulation
CTF4	2.99	SF	No	No	DNA repair
ASC1	2.89	SF	No	No	unknown
GAS5	2.88	SF	No	No	unknown
YCL060C	2.80	SF	No	No	unknown

FAB1	2.72	SF	No	No	phospholipid metabolism
SKT5	2.69	SF	No	No	cell wall chitin biosynthesis
YDR520C	2.63	SF	No	No	unknown
NPL3	2.62	SF	No	No	mRNA-nucleus export
PAT1	2.43	SF	No	No	unknown
SPH1	2.40	SF	No	No	actin filament organization
UBC4	2.39	SF	No	No	protein ubiquitination
YOR024W	2.38	SF	No	No	unknown
DUN1	2.38	SF	No	No	DNA damage response
EXO1	2.31	SF	No	No	DNA mismatch repair
CSM1	2.29	SF	No	No	chromosome segregation
NSG2	2.19	SF	No	No	unknown
NUP170	2.18	SF	No	No	Nuclear transportation
UME6	2.09	SF	No	No	entry into meiosis
VIP1	2.08	SF	No	No	actin cytoskeleton
MTF1	2.03	SF	No	No	transcriptional regulation
PIF1	2.01	SF	No	No	DNA recombination
MMS1	1.99	SF	No	No	DNA repair
LSM1	1.98	SF	No	No	mRNA catabolism
UAF30	1.88	SF	No	No	transcriptional regulation
XRS2	1.81	SF	No	No	DNA repair

Notes: [a] In each *sgs1*□ dSLAM experiment, useful UPTAG and DOWNTAG ratios were averaged to obtain a single/double (C/E) hybridization ratio for each YKO. Each of the interactions listed was individually re-tested by random spore analysis (on synthetic haploid selection media): SL-synthetic lethal; SF-synthetic fitness defect or synthetic sick. [b] "Yes" means that synthetic interaction was identified by that method; [c] "No" means that synthetic interaction was not identified by that method.

Table S8. Potential *cdc101-1* synthetic interactions

Gene Name □	control/experiment mean ratio [a]			
	cdc102-1 **(30°C)**	***CDC102*** **(30°C)**	***cdc102-1*** **(28°C)**	***CDC102*** **(28°C)**
MDM39	12.17	1.27	7.09	1.51
NHX1	11.40	1.20	6.27	1.25
RMD7	9.06	1.41	12.00	1.40
NBP2	8.09	1.26	2.88	1.08
YDR455C	7.50	0.96	2.50	1.19
PTC1	6.64	1.32	2.58	0.81
ARR4	6.16	1.22	2.68	1.41
APL5	5.96	1.33	1.98	1.59
ARL1	5.94	1.32	2.44	0.84
VPS25	5.58	1.50	2.75	1.17
YGL072C	5.27	1.26	2.12	1.30
NKP2	5.14	0.99	1.73	0.74
YCR051W	5.01	0.48	1.70	1.27
VPS36	4.96	1.03	2.18	1.08
RIM20	4.96	1.46	2.27	1.40
YER084W	4.87	1.40	2.46	1.18
SPF1	4.86	1.28	2.62	1.03
MON2	4.82	1.32	2.41	0.78
APM1	4.75	1.35	2.62	1.71
HTZ1	4.66	1.50	3.02	1.49
APL6	4.34	1.31	2.04	1.58
VTC4	4.18	1.24	1.67	1.18
CUE1	4.15	1.67	1.95	1.38
COG8	4.08	1.58	2.68	1.19
ERG4	4.07	1.05	1.93	1.09
YFR024C	4.05	1.62	2.31	1.27
APS3	3.98	1.15	2.20	1.47
WHI2	3.89	1.56	1.67	0.80
PMP3	3.83	0.81	3.84	0.66
SMI1	3.82	0.61	2.07	1.24
GYP1	3.81	1.54	2.27	1.43
SAC7	3.80	1.03	2.03	1.18
API2	3.73	1.32	2.04	1.20
IMP2'	3.71	0.99	2.07	0.99
YER119C-A	3.68	1.37	2.05	1.27
YKL136W	3.66	1.37	2.26	1.30
LSM1	3.63	1.44	2.60	1.20
APM3	3.59	1.29	1.72	1.21
UBP14	3.46	1.24	2.30	1.09

COG6	3.45	1.34	1.97	1.17
PFD1	3.41	1.26	2.81	1.24
RIM21	3.35	1.39	2.26	1.49
VPS71	3.28	1.13	2.46	1.01
SYS1	3.27	1.66	2.21	1.32
YLR057W	3.24	1.22	1.91	1.45
VAM10	3.23	1.26	1.85	1.19
SCS2	3.17	1.50	2.28	1.32
YDR334W	3.15	1.23	2.11	1.65
OPI3	3.13	1.59	2.43	0.83
CTK3	3.12	0.86	2.41	0.68
GEF1	3.11	1.11	1.86	1.38
APL2	3.11	1.19	1.88	1.05
CKB2	3.09	1.30	2.24	0.91
LTE1	3.05	1.02	2.69	1.20
RER1	3.02	0.81	2.00	1.16
RIM101	3.02	1.21	1.66	1.22
GSG1	3.00	1.80	2.01	1.26
OST3	2.99	1.13	1.83	1.54
INP51	2.97	1.09	2.06	1.15
RPA14	2.96	0.19	1.61	1.33
YLR374C	2.93	1.50	2.23	1.14
SEC72	2.90	0.88	1.78	0.89
KTR3	2.89	1.33	1.54	1.14
YBT1	2.88	1.56	3.21	1.32
MCK1	2.86	1.31	1.95	1.22
APS1	2.86	1.27	1.81	1.48
SAC1	2.85	1.24	1.87	0.86
YKL207W	2.85	1.24	2.54	1.31
SNF8	2.81	0.89	1.83	0.87
KHA1	2.81	1.17	1.71	1.04
ALG8	2.79	1.08	1.50	1.26
VPS67	2.77	0.94	2.03	1.06
YGR122W	2.67	1.65	2.46	1.76
SWC1	2.66	1.09	3.20	1.85
RIM13	2.65	1.39	1.85	1.10
RIC1	2.65	1.09	1.84	0.80
LGE1	2.64	1.02	2.12	1.42
YGL046W	2.62	0.82	1.51	1.30
YLR294C	2.60	0.74	1.84	0.91
YDL072C	2.58	1.18	1.60	1.31

Notes: [a] Each of the heterozygous double YKO pools containing the indicated plasmid-borne alleles of *CDC102* were sporulated and selected to generated a *MAT***a** haploid pool of both single and double deletion mutants (control) and a *MAT***a** haploid double deletion pool (experiment). The abundance of each *kanMX* YKO mutant in both pools was compared by microarray hybridization of the TAGs. A high C/E ratio indicates synthetic interactions between the corresponding YKO and the *CDC102* allele.

Table S9. PCR primers for amplifying the gene-disruption cassettes.

Cassette	Forward primer sequence	Reverse primer sequence
bim1Δ::URA3	5'ATTAGACCAACTATACGCCGAAGG3'	5'AACGTGCCCTTCTTGTCAGTATCA3'
bub2Δ::URA3	5'CGGAGGGTCTTTATCGGCGACT3'	5'TACCGTCTTTAATGTGATCCTAACC3'
cdc102Δ::natMX	5'CCATTAATCCTTTTTATGTAGTCATGC3'	5'AAGGATGATCAGTATGCGAAATATCTG3'
cin8Δ::URA3	5'GACTTTGTTGAGAGAGACTCTATTG3'	5'CCGAATGCCTCATACCAATTGATG3'
dot1Δ::URA3	5'TTGTTTTCCTTGCGTGCCCAATG3'	5'TGTGCATACCGCTACTTCTTCATC3'
dun1Δ::URA3	5'GTTGGTTCAATGCAAATTATTACATC3'	5'AGAGAGATTGAATCTTAAAATTGACG3'
ira2Δ::URA3	5'GACAATTCATTGTATTTCCAGTTGTTT3'	5'CCGTCTGAGTTCATATATAATTCAC3'
mad2Δ::URA3	5'TGCATAGTCTAACCTATAGTATTTAG3'	5'GCCGAAGTACCCATCTAATGAAAC3'
mre11Δ::URA3	5'GGATATCACTCAAGCAGAAAAAATCA3'	5'ATGGGCTTTCTGGCCTGATCAAC3'
rad51Δ::URA3	5'TCGTACTAATTGCTGACAAACCCG3'	5'CTAGAAGGTACTGTGCATCAGGG3'
rad61Δ::URA3	5'TCTTTGAACTTGTTGCAATTGG3'	5'CCTCATGTTGTCTAACTTCCAA3'
rad9Δ::URA3	5'AGCTCTTGAACAACATACTCTCAG3'	5'GAGATTCATCAAACAGATTGATCGC3'
sgs1Δ::URA3	5'GGTAATAGCGCGATGAAACAACGTC3'	5'GTGCTCAAGGTGAATATACTGGTC3'
sml1Δ::URA3	5'CATGATGGTGTAAGTCACAAAGAC3'	5'ACGATACGTGAAGGCATATGAA3'
tub1Δ::URA3	5'GTGCTTGCCAACACCCATATT3'	5'GTCCATATTAAATCCGCTGATAG3'
ura3Δ::URA3	5'TCCCGGTTAGTACAGATGC3'	5'GATGTGGTGCTGATTCAGG3'
ykl088wΔ::natMX	5'TGATTTTGCCACACCAATCACACAG3'	5'CTGCTAGTGCCTACTCTAGTTGTTG3'
ykr079cΔ::natMX	5'GGTATCTGACATTATGGTACAGGTT3'	5'GGGCACTGGACAAAAAGATAACATT3'
yor145cΔ::natMX	5'TCAAACTTCGAGCTTGCCATCCTAT3'	5'CACAAAGCTTGCTGATCATTGCCCA3'

Reference

S1. Bennett, C. B., Lewis, L. K., Karthikeyan, G., Lobachev, K. S., Jin, Y. H., Sterling, J. F., Snipe, J. R., and Resnick, M. A. (2001). Genes required for ionizing radiation resistance in yeast. Nat Genet 29, 426-434.

S2. Chang, M., Bellaoui, M., Boone, C., and Brown, G. W. (2002). A genome-wide screen for methyl methanesulfonate-sensitive mutants reveals genes required for S phase progression in the presence of DNA damage. Proc Natl Acad Sci U S A 99, 16934-16939.