

TABLE 2A. Microarray primers

Gene	Stanford orf6	5' primer	3' primer
AAF1	orf6.8596	CAAGGGCAACCACAGTCG	ATCAGCATTTCGGGCAGG
ABP1	orf6.5487	CACTGAAACAGGGGACGG	TGGAGCAACAGGCTTCCC
ACT1	orf6.8002	GGTTTTGCCGGTGACGAC	TCGAAATCCAAAGCAACG
ALS1	orf6.2112	TGTGCTGGCAGTCGTCTG	TCGGTACCACCTGGAGGA
ASF1	orf6.5313	TGGACCTGTCCCGTAGG	TCCACCACTGCATCACCA
ASH1	orf6.8332	GCACCACCATCTCCTCCA	CTCGGCGGCCAACTCTAG
ATX3	orf6.6119	TTGATGGATGGAGCCACC	TGCTGGAACAACGGTGAA
AXL1	orf6.8423	ATTTAATCCGGCGATGGG	CCTGGTGGTGGTGGTGT
BDF1	orf6.8227	GCATCCCGTGGACACTGT	CCAATCGGTGTCCCATCA
BEM1	orf6.1490	GCGGAAGCTAATGGATGG	TTGAACCAAGGGGGATTG
BEM2	orf6.7561	GGTGGTGGCGGTACAACA	CAATGGAGGTGGATGTGC
BEM3	orf6.6581	TGAACCAGAGCCTGAGCC	AGCGGCACCAAGAGTGCT
BMH1	orf6.7751	CCTCCCGTGAAGATTCCG	GGTTGGTGGCAACTCGGT
BOI2	orf6.8230	TGGTTGGTACATGGGCAA	GCAAATTTCCCAGCCACA
BUB1	orf6.5556	TGTTGAGCAGGTGCACA	TCCACTACGGTGGGATGG
BUB2	orf6.6151	TGGTTTGTGCGAGCTTCG	CAAAGGCGGAGTACACGC
BUD2	orf6.8189	GGACCTAAAGCACCCGTG	ATGGGAACCCCCACATTC
BUD3	orf6.8474	ATCCCGCAAGCAGCAAT	GGTGGTCCAAGTCTCCC
BUD5	orf6.1252	CCAACGGCGCAACTTCTA	TCACCAAGGATTGACCCA
BUD6	orf6.6289	AACTCAGTGGGCACGCAA	ACCGCTTTGATGCACGAC
BUD7	orf6.3464	GGCTCCCGAGACTCGCAAG	TCCTTCCCAAGCAACAA
CAC1 (RLF2)	orf6.633	GAGTCGCCAGTCTGACGG	TTTCTGCTTCCTTGGCCA
CAC2	orf6.6779	CGGTTTCATTGGCACAACG	CGGCTGACTGGCTGACAA
CAC3 (MSI1)	orf6.5748	TGCCCCAAAAGCCTAACA	CCAGTGGCATACCCAGGA
CAG1	orf6.7428	TGCGTCAACAAAACCTCGA	CCCAGTCCAACTTCCAT
CAP1	orf6.787	TATTCAAGTGGGGCTGCC	ACCCAATTCTCGGGAAAC
CBF1	orf6.4385	TGCCCACACTGACACTGC	TGCCATTCTCTGATCCG
CCL1	orf6.6688	TATGGTCAGCGATGTGGC	TCGCAACATCCTGATTCC
CDC1	orf6.7427	TGTACCGGGGAATCATGA	ATTTCTTGCCCATTGCCA
CDC10	orf6.6760	GACACACCAGGGTTTGGC	TCCAGCAATTGCAAATGG
CDC11	orf6.4569	TCATCTGCCGCTTTGAGA	AGGCGTTAACGAGTCGGC
CDC12	orf6.7750	TGGTGGCTGGTGAAAGTG	CCAATTCTTGTTGGCGACA
CDC14	orf6.2743	CTCAACCCAAAGGGAAGGG	TGGACGTTGTTTTCCACG
CDC15	orf6.4291	CACACGAGCCAGAATGCA	CTGTTGTTGCTTGCGGAG
CDC16	orf6.4371	AGTGCCTATGCCTTTGCC	TGGAGAAATTGCCAATGC
CDC19	orf6.5754	CAACGTGGACGTTTGGT	CAACATCGGTACCTGGCA
CDC20	orf6.2609	TGTGTCAATTTACGCGGC	TGATGAGGAACCGCCTTG
CDC23	orf6.7817	AAACAACAGCCGGTGACG	TGTAGACTCTGGCGGGCT
CDC24	orf6.1482	AATCCCTGGCATGGAACC	TGCGTCTTGACGGCAATT
CDC25	orf6.7312	CGATTTCCCTGGAACCCA	TGCGAAGGTGGTTGCATC
CDC27	orf6.8231	GTTCCGATGCCGCTTTAC	TGCAGAAGTGCCCTGATG
CDC28	orf6.5246	CAAGGAGTTGGACTAGGGGC	GCATCCAACTTGGAATGCG
CDC3	orf6.4934	TGCAACACGATTCCGATG	ACCAACAACGGCAAAATGG
CDC31	orf6.7086	CAATGGCGTCTACCAAAA	TAACCTAAAGGCACGGCG
CDC34	orf6.7631	CTTTCCCTTTTCGCCACC	TCTTCGTCAACCGGTTC
CDC36	orf6.7619	CGCTACCGCCAGAAAGAAG	TTGATCAAGACGGGCTCC
CDC39	orf6.1533	TGCCAAAGGCGCTCAATT	AATGCAGCGGCCAAAATA
CDC4	orf6.3808	TCTCAGCAACCTTCGGCA	TGCCTTCCCCTGTAAGGA
CDC42	orf6.6274	GTTGTCCGGTATGGTGCC	TCACCTGTTCCTGGGTG
CDC45	orf6.1287	AGTGCCATCGGTGAGACC	TTGTTGAGACCAACCCCG
CDC46	orf6.4181	CCAGTTGGTGAAATGCCA	CGGTACCAGGATCTCCCA
CDC47	orf6.5934	CGGCAGCTGTGCTTCCTA	TGCAGCAGCAGAATCAGG
CDC48	orf6.5568	TGCGTGTGAGATTGGGAG	ACCGGTACCAGGTGGACC
CDC5	orf6.5090	GGCGCTTCGTTTACAACC	ATGGCACCACAATTTGC
CDC50	orf6.4914	ACGATTGAAAGCCTGGCA	CACTTGACAAGGCCTCCC
CDC53	orf6.1083	AGACGTGGAACAACCCCG	ATTCCATGGTGGCTTCCA
CDC54	orf6.3958	TGCCAATGCCACCACTAG	CACGATCACGACACGAC
CDC55	orf6.7105	TCCAAAGTCATGATGCCG	TTGATCAGCAATGCCCAA
CDC6	orf6.769	TTCAACGTGGATCCAACG	CCGGGTGGAATAATTTCTT
CDC7	orf6.1601	ATGCTTTACAGGAATTCTCG	AGAATTTGTGGTGGTGGTG
CDC9	orf6.6632	ATTCGCCGAAAAGTCGGG	TATATCCATCCGGGTGCC

CDC91	orf6.1849	CCAACAATAATTTTCCCCCA	TCGAATTTCCCAGAAGTCCC
CDC95	orf6.1128	GCCGTTGGTGGATCAGAA	CCAGCAACACTGAGCCAA
CDR1*	orf6.9037	ATGTCAGATTCTAAGATGTC	TCGATACCTTCACCTCTG
CDR2	orf6.9079	CGTCTTTGTGCGAACAGC	GGGTCTCCCCAAAACCAC
CDR3	orf6.3101	CCATGCACCCTAATGGGA	TGGGTTTCCGTTTCAGCA
CDR4	orf6.6297	ATGGCAGATGCCGATACG	ACAACGGTCAACTCGCCC
CEK1 (ERK1)	orf6.1819	CAGCTAACGCTGCAGCTACTAC	CTTGTGAAGCAATTGATCTTGC
CFL1	orf6.5730	TCGATGCAAGAACACCGA	GGATGTACCGCTGTTGCC
CFL99	orf6.5731	AATGGTTGACTGGCTGGG	AATGCATGTCCACCAGCA
CGR1	orf6.2697	ATTGATCCATGGGGGAAT	GTTGGTCTTTTGGCAGCA
CHL1	orf6.6360	TCCAGTTGATGGATGCCA	CCTGCTGCTGTCATGGCT
CHS1	orf6.3499	ACACAGCGTGCACCTTCGC	TTGGGGTCCAAGACAGGA
CHS2	orf6.8379	GCCGTCGAGACGATTTCAG	TGACACGTTTCAGTGGGGA
CHS3	orf6.6053	GGATGAAAGCCATCCACG	AAGCAACAAATGCCCCAA
CHS4	orf6.8509	CACCGCGTGATCAAGCAC	CCGCCAAATTGTTTTCCG
CHS5	orf6.2544	TGGGGGCAAAAATATCCAG	GGTTTCAACCGCAACAGG
CHT1	orf6.8769	GGGTCAAAATGCTGGAGG	CCAACCGACTCATAGGG
CHT2	orf6.2344	GCATCATCAGCTTTGGCC	TGGACATTGTGGAGCAGC
CHT3	orf6.8934	TGGTGGTTCCCAACAACG	ACCAACAGAAGCATCGGG
CKA1	orf6.9000	AAAATTGGGACGAGGCAA	CACCCAAACGACCACATG
CLA4	orf6.3334	TGGTCTGGCAGTTTGGC	GTTGCCGTTCAAGGAACC
CLG1	orf6.5668	TTTATTGGATGGGCTTGC	TCAGAATGACAGCTGCCA
CLN1	orf6.4392	GCAAAATAGCCAACCTCAAGG	TGTTGTGATGACCATGATGG
CLN2	orf6.5045	TGCTGAAGACCAGTTTGAGG	TGTGTAACCAGCAATGGTTG
CLN99	orf6.3156	CAAACAAATCAAACCTCCGCT	CATCATCATCGTCATCATCA
CMD1	orf6.2969	TTGCTGAATTCAAAGAAGCA	CCATCATTTGTTGGTATCAGC
CMK2	orf6.4095	AGGAGCAGGATCATTGG	TATGACTTCAGGGGCGAGC
CMP1	orf6.3161	AAGTGTTCCGGCACCAGT	CATTAACCCCTTGGTCGG
CPH1	orf6.695	GCTCCAGCAAAATTGGCAA	AGGATACACCGGTGTCGG
CPP1	orf6.7345	CATCGTCAGATGCTGCGC	TTGCTGGGTGAATCCATG
CSE1	orf6.5086	TGGTTAGATGGTGTGTTGA	TGATCTTCGAAAAATCCGG
CST20	orf6.6603	GGGTCTCCAATGCACGAG	TGCGGGGTGCAGATAATC
CTF1	orf6.3543	TTCCACTGACACCCCCAC	TGGTTGCAGTTGCCTCTG
CTK1	orf6.6453	AAAAGACCGTTGCCTTCG	TCGAATTGCCGTAATTGGG
CTR9	orf6.8486	GGGTATGCAAAATTGGGG	CCCATGCCTGTATTGCCA
CYB1	orf6.7127	TTGGGTGATGTTTCAAATCA	TTCTTCATCCAAATCCTGCC
CYB4	orf6.8086	ATTGCCAATTGAGCAGC	CCACATTGGTTGCATGGG
DBF4	orf6.6970	GCAAAACCCAGACAGCCG	TCGTCTACCCCGGTCTGG
DFG5	orf6.7480	CGGCATCTGTGCAATCAT	ACCTTGCCGCTAAATGGA
DOT1	orf6.8562	TTGGCAACATGAAGTCGC	TTCGAGATAAATCCCGCG
DOT4 (UBP10)	orf6.2890	TGTCACCACAAGCATCCG	ATAATGTTGCATTGCCGG
ECE1	orf6.2886	AGATGTTGCTCCAGCTGC	AACAGTTTCCAGGACGCC
ECM21	orf6.3331	CGCAGCCACCAATTCTCA	AACGCCGCCATTTTCATC
EFG1	orf6.2978	ATAACGGTATGCCCCAGC	GTGGTTGGAATTGCCCA
EGT2 (ORF near EGT2)	orf6.2978	CGCTTGATGAGCTGATGC	TCCTCGAGCCAAGTCACA
ELM1	orf6.1589	GGTCAAGGGCAATATGGG	GCCAATTCTTTGGCGTCA
ENG1 (YNR067)	orf6.7803	GGCAGAGAACCTGGCTCA	TCACAGCACCATTGGAGC
ENG2	orf6.2732	AGACCTCCAGCTCCTCCG	AGCAGTTACCGAAAGGGC
ENX3	orf6.3059	GCAATCAAGTTGCCCAGA	TAAATGGGCTGCTGCCAA
EPL1	orf6.8781	TCGGTAAAGCAGCCCTTG	GAATGTTGCTGGGGTCCA
ERG1*	orf6.2816	GAGTTCAGTTAAGTATGATGC	GCAGCCCCAGCTACTC
ERG11*	orf6.2866	GAGAACAGCCACACGACAA	AGTTTCCTTAATAGTGTTATT
ERG2*	orf6.3930	CGGTACAGCAATTGGG	CTTGATCATATCTTTACCAGT
ERG24*	orf6.1086	AATGGTTTGAGCATGAGT	CCATAATAACATCCCGG
ERG25	orf6.1690	CTTCCATTAGTAATGTTTATCA	TTAGGGAATGGTACTTGATA
ERG26	orf6.6113	TTCAGCTTCACCGATGCA	TGCTGCCAAAACATGAGC
ERG27	orf6.8240	TTGCAGTCATTACCGGGA	TCCCACCATTTTCCAACA
ERG3*	orf6.3667	TCGTACTAGAAATTTGTGACTA	ATGATAAGTAAGCCACAATG
ERG4*	orf6.4141	TCTCGTTATATTCCCAAAG	GTTCAATGAGTCAATTGGT
ERG5	orf6.6958	TTCAATTGCTGGTCCCCG	ACCAACTCCAAAGCAGCG
ERG6	orf6.6441	TGCTGCTTCTGTTGCTGC	TGGAGCATGAACGGTAGC
ERG7*	orf6.6427	TCAGAGGAAATTGGTCTTC	TATCAACAGAATGAAGTCCC
EST1	orf6.4411	ACGGTCGAGAACTGGCG	TGGTGTGCTAAAGCGCC
EST2	orf6.6287	ACAAGCAATGACGTGCCA	GCGTGAGAAGTCCCTGGA

FET3	orf6.5008	GACGCAAATCCTGATGGG	TCCAGGTTTCGACCTTCCA
FKH2	orf6.8625	GCCACAGAAATCCAAGCC	AAACTTGTGGAGCCACCG
FKS1; GSC1	orf6.3785	GCCACCTCATCAAGGAGG	AGGCCTGAGCTGGTGACA
FKS2; GSL1	orf6.6176	CCCCAATAAGTCACCGC	CTTTGGTTGAAACCGGCA
FKS3; GSL2	orf6.8270	CTAGATTGGGGCCAACCC	TCTTTATCGCGACGACGG
FLU1	orf6.7565	CCAACAGCAATCACAACG	GGCAGCAAGACCAACAGA
FUN2 (YAR014)	orf6.4646	CCCCGATGAGATTTTCCA	TTTCGAATGAGCCACCAA
FUS3	orf6.2854	GCATTGTTGCTTTGGCAG	CCACCGACCAAAGATCGA
GCN5	orf6.6803	CCACCACAAGTGAAAGCG	TGGTTGCTCTTCCACACC
GDH1	orf6.3152	TGAGAAACAAGTGGGCGG	GCTTCTTTGGTGGAACCC
GDH2	orf6.3428	GATATTGCCCGTGGTGGT	CGGATCTTTGCATCGTCA
HAP1	orf6.5234	AACAACATATCGCCCCGCA	TTGCGAATCACTTGGCAG
HAP2	orf6.868	AGGTGTGGGAATGGGAGT	TCAGCAATTTTCAGCAGCA
HAP3	orf6.6729	GTTGAGGGAGCAAGACCG	ACTTCCTGGCTTCTCGGT
HAP5	orf6.1862	AGACGAACAGCTTCCGCA	CATCACAACCCCTTGGCAA
HAT1	orf6.4117	CCAGAGCAATGGACGACA	GCCGTGGTAAACCCAAT
HAT2	orf6.5380	GGCATTGTATGTGGCCATC	TTGCCGTTGAATTGGTGTC
HCM1	orf6.7358	TCAGAAGATCCGACGCAA	TTGCTCCTCACATCCTGG
HDA1	orf6.3593	GGTCATCATGCTGAGCCC	GCCAAATTTTCTCTGGCG
HDF1	orf6.1909	TTTGGGTGTCACCAGAAG	TCAGCACCAACAGTGGCA
HDF2	orf6.3865	TTACGCGGGCACTGGAAT	ACACCTTGGGGCAATCAA
HF11	orf6.4445	CGCATGGCACTCAACTA	TGCTGCCATTGAACCAA
HHF1	orf6.4930	TGTCTGGTACCGGTAGAGGA	AACCACCGAAACCATACAAG
HHT1	orf6.8840	ATGGCAAGAACAAAACAAACAG	TTCAACAGCTTCTGTAAAGCA
HIR2	orf6.5191	AGTTTCTGGTGGGACGGA	TGAGTGTCTGTCACCCACG
HIR3	orf6.6868	TGATGCACCCAATCAAGG	GGCAAAACAAACAGTGCC
HMG1*	orf6.3220	CACTTGAAGAATGTGTTAAAG	TTACAACCACGCATGG
HOG1	orf6.7282	TGAGCTAAATCCCGTGGG	CGGGGAATAGTGGTTTCC
HOP1	orf6.7201	ATGATGGTAGGGCAAGCA	CGAACTGGACAGGATCTG
HOS1	orf6.2971	TCCCGTCCAATAAGGGAA	CCATCCCCATGATGCAAA
HOS2	orf6.4139	TATGGTGCCTTCATCCA	TTGAACCCCATCACCATG
HOS3	orf6.6580	GCTGAACATGCTTTCGGG	TGATGTCCCGGTGGTCTT
HPA3	orf6.5516	CCTCCCGTGTATGTCCCG	ACAACAACCTGGGCACGGT
HSL1	orf6.4613	CAGGTCAATTAGCCGCTG	GCAGCCATACCAAAATCG
HST1	orf6.4594	ATGACCAGGACAAACGACG	AGTTTCCGTTTGGGGACA
HST2	orf6.4681	TTTCGACAGGTGCAGGGA	GTACCTGCCACAATGGCG
HST20	orf6.6603	CCTGGACCTGGACCTGAA	TGCGGGGTGCAGATAATC
HST3	orf6.5604	TAATGCGGGAATACCCGA	GCATTCTGGATTGAGCCC
HST7	orf6.3212	ACCACCAGTGCCCTTACC	GCTGGCGATGATGGTTCA
HTA1	orf6.7310	TCAGCCAAAGCTGGTTTG	TAACACACCACCTTGGGC
HTA3	orf6.5631	CTGGGAAGGGAAAAGTGC	ATATGAGGCAACACCCCA
HWP1	orf6.4883	TCAATTGGGGCCACTGTC	TGGAATCCAATCGGTTGG
HYR1	orf6.3143	TGACCGTGGTGGAAATTCA	ACGCAACAAATTTGGCC
INT1	orf6.1732	TTGCAAGACGCTTCGAAA	CTTCAGGCTCTGCCGCTT
IPL1	orf6.4985	CACCTCCTCATATCCCA	TTGCTTCTTCTGATGGGG
IQG1	orf6.7624	TTGAACTCCCCGACAAAG	GCAAGGTGGATCCCATT
KAR4	orf6.1096	CACCATCTCCTCGAGCAA	CCAGAGTCGTGGGGATAA
LAS1	orf6.3193	CATCCACTGTGCACGGCA	CGAAATTCACGGCATCA
MCD4	orf6.7698	ATCCACTTGGACCCACC	CGATAAGCATGTCCCGCA
MCM1	orf6.7951	TGACGATGATGACGATGG	ATGAGAAGGCATTGGTGC
MCM10 (DNA43)	orf6.7254	TGAAGGACTTGGTGCAGG	CGCACCAAAAGGCAACA
MCM2	orf6.2810	GTCAAGTCCACCAGCTGC	TGCTCCTCTTCGAGAACG
MDR1	orf6.5068	TGCCCATCCAGAAGAAGC	GGCGAAGAATCCACCCAA
MET3	orf6.7984	TGCTGGTCCAGGGAAGAAA	TGGAACAATAACCCCGGA
MKC1	orf6.8775	AGTCAAGGAGTTGGGCCA	AACCCAGCATTTTCGTCG
MKK1	orf6.7153	TGGCCCTGGTACCTCCAC	TCCATTACCTTCGCCCAA
MLP1	orf6.5453	ACCCATTAAGTGCAGCCG	CACCGATTTTGCCGATTG
MPR1	orf6.8164	GCCAAGGTGCCGATTAG	GGCTCTTGGCCCATCATT
MSB1	orf6.1506	TGGACTTGGTTGCGTCA	CGAAGTGGATGTGCCAGC
MSB3	orf6.4728	GCAGGGGACATCCAATGA	CTGTGCAAAGGCAACCAA
MTLa1		ATGAACTCAGAAATAGAAAG	CTAAACACGGTGACATACCT
MTX6	orf6.5210	GCTGGTTTCGAATCTGCC	CTGGTTGCAAAGCAGCAG
MUB1	orf6.8572	CACATTCCATCAGGCCTC	TCCGTCTCGTTATTCCCC
NFI1	orf6.4736	CAAGTTCAAAACCGGCCA	TGCATCCACCTCATCAGC

NIK1	orf6.547	TCAGCGACCTGAGCTTT	AAGGATTTACCCCTGGGC
NPR1	orf6.1586	GCAGCAAAGTCAACTGCC	CCACCACCAGGAGCAGAA
NPS1	orf6.2685	ATGCCCAAGCCAAATTGG	ATGCCATCAGTATCGCCA
OPS4	orf6.6056	CGTCCAGCCAACATTGT	GAGCAGCAGCAGCAGCTG
PAB1	orf6.7774	TCATCTGGTGTGGCCGAG	TCAATGGCAGCTTCAGCA
PBS2	orf6.8548	GAAAAATTCACGATGCGCC	TGATGCTTTGCCAGCAAA
PCL1	orf6.1258	ACAAATGGCAAATGCTGC	TTTTGTGCCGTCAATTCA
PCL2	orf6.6261	TTCCAACGTACAAACCCC	ATTTGAAGAACCAACGGC
PCL6	orf6.5131	CAAACCTACACCCGTGGCC	CGGGCTGAGCTATCGATG
PFY1	orf6.6300	GCCTTATATTCAAGAGCCGG	GTGGTAGCTTCACCTGGTTG
PGK1	orf6.3310	TCAACGTCCCATTTGGACG	CCAGCAGCTCTCTGTGGA
PHO12	orf6.897	TTTCTTGGCGGTAGTGCC	TTGGCACCAAGATCAGCA
PHO4	orf6.5720	AGCGGGACAACACCAGGA	ATGCCCAAGGCACCAGAA
PHO80	orf6.1302	CAACATCTCCGACCTCGC	ACCCACCAACTTTTGCA
PHO85	orf6.6995	TTTTGGGTTAGCTCGTGC	TGGGCTGATGTGGATGTT
PHR1	orf6.7524	TATCAGCAAGATGCCGCG	AAATAATCGGCAATGGCG
PHR2	orf6.6260	GCCGAAGATTTGCCTGCT	TGGCGGAATCATCATTTGG
PHR3	orf6.2069	GACCATGTTGGCCAAAGC	GCAACACCTCGTTGCACC
PHX1	orf6.6653	ATTAGTGGGGGCCGGACT	CCGTCAATTGCCGTCACTA
PRA1	orf6.6934	TTTCCGTGTGTCACCAG	CACCGGAGCATAGTTGGG
PRY1 (YJL079)	orf6.5424	TCGGATTCTCAGCCAATG	CTGGCAACTTTGTTGGCA
PRY2	orf6.8118	AGTCAAACCGTTGTGGCC	GCAGCCAAATTTTACCGG
PRY3	orf6.5572	TGGTAGTGGAAAGTGGAAACC	TGGGAAAACATTTTGTGAGG
RAD6	orf6.8095	TCCTAATGTATATGCCAGTGGA	TATCATCATCATCATCGTCCTC
RAM2*	orf6.5223	ATGTCCACAGAATCCAAGTA	TACCTTGGTAATTACACCG
RAP1	orf6.1679	TTCGCCTCCTAAACCCAT	TGACCCAGTGATCCTCGT
RAS1	orf6.4089	TGGTAAATCCGCTTTAACCA	TTGTTTTTCAGCTTCAGCAA
RAS2	orf6.9043	ATGCTGGTCAAAGCCCGTAA	TCTCTGACGGAAGTTTCCAA
RBF1	orf6.4128	TCCGAGATTGGTGCTTCA	CCCGATCTTTCACATTGG
RBT1	orf6.4889	CTTTTGGAAAGCGCTGGTG	TCTCTTGGCAGGGAAGGC
RBT2	orf6.6384	TGCCGTGCAAGCATGTAA	CGCATTAGAAATTCCCCC
RBT4	orf6.537	TTGCCACTACTGCTGCCA	TGGCGTCAGGAGTAGCAA
RBT5	orf6.4505	AACCGCTTCCATCAACGG	TGGTGGTTTCAGCAGCCT
RBT7	orf6.4791	CTTTGTGGAAATTGCGG	GGCTGGTGAAACAGGATG
RCK2	orf6.859	TGGAATATTGTGATGGTGGA	TGAACCTGAACCTGAACCTG
RHO1	orf6.4937	ATGGTTAACGGTCCAGCTG	CCAAGTAATCAGCAGCACC
RHO2		GGACAAGCCATGGCAGAT	GCAAACCTAGTCCGAACGG
RHO3	orf6.606	ATGGGTAGGGGAAATTGC	TGGCACCTTTAGGTTTGG
RIM101	orf6.8147	CCAGCAGCTTTTGCTCCT	GCTTCAATGGGACATGGA
RIM8	orf6.6250	TTAACGACTCCGCCATT	AGTACTGGCATTGTCCGG
RIS1	orf6.6915	TAACAGGCAATGGGACCG	TTCCAAGTCGTCATCGCC
ROX1	orf6.1166	TATTCAAGTGGGGCTGCC	ACCCAATTCTCGGGAAAC
RPD3	orf6.4495	CAATGGAAGGTGCAGCAA	TGCCCATGTTCTCGCAAC
RPL39		TGGCTAAGTCAGGAATTGCT	GCTCTCTTTTACCAGCATT
RPL43	orf6.7571	ATGGGTACCACTGATGTT	CTATTCATCATCTTCAAC
RPS26	orf6.7103	AAAGAGAGCTTCCAACGG	AGCAGCATCTTGTGAGAG
RPS7	orf6.8330	CCACCTACCCAGCTGGTT	GACCCATGGTTTACCGGC
RSC1	orf6.6652	GCAGATTCAATGGTGGCA	TCGGTCTCTCTGGGTCGG
RSC4	orf6.5980	TGGCGATGAAGAATTGGC	GGGGCCACTCAAAACTCC
RSC8	orf6.8134	AACCAGACGCCGCAAGTC	TGCCTTGTCAATTTCGGC
RVS161	orf6.5778	TTAATCGAGCTGGAACCTAA	GAATTGAATCTGGCAATTGG
RVS167	orf6.3078	GGAGCCCAGTGCTACGGT	AATGTTCCCCTTCTTGCC
SAC1	orf6.7346	TTGCCAATGCAAAAACCA	TCCCATTGAAAACAGCGG
SAC2	orf6.9008	CGCCAGAAATTGCTCGAT	CATTGCCGATTGGTCAGA
SAC6	orf6.1299	TTTTGTGCGTTGGTTCA	AAGTGACACCACTGGCGG
SAC7	orf6.8438	GAAACCAGTGTGCGCCAG	AGGCTGGCTCATATCGGG
SAN1	orf6.6179	GGGTCAATCGAATGGCAGA	TGCATTGTTTGGCAAGGA
SAP1	orf6.4644	CCTCGTCTGGTCAATCA	CAGCTTGAAGGCATCAA
SAS10	orf6.2702	TGATGGAAGATTGGCAGAA	TTTGGCGTCAACAAAATTG
SAS2	orf6.7468	TCCCCATGATCTATCGCA	AAGTGGGAATTCTGGGCC
SAS4	orf6.3737	CTCCAATTGTGCGGACGT	TGCGTCAACCTCTCCAAC
SBE22	orf6.6130	CCATCCCTTTGGAGGAAC	AGGGGTGGTGGCTGAGAT
SCC2	orf6.3741	GGTTCCGCGAAATGTTTG	GCAATGAATGAGGGGCTG
SCW11 (YGL28)	orf6.2346	TCCAGCACATCTCAACC	AGTGGCAGGTGGTTCAGA

SFL1	orf6.2746	TGCATGATCCAGCGTTGA	TGGAGGTAGTGATGGCGG
SHS1	orf6.3490	GCAGATTCCCTGGTTTGCTT	TCACTATTGCTTGTGCCTGC
SIN4	orf6.2645	CGCAATCACAACTGGTG	AGCTCCATTTCATCCCCG
SIR2	orf6.6367	CAATCGCCAAAATGGTG	CATCGCCTAATTCTCCCA
SIS1	orf6.5251	AGGGGGAATGCACCAGCT	AATCACCTTCGTTGGCAA
SIT1	orf6.6084	CGTTTTCGCCATCCGATA	CCAACGGCAGCAGTAACA
SKN1	orf6.8522	TCCAGAAGACAAGCCCCA	TCAGTGGCGGAATCAGGT
SKN7	orf6.8220	GCTCCAACCAAAGTGGCT	TAGCGGAAACAAGCTGGG
SLA1	orf6.7099	TGAAGAAACGGGTCGTCG	GAACCCAAAGACCTTGGC
SLA2	orf6.8101	TGCCCTTTTGGAATGCTG	TCCGCTCAATGCATCATC
SLN1	orf6.8256	GGGATTTCGACCCCAATTA	ACCGGTACGGTGATCCCC
SMF1	orf6.460	CTGGGAATTATGCCACGG	GCCACCGTCATACCATT
SMT3	orf6.6563	CACAGGAGGCTCACCACC	CAACCACCAATTTGTGCA
SMT4	orf6.8677	TTTTCTGCAAAACCTCGG	AGTAAATGCTGTCCGGCGA
SNF12	orf6.5881	TGGCGGAATCATCTTGGA	GGAAGTTTCAACCGCTGG
SPS4	orf6.7786	TGAGCGGCAAAAGCTCAA	TCCAGAACGGTGTTCCAA
SPX45; CHS6	orf6.6981	CCGTTCCATTTATGCCGG	AGGAGCTCCACACCCAGA
SRO4	orf6.3942	GCCATTGATTAGGCGTC	CTATCGGCTGATCGACCA
SRV2	orf6.7066	GCAGCAACGTCTCGTCTT	TGTAGGGATCCCAATCCA
SSA2	orf6.4924	CCAAGCTAAGAACCAATTGG	CTTCAACAGTTGGACCATCG
SSK1	orf6.7978	CAGGCAAGCAATTCGACA	TGCATGGCCATTCCATTA
SSN8	orf6.8515	CTACTACCACCACTGCCCA	TGCCTTTTAAACCCCTTGT
STE11	orf6.3750	TCGAAATGATGCAAAAGGAA	CCTTTTAATTGCTTGGGCA
SWE1	orf6.2582	TACCTACAATCTGCACGTACGG	TATAGCAGCAAATATGTCCGGC
SWI1	orf6.6897	AAGCTCCACAGGTTGCGC	GAATGGAGATCCCGCTCC
SWI3	orf6.2949	TGCTTCACCTCCAGAGGA	AGCATCAACGTTGGTTGG
SWI4	orf6.6691	GTCCAAGGTGGGTTTGGA	CTGTTGGGCAGTTGGTGG
SWI5 or ACE2	orf6.5105	TCGACCAAAGGGTCAACC	GCTCATCCTCCTCAAGCA
SWI6	orf6.3187	TTTTGGGTCATCCAGCAA	CCTTGACAATGCGTCTGC
TEC1	orf6.9129	CGTGAGAAATGCCGATGG	CCACAAGATCTACCGGCA
TEL1	orf6.4422	CCGTGACAATTATCGGGA	TGGCCAATTTCAAGGAGA
TEL2	orf6.8452	GGCGGTGGTCAATGAAGC	CTGAACCTTTTCGTGCGC
TEM1	orf6.4863	CATTCTGGAGGAATGCCA	TTTCATCGCACTTCCGAA
TFS1	orf6.1861	TGGCCCAACTGAATTGGTC	CTTTGACACCACTGCTTGG
TOM1	orf6.3949	CGTCAAGGTTTCTGCGC	CTGCATGGCATCACTGCT
TPK1	orf6.4228	TGGAACCAGCAGACACAA	AATCTTGGAATGTCCCCC
TPK2	orf6.3564	TTCACATCACCAAGCTGCA	ACCAAAGGAACCTGTTCCC
TUB1	orf6.8389	TCCGGTTTGGGTTCTTTG	ACAAACAGGTGGCCATGT
TUB2	orf6.7578	CCCATCACAAAAGTTTCC	CTGGTTTGGATTTTGTGCA
TUP1	orf6.6232	CGCCTCAAACGAAGCAAG	CGCAGCAAACAACTGACG
UTH1	orf6.2071	TGCTCCAGCTTTTGAAGC	AATACCGGACCAACCACC
WAP1	orf6.8439	TGCCAGAGTGTGCCAAGC	TTCAGGAGTTGATGGGGC
WHI2	orf6.7962	AAATGGGGATGTCGATCAT	ATTCTGGGGCATCAATTC
WHI3	orf6.3359	GCAGTCAAACGGACCACC	TTGCCGTTTCGAAAGCAT
WHS11		ATTGGTGATAAAATCGAATCCA	TTTGAATCACCAAAAATAGCA
XBP1	orf6.3453	CACCAACCTCCACAGCAA	GAATGGTTGCGTTTTGGC
YBL64	orf6.6956	GCCACGCACACTACCATG	TCTACCGGTCGAGGCAGG
YBR103	orf6.2600	TGGCTGCAGAACAAGAGG	TTTCAATTTCCCATCCGG
YBR158 (CST13)	orf6.1307	TGGGACAATTTAAATGTGGTGA	ATAATTGGAGTTGGGAGTTTG
YBR183	orf6.6941	GCTTTGGCAACATTTGCG	CCATCCGTGTCTTCCAA
YCL066 (MATalpha1)	orf6.4399	CGCGATGCTCCAAGAAGA	TGTAATCCAAAGCCTCGC
YCL067 (MATalpha2)	orf6.4403	TGAATTCACATCTGGAGGCA	TGGTCTTTTTCAGATACGG
YCR27	orf6.9043	ATGCTGGTCAAAGCCGTAA	TTCTCTGACGGAAGTTTCCA
YDL160 (DHH1)	orf6.5427	TTTGAAAAGCCTTCGCCT	TTTCACGGCAAGAGGGAA
YDL225	orf6.875	TGCCTTGACGGAACCTCA	CGTGACAACAGCAAATGG
YDR371	orf6.3398	AATGCCACAACCATCACC	GACCAGCTTTCACCAGCA
YDR533C	orf6.1991	TTGCTGAAAAGGAAGGTG	TTACATTCAAAAGCAGCA
YER053C	orf6.1991	CCGATAAATTGACCGGTG	TGGTTTCCCAAGGACACA
YER175 (BRR2)	orf6.6947	GAAGAGATTCCCGCCAGC	CTGTTGAAGCCAATGCCA
YGL29	orf6.5536	GCTCCTAAAGACAAAGGGG	TCCACTTTTTTAGCATGCA
YGL37	orf6.6793	CCGCCTAATGGATCATTG	CCCCCAACAATCTTGGA
YML131	orf6.5876	ATCCAATGACCAACCCA	GAAGATCCAAGTGGCACCA
YNL288	orf6.8098	ACCGATTCTACGGCTTCC	ATGCTCCAATCACACCCA
YNL320	orf6.8975	AATGATTGCCCAAGCTGG	TAGCAACTGCACCTCCCA

YPL110	orf6.2299	CAATCGATTCTGCTGCCA	TTGGAAGCCTCTGTGCCA
ZDS1	orf6.7518	ATGATCCCGACTTGCCAC	CCCACAACAAAGGGGATG

* primers obtained from Theodore White (University of Washington, Seattle)