

Supplemental Table S2. List of 166 Transcription Factors Deleted in Mutants Assayed in this Study

ORF	Gene	Description
YER045C	ACA1 ^{sa}	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family, may regulate transcription of genes involved in utilization of non-optimal carbon sources
YLR131C	ACE2 [*]	Transcription factor that activates expression of early G1-specific genes, localizes to daughter cell nuclei after cytokinesis and delays G1 progression in daughters, localization is
YDR448W	ADA2 ^b	Transcription coactivator, component of the ADA and SAGA transcriptional adaptor/HAT (histone acetyltransferase) complexes
YDR216W	ADR1 [*]	Carbon source-responsive zinc-finger transcription factor, required for transcription of the glucose-repressed gene ADH2, of peroxisomal protein genes, and of genes required for
YGL071W	AFT1	Transcription factor involved in iron utilization and homeostasis; binds the consensus site PyPuCACCCPu and activates the expression of target genes in response to changes in iron
YPL202C	AFT2 [*]	Iron-regulated transcriptional activator, required for iron homeostasis and resistance to oxidative stress; similar to Aft1p
YMR042W	ARG80 [*]	Transcription factor involved in regulation of arginine-responsive genes; acts with Arg81p and Arg82p
YML099C	ARG81 [*]	Zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type, involved in the regulation of arginine-responsive genes; acts with Arg80p and Arg82p
YDR421W	ARO80 [*]	Zinc finger transcriptional activator of the Zn2Cys6 family; activates transcription of aromatic amino acid catabolic genes in the presence of aromatic amino acids
YPR199C	ARR1 [*]	Transcriptional activator of the bZIP family, required for transcription of genes involved in resistance to arsenic compounds
YKL185W	ASH1 [*]	Zinc-finger inhibitor of HO transcription; mRNA is localized and translated in the distal tip of anaphase cells, resulting in accumulation of Ash1p in daughter cell nuclei and inhibition of
YGR097W	ASK10 [*]	Component of the RNA polymerase II holoenzyme, phosphorylated in response to oxidative stress; has a role in destruction of Ssn8p, which relieves repression of stress-response
YOR113W	AZF1 [*]	Zinc-finger transcription factor, involved in induction of CLN3 transcription in response to glucose; genetic and physical interactions indicate a possible role in mitochondrial
YKR099W	BAS1 [*]	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways
YLR399C	BDF1	Protein involved in transcription initiation at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal
YKL005C	BYE1 [*]	Negative regulator of transcription elongation, contains a TFIIS-like domain and a PHD finger, multicopy suppressor of temperature-sensitive <i>ess1</i> mutations, probably binds RNA
YDR423C	CAD1 [*]	AP-1-like bZIP transcriptional activator involved in multiple stress responses, iron metabolism, and pleiotropic drug resistance; controls a set of genes involved in stabilizing
YMR280C	CAT8	Zinc cluster transcriptional activator necessary for derepression of a variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive
YJR060W	CBF1 [*]	Helix-loop-helix protein that binds the motif CACRTG, which is present at several sites including MET gene promoters and centromere DNA element I (CDEI); required for
YLR098C	CHA4 [*]	DNA binding transcriptional activator, mediates serine/threonine activation of the catabolic L-serine (L-threonine) deaminase (CHA1); Zinc-finger protein with Zn[2]-Cys[6] fungal-type
YOR028C	CIN5 [*]	Basic leucine zipper transcriptional factor of the YAP-1 family that mediates pleiotropic drug resistance and salt tolerance; localizes constitutively to the nucleus
YDR223W	CRF1	Transcriptional corepressor involved in the regulation of ribosomal protein gene transcription via the TOR signaling pathway and protein kinase A, phosphorylated by activated Yak1p
YNL027W	CRZ1 [*]	Transcription factor that activates transcription of genes involved in stress response; nuclear localization is positively regulated by calcineurin-mediated dephosphorylation
YIL036W	CST6 [*]	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family, activates transcription of genes involved in utilization of non-optimal carbon sources; involved in
YDR151C	CTH1	Member of the CCCH zinc finger family; has similarity to mammalian Tis11 protein, which activates transcription and also has a role in mRNA degradation; may function with Tis11p in
YGL166W	CUP2	Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated copper concentrations
YPL177C	CUP9 [*]	Homeodomain-containing transcriptional repressor of PTR2, which encodes a major peptide transporter; imported peptides activate ubiquitin-dependent proteolysis, resulting in

YKR034W	DAL80*	Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA-binding family, forms
YIR023W	DAL81*	Positive regulator of genes in multiple nitrogen degradation pathways; contains DNA binding domain but does not appear to bind the dodecanucleotide sequence present in the promoter
YNL314W	DAL82*	Positive regulator of allophanate inducible genes; binds a dodecanucleotide sequence upstream of all genes that are induced by allophanate; contains an UISALL DNA-binding, a
YNL023C	FAP1	Protein that binds to Fpr1p (FKBP12), conferring rapamycin resistance by competing with rapamycin for Fpr1p binding; has similarity to putative transcription factors, including D.
YIL131C	FKH1*	Transcription factor of the forkhead family that regulates the cell cycle and pseudohyphal growth; also involved in chromatin silencing at HML and HMR
YNL068C	FKH2*	Transcription factor of the forkhead family that regulates the cell cycle and pseudohyphal growth; also involved in chromatin silencing at HML and HMR; potential Cdc28p substrate
YER109C	FLO8	Transcription factor required for flocculation, diploid filamentous growth, and haploid invasive growth; genome reference strain S288C and most laboratory strains have a mutation in this
YGL254W	FZF1*	Transcription factor involved in sulfite metabolism, sole identified regulatory target is SSU1, overexpression suppresses sulfite-sensitivity of many unrelated mutants due to
YDR009W	GAL3*	Transcriptional regulator involved in activation of the GAL genes in response to galactose; forms a complex with Gal80p to relieve Gal80p inhibition of Gal4p; binds galactose and ATP
YPL248C	GAL4*	DNA-binding transcription factor required for the activation of the GAL genes in response to galactose; repressed by Gal80p and activated by Gal3p
YML051W	GAL80*	Transcriptional regulator involved in the repression of GAL genes in the absence of galactose; inhibits transcriptional activation by Gal4p; inhibition relieved by Gal3p or Gal1p
YFL021W	GAT1*	Transcriptional activator of genes involved in nitrogen catabolite repression, member of the GATA family of DNA binding proteins; activity and localization regulated by nitrogen limitation
YMR136W	GAT2	Protein containing GATA family zinc finger motifs; similar to Gln3p and Dal80p; expression repressed by leucine
YLR013W	GAT3*	Protein containing GATA family zinc finger motifs
YIR013C	GAT4	Protein containing GATA family zinc finger motifs
YEL009C	GCN4*	Transcriptional activator of amino acid biosynthetic genes in response to amino acid starvation; expression is tightly regulated at both the transcriptional and translational levels
YNL199C	GCR2*	Transcriptional activator of genes involved in glycolysis; interacts and functions with the DNA-binding protein Gcr1p
YDR096W	GIS1	Transcriptional factor, involved in the expression of genes during nutrient limitation; also involved in the negative regulation of DPP1 and PHR1
YER040W	GLN3*	Transcriptional activator of genes regulated by nitrogen catabolite repression (NCR), localization and activity regulated by quality of nitrogen source
YGL181W	GTS1*	Protein containing a zinc-finger in the N-terminus and a long Gln-rich region in the C-terminus; regulates ultradian rhythm, cell size, cell cycle, lifespan, sporulation, heat
YJL110C	GZF3*	GATA zinc finger protein and Dal80p homolog that negatively regulates nitrogen catabolic gene expression by competing with Gat1p for GATA site binding; function requires a
YPR008W	HAA1*	Transcriptional activator involved in the transcription of TPO2, HSP30 and other genes encoding membrane stress proteins; despite sequence similarity with the transcription factor
YFL031W	HAC1*	bZIP transcription factor (ATF/CREB1 homolog) that regulates the unfolded protein response, via UPRE binding, and membrane biogenesis; ER stress-induced splicing pathway
YOL089C	HAL9*	Putative transcription factor containing a zinc finger; overexpression increases salt tolerance through increased expression of the ENA1 (Na ⁺ /Li ⁺ extrusion pump) gene while gene
YGL237C	HAP2*	Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; contains
YBL021C	HAP3*	Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; contains
YKL109W	HAP4*	Subunit of the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; provides the
YOR358W	HAP5*	Subunit of the heme-activated, glucose-repressed Hap2/3/4/5 CCAAT-binding complex, a transcriptional activator and global regulator of respiratory gene expression; required for
YCR065W	HCM1	Forkhead transcription factor that drives S-phase specific expression of genes involved in chromosome segregation, spindle dynamics, and budding; suppressor of calmodulin mutants

YBL008W	HIR1*	Non-essential transcriptional corepressor involved in the cell cycle-regulated transcription of histone H2A, H2B, H3 and H4 genes; contributes to nucleosome formation, heterochromatic
YOR038C	HIR2*	Non-essential transcriptional corepressor involved in the cell cycle-regulated transcription of histone H2A, H2B, H3, and H4 genes; recruits Swi-Snf complexes to histone gene
YJR140C	HIR3*	Transcriptional corepressor involved in the cell cycle-regulated transcription of histone genes HTA1, HTB1, HHT1, and HHT2; involved in position-dependent gene silencing and
YOR032C	HMS1*	Basic helix-loop-helix (bHLH) protein with similarity to myc-family transcription factors; overexpression confers hyperfilamentous growth and suppresses the pseudohyphal
YJR147W	HMS2*	Protein with similarity to heat shock transcription factors; overexpression suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 homozygous null mutant
YMR172W	HOT1	Transcription factor required for the transient induction of glycerol biosynthetic genes GPD1 and GPP2 in response to high osmolarity; targets Hog1p to osmostress responsive
YBR215W	HPC2	Highly charged, basic protein required for normal cell-cycle regulation of histone gene transcription; mutants display strong synthetic defects with subunits of FACT, a complex that
YJR094C	IME1*	Master regulator of meiosis that is active only during meiotic events, activates transcription of early meiotic genes through interaction with Ume6p, degraded by the 26S proteasome
YIL154C	IMP2'	Transcriptional activator involved in maintenance of ion homeostasis and protection against DNA damage caused by bleomycin and other oxidants, contains a C-terminal leucine-rich
YDR123C	INO2*	Component of the heteromeric Ino2p/Ino4p basic helix-loop-helix transcription activator that binds inositol/choline-responsive elements (ICREs), required for derepression of phospholipid
YOL108C	INO4*	Transcription factor required for derepression of inositol-choline-regulated genes involved in phospholipid synthesis; forms a complex, with Ino2p, that binds the inositol-choline-
YKL032C	IXR1*	Protein that binds DNA containing intrastrand cross-links formed by cisplatin, contains two HMG (high mobility group box) domains, which confer the ability to bend cisplatin-modified
YCL055W	KAR4	Transcription factor required for induction of KAR3 and Clk1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative
YLR451W	LEU3*	Zinc-finger transcription factor that regulates genes involved in branched chain amino acid biosynthesis and ammonia assimilation; positively regulated by alpha-isopropylmalate, an
YDR034C	LYS14	Transcriptional activator involved in regulation of genes of the lysine biosynthesis pathway; requires 2-aminoadipate semialdehyde as co-inducer
YMR021C	MAC1*	Copper-sensing transcription factor involved in regulation of genes required for high affinity copper transport
YGR288W	MAL13*	MAL-activator protein, part of complex locus MAL1; nonfunctional in genomic reference strain S288C
YBR297W	MAL33*	MAL-activator protein, part of complex locus MAL3; nonfunctional in genomic reference strain S288C
YOR298C-A	MBF1*	Transcriptional coactivator that bridges the DNA-binding region of Gcn4p and TATA-binding protein Spt15p; suppressor of frameshift mutations
YDL056W	MBP1*	Transcription factor involved in regulation of cell cycle progression from G1 to S phase, forms a complex with Swi6p that binds to MluI cell cycle box regulatory element in promoters of
YIL128W	MET18*	DNA repair and TFIIH regulator, required for both nucleotide excision repair (NER) and RNA polymerase II (RNAP II) transcription; involved in telomere maintenance
YIR017C	MET28*	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism
YPL038W	MET31*	Zinc-finger DNA-binding protein, involved in regulating expression of the methionine biosynthetic genes, similar to Met32p
YDR253C	MET32*	Zinc-finger DNA-binding protein, involved in regulating expression of the methionine biosynthetic genes, similar to Met31p
YGR249W	MGA1*	Protein similar to heat shock transcription factor; multicopy suppressor of pseudohyphal growth defects of ammonia permease mutants
YIR033W	MGA2	ER membrane protein involved in regulation of OLE1 transcription, acts with homolog Spt23p; inactive ER form dimerizes and one subunit is then activated by
YGL035C	MIG1*	Transcription factor involved in glucose repression; C2H2 zinc finger protein similar to mammalian Egr and Wilms tumor proteins
YGL209W	MIG2*	Protein containing zinc fingers, involved in repression, along with Mig1p, of SUC2 (invertase) expression by high levels of glucose; binds to Mig1p-binding sites in SUC2 promoter
YER028C	MIG3*	Probable transcriptional repressor involved in response to toxic agents such as hydroxyurea that inhibit ribonucleotide reductase; phosphorylation by Snf1p or the Mec1p pathway

YMR070W	MOT3*	Nuclear transcription factor with two Cys2-His2 zinc fingers; involved in repression of a subset of hypoxic genes by Rox1p, repression of several DAN/TIR genes during aerobic
YOL116W	MSN1*	Transcriptional activator involved in regulation of invertase and glucoamylase expression, invasive growth and pseudohyphal differentiation, iron uptake, chromium accumulation, and
YMR037C	MSN2*	Transcriptional activator related to Msn4p; activated in stress conditions, which results in translocation from the cytoplasm to the nucleus; binds DNA at stress response elements of
YKL062W	MSN4*	Transcriptional activator related to Msn2p; activated in stress conditions, which results in translocation from the cytoplasm to the nucleus; binds DNA at stress response elements of
YMR164C	MSS11*	Transcription factor involved in regulation of invasive growth and starch degradation; controls the activation of MUC1 and STA2 in response to nutritional signals
YHR124W	NDT80*	Meiosis-specific transcription factor required for exit from pachytene and for full meiotic recombination; activates middle sporulation genes; competes with Sum1p for binding to
YDR043C	NRG1*	Transcriptional repressor that recruits the Cyc8p-Tup1p complex to promoters; mediates glucose repression and negatively regulates a variety of processes including filamentous
YBR066C	NRG2	Transcriptional repressor that mediates glucose repression and negatively regulates filamentous growth; has similarity to Nrg1p
YNR009W	NRM1	Transcriptional co-repressor of MBF (MCB binding factor)-regulated gene expression; Nrm1p associates stably with promoters via MBF to repress transcription upon exit from G1 phase
YAL051W	OAF1*	Oleate-activated transcription factor, acts alone and as a heterodimer with Pip2p; activates genes involved in beta-oxidation of fatty acids and peroxisome organization and biogenesis
YHL020C	OPI1*	Transcriptional regulator of a variety of genes; phosphorylation by protein kinase A stimulates Opi1p function in negative regulation of phospholipid biosynthetic genes; involved in telomere
YGL013C	PDR1*	Zinc cluster protein that is a master regulator involved in recruiting other zinc cluster proteins to pleiotropic drug response elements (PDREs) to fine tune the regulation of multidrug
YBL005W	PDR3*	Transcriptional activator of the pleiotropic drug resistance network, regulates expression of ATP-binding cassette (ABC) transporters through binding to cis-acting sites known as
YLR266C	PDR8	Transcription factor; targets include ATP-binding cassette (ABC) transporters, major facilitator superfamily transporters, and other genes involved in the pleiotropic drug
YKL043W	PHD1*	Transcriptional activator that enhances pseudohyphal growth; regulates expression of FLO11, an adhesin required for pseudohyphal filament formation; similar to StuA, an A.
YDL106C	PHO2*	Homeobox transcription factor; regulatory targets include genes involved in phosphate metabolism; binds cooperatively with Pho4p to the PHO5 promoter; phosphorylation of
YFR034C	PHO4*	Basic helix-loop-helix (bHLH) transcription factor; binds cooperatively with Pho2p to the PHO5 promoter; function is regulated by phosphorylation at multiple sites and by phosphate
YOR363C	PIP2*	Autoregulatory oleate-specific transcriptional activator of peroxisome proliferation, contains Zn(2)-Cys(6) cluster domain, forms heterodimer with Oaf1p, binds oleate response elements
YIL122W	POG1	Putative transcriptional activator that promotes recovery from pheromone induced arrest; inhibits both alpha-factor induced G1 arrest and repression of CLN1 and CLN2 via SCB/MCB
YLR014C	PPR1*	Zinc finger transcription factor containing a Zn(2)-Cys(6) binuclear cluster domain, positively regulates transcription of genes involved in uracil biosynthesis; activity may be modulated by
YKL015W	PUT3*	Transcriptional activator of proline utilization genes, constitutively binds PUT1 and PUT2 promoter sequences and undergoes a conformational change to form the active state; has a
YOR380W	RDR1*	Transcriptional repressor involved in the control of multidrug resistance; negatively regulates expression of the PDR5 gene; member of the Gal4p family of zinc cluster proteins
YCR106W	RDS1*	Zinc cluster protein involved in conferring resistance to cycloheximide
YPL133C	RDS2	Zinc cluster protein involved in conferring resistance to ketoconazole
YLR176C	RFX1*	Protein involved in DNA damage and replication checkpoint pathway; recruits repressors Tup1p and Cyc8p to promoters of DNA damage-inducible genes; similar to a family of
YMR182C	RGM1*	Putative transcriptional repressor with proline-rich zinc fingers; overproduction impairs cell growth
YKL038W	RGT1*	Glucose-responsive transcription factor that regulates expression of several glucose transporter (HXT) genes in response to glucose; binds to promoters and acts both as a
YHL027W	RIM101*	Transcriptional repressor involved in response to pH and in cell wall construction; required for alkaline pH-stimulated haploid invasive growth and sporulation; activated by proteolytic
YPL089C	RLM1*	MADS-box transcription factor, component of the protein kinase C-mediated MAP kinase pathway involved in the maintenance of cell integrity; phosphorylated and activated by the

YGR044C	RME1*	Zinc finger protein involved in control of meiosis; prevents meiosis by repressing IME1 expression and promotes mitosis by activating CLN2 expression; directly repressed by a1-a2
YPR065W	ROX1*	Heme-dependent repressor of hypoxic genes; contains an HMG domain that is responsible for DNA bending activity
YER169W	RPH1*	Transcriptional repressor of PHR1, which is a photolyase induced by DNA damage; binds to AG(4) (C(4)T) sequence upstream of PHR1; Rph1p phosphorylation during DNA damage is
YDL020C	RPN4*	Transcription factor that stimulates expression of proteasome genes; Rpn4p levels are in turn regulated by the 26S proteasome in a negative feedback control mechanism; RPN4 is
YJR127C	RSF2	Zinc-finger protein involved in transcriptional control of both nuclear and mitochondrial genes, many of which specify products required for glycerol-based growth, respiration, and other
YOL067C	RTG1*	Transcription factor (bHLH) involved in interorganelle communication between mitochondria, peroxisomes, and nucleus
YGL252C	RTG2	Sensor of mitochondrial dysfunction; regulates the subcellular location of Rtg1p and Rtg3p, transcriptional activators of the retrograde (RTG) and TOR pathways; Rtg2p is inhibited by
YBL103C	RTG3*	Basic helix-loop-helix-leucine zipper (bHLH/Zip) transcription factor that forms a complex with another bHLH/Zip protein, Rtg1p, to activate the retrograde (RTG) and TOR pathways
YOR315W	SFG1	Nuclear protein, putative transcription factor required for growth of superficial pseudohyphae (which do not invade the agar substrate) but not for invasive pseudohyphal growth; may act
YOR140W	SFL1*	Transcription repressor involved in regulation of flocculation-related genes, inhibits transcription by recruiting general corepressor Cyc8p-Tup1p to different promoters;
YLR403W	SFP1*	Transcription factor that controls expression of many ribosome biogenesis genes in response to nutrients and stress, regulates G2/M transitions during mitotic cell cycle and DNA-damage
YNL257C	SIP3*	Protein that activates transcription through interaction with DNA-bound Snf1p, C-terminal region has a putative leucine zipper motif; potential Cdc28p substrate
YJL089W	SIP4*	C6 zinc cluster transcriptional activator that binds to the carbon source-responsive element (CSRE) of gluconeogenic genes; involved in the positive regulation of gluconeogenesis;
YHR206W	SKN7*	Nuclear response regulator and transcription factor, part of a branched two-component signaling system; required for optimal induction of heat-shock genes in response to oxidative
YNL167C	SKO1*	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family, forms a complex with Tup1p and Ssn6p to both activate and repress transcription; cytosolic and nuclear
YBR182C	SMP1*	Putative transcription factor involved in regulating the response to osmotic stress; member of the MADS-box family of transcription factors
YMR016C	SOK2*	Nuclear protein that plays a regulatory role in the cyclic AMP (cAMP)-dependent protein kinase (PKA) signal transduction pathway; negatively regulates pseudohyphal differentiation;
YKL020C	SPT23*	ER membrane protein involved in regulation of OLE1 transcription, acts with homolog Mga2p; inactive ER form dimerizes and one subunit is then activated by ubiquitin/proteasome-
YMR053C	STB2*	Protein that interacts with Sin3p in a two-hybrid assay and is part of a large protein complex with Sin3p and Stb1p
YHR178W	STB5*	Activator of multidrug resistance genes, forms a heterodimer with Pdr1p; contains a Zn(II)2Cys6 zinc finger domain that interacts with a PDRE (pleiotropic drug resistance
YDR463W	STP1*	Transcription factor, activated by proteolytic processing in response to signals from the SPS sensor system for external amino acids; activates transcription of amino acid permease
YHR006W	STP2*	Transcription factor, activated by proteolytic processing in response to signals from the SPS sensor system for external amino acids; activates transcription of amino acid permease
YDR310C	SUM1*	Transcriptional repressor required for mitotic repression of middle sporulation-specific genes; involved in telomere maintenance, regulated by the pachytene checkpoint
YGL162W	SUT1*	Transcription factor of the Zn[II]2Cys6 family involved in sterol uptake; involved in induction of hypoxic gene expression
YPR009W	SUT2*	Putative transcription factor; multicopy suppressor of mutations that cause low activity of the cAMP/protein kinase A pathway; highly similar to Sut1p
YER111C	SWI4*	DNA binding component of the SBF complex (Swi4p-Swi6p), a transcriptional activator that in concert with MBF (Mbp1-Swi6p) regulates late G1-specific transcription of targets including
YDR146C	SWI5*	Transcription factor that activates transcription of genes expressed in G1 phase and at the G1/M boundary; localization to the nucleus occurs during G1 and appears to be regulated by
YLR182W	SWI6*	Transcription cofactor, forms complexes with DNA-binding proteins Swi4p and Mbp1p to regulate transcription at the G1/S transition; involved in meiotic gene expression; localization
YBR083W	TEC1*	Transcription factor required for full Ty1 expression, Ty1-mediated gene activation, and haploid invasive and diploid pseudohyphal growth; TEA/ATTS DNA-binding domain family

YBR240C	THI2*	Zinc finger protein of the Zn(II)2Cys6 type, probable transcriptional activator of thiamine biosynthetic genes
YLR183C	TOS4	Transcription factor that binds to a number of promoter regions, particularly promoters of some genes involved in pheromone response and cell cycle; potential Cdc28p substrate;
YGL096W	TOS8*	Homeodomain-containing transcription factor; SBF regulated target gene that in turn regulates expression of genes involved in G1/S phase events such as bud site selection, bud
YCR084C	TUP1	General repressor of transcription, forms complex with Cyc8p, involved in the establishment of repressive chromatin structure through interactions with histones H3 and H4, appears to
YOR344C	TYE7*	Serine-rich protein that contains a basic-helix-loop-helix (bHLH) DNA binding motif; binds E-boxes of glycolytic genes and contributes to their activation; may function as a transcriptional
YDL170W	UGA3*	Transcriptional activator necessary for gamma-aminobutyrate (GABA)-dependent induction of GABA genes (such as UGA1, UGA2, UGA4); zinc-finger transcription factor of the Zn(2)-
YPL139C	UME1	Negative regulator of meiosis, required for repression of a subset of meiotic genes during vegetative growth, binding of histone deacetylase Rpd3p required for activity, contains a NEE
YDR207C	UME6*	Key transcriptional regulator of early meiotic genes, binds URS1 upstream regulatory sequence, couples metabolic responses to nutritional cues with initiation and progression of
YDR213W	UPC2*	Sterol regulatory element binding protein, induces transcription of sterol transport and biosynthetic genes; involved in the anaerobic induction of DAN/TIR mannoproteins and
YML076C	WAR1*	Homodimeric Zn2Cys6 zinc finger transcription factor; binds to a weak acid response element to induce transcription of PDR12 and FUN34, encoding an acid transporter and a
YOR230W	WTM1*	Transcriptional repressor involved in regulation of meiosis and silencing; contains WD repeats
YOR229W	WTM2*	Transcriptional repressor involved in regulation of meiosis and silencing; contains WD repeats
YIL101C	XBP1*	Transcriptional repressor that binds to promoter sequences of the cyclin genes, CYS3, and SMF2; expression is induced by stress or starvation during mitosis, and late in meiosis;
YML007W	YAP1*	Basic leucine zipper (bZIP) transcription factor required for oxidative stress tolerance; mediates pleiotropic drug and metal resistance; localized to the nucleus in response to the
YHL009C	YAP3*	Basic leucine zipper (bZIP) transcription factor
YIR018W	YAP5*	Basic leucine zipper (bZIP) transcription factor
YDR259C	YAP6*	Putative basic leucine zipper (bZIP) transcription factor; overexpression increases sodium and lithium tolerance
YOL028C	YAP7*	Putative basic leucine zipper (bZIP) transcription factor
YDR451C	YHP1*	One of two homeobox transcriptional repressors (see also Yox1p), that bind to Mcm1p and to early cell cycle box (ECB) elements of cell cycle regulated genes, thereby restricting ECB-
YML027W	YOX1*	Homeodomain-containing transcriptional repressor, binds to Mcm1p and to early cell cycle boxes (ECBs) in the promoters of cell cycle-regulated genes expressed in M/G1 phase;
YOR172W	YRM1	Zn2-Cys6 zinc-finger transcription factor that activates genes involved in multidrug resistance; paralog of Yrr1p, acting on an overlapping set of target genes
YOR162C	YRR1*	Zn2-Cys6 zinc-finger transcription factor that activates genes involved in multidrug resistance; paralog of Yrm1p, acting on an overlapping set of target genes
YJL056C	ZAP1*	Zinc-regulated transcription factor, binds to zinc-responsive promoter elements to induce transcription of certain genes in the presence of zinc; regulates its own transcription; contains

^aGenes marked with an asterisk encode DNA-binding transcriptional regulators as described in Harbison et al., 2004, Nature, 431:99

^bGenes without an asterisk are annotated as encoding transcription factors in the SGD database (www.yeastgenome.org)