Table 5. List of modules

For each of 165 modules, we list the expression regulators, chromosomal markers, and the module genes. These modules can be interactively viewed by using our visualization software Genomica (can be downloaded from http://genomica.weizmann.ac.il/index.html) and the file containing the modules information (can be downloaded from http://ai.stanford.edu/~koller/seqvar.gxp). The visualization gives access to the modules gene expression and annotations as well as interactive viewing of the information in this table. For the expression regulators and module genes, it provides ORF name, gene name, and SGD desciprtion. For the genotype regulators, we listed the genes that are located within 10 kb upstream/downstream of the genomic region the markers corresponding to the genetic regulator cover. For each of these genes, we provided the number of coding SNPs and upstream SNPs inside the parenthesis.

(1) MODULE 1		
Expression regulators		
YNL145W	MFA2	lipopeptide mating pheromone; mating a-factor pheromone precursor
YHR005C	GPA1	Alpha subunit of G protein coupled to mating factor receptors, involved in the mating pheromone signal transduction pathway; component of pheromone response pathway common to both a and alpha cells
Module genes		
YCL065W	None	
YKL177W	None	
YCL067C	HMLALPHA2	Silenced copy of ALPHA2, encoding a homeobox-domain containing protein that associates with Mcm1p in haploid cells to repress a-specific gene expression and interacts with A1p in diploid cells to repress haploid-specific gene expression
YCR040W	MATALPHA1	Transcriptional co-activator involved in regulation of mating-type-specific gene expression; targets the transcription factor Mcm1p to the promoters of alpha-specific genes; one of two genes encoded by the alpha mating type cassette
YCL066W	HMLALPHA1	Silenced copy of ALPHA1, encoding a transcriptional coactivator involved in the regulation of mating-type alpha-specific gene expression
YJR004C	SAG1	Alpha-agglutinin of alpha-cells, binds to Aga1p during agglutination, N-terminal half is homologous to the immunoglobulin superfamily and contains binding site for a-agglutinin, C-terminal half is highly glycosylated and contains GPI anchor
YGL090W	LIF1	Protein involved in DNA double-strand break repair; physically interacts with DNA ligase 4 (Lig4p); homologous to mammalian XRCC4 protein
YLR041W	None	
YCR041W	None	
YPL187W	MF(ALPHA)1	mating factor alpha
YCR039C	MATALPHA2	Homeobox-domain containing protein which, in haploid cells, acts with Mcm1p to repress a-specific genes; in diploid cells

		Alpha2p acts together with A1p to repress transcription of haploid-specific genes
YOR090C	PTC5	Phosphatase type Two C; Type 2C Protein Phosphatase
YCR096C	HMRA2	Silenced copy of A2, encoding a protein of with similarity to Alpha2p that is required along with A1p for inhibiting expression of the HO endonuclease in a/alpha HO/HO diploid cells with an active mating-type interconversion system
YGL089C	MF(ALPHA)2	alpha mating factor
YLR040C	None	
YKL178C	STE3	Cell surface a factor receptor, transcribed in alpha cells and required for mating by alpha cells, couples to a MAP kinase cascade to mediate pheromone response; ligand bound receptors undergo endocytosis and recyling to the plasma membrane
(2) MODULE 2		
Genotype regulators		
M8_5776_19171		MUP3(0,5) YHL037C CBP2(45,5) YHL039W ARN1(3,0) YHL041W YHL042W ECM34(2,6) YHL044W YHL045W YHL046C YHL046W-A ARN2(308,525) YHL048C-A COS8(79,2) YHL049C YHL050C YHL050W-A
Module genes		
YHL047C	ARN2	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to the siderophore triacetylfusarinine C
YHL044W	None	
(3) MODULE 3		
Expression regulators		
YDR225W	HTA1	One of two nearly identical (see also HTA2) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p
YDL101C	DUN1	Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and Sml1p, and transient G2/M arrest after DNA damage; also regulates postreplicative DNA repair
Genotype regulators		
M1_1_37068		ACS1(2,7) PEX22(3,3) YAL056C-A GPB2(10,6) CNE1(9,5) YAL058C-A YAL059C-A ECM1(4,2) BDH1(6,5) YAL061W GDH3(0,50) FLO9(880,506) YAL063C-A YAL064C-A YAL064W YAL064W-B YAL065C YAL066W SEO1(370,503) YAL067W-A YAL068C YAL068W-A YAL069W
Module genes		
YAR062W	None	
YAL065C	None	
YAR050W	FLO1	Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers floc-forming ability that is chymotrypsin sensitive and heat resistant; similar to Flo5p

YHR213W	None	
YAL064W-B	None	
YAL063C	FLO9	Lectin-like protein with similarity to Flo1p, thought to be expressed and involved in flocculation
YHR211W	FLO5	Lectin-like protein involved in flocculation, cell wall protein that binds to mannose chains on the surface of other cells, confers floc-forming ability that is chymotrypsin resistant but heat labile; similar to Flo1p
(4) MODULE 4		
Expression regulators		
YOR210W	RPB10	RNA polymerase subunit, found in RNA polymerase complexes I, II, and III
YAL040C	CLN3	role in cell cycle START; involved in G(sub)1 size control; G(sub)1 cyclin
YPL075W	GCR1	Transcriptional activator of genes involved in glycolysis, functions and interacts with Gcr2p
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 DNA; mediates aerobic transcriptional repression of COX5b
Genotype regulators		
M13_46070_69122		VPS9(7,4) TAF13(3,0) ARG81(14,0) YML099W-A TSL1(3,1) YML100W-A CUE4(0,0) YML101C-A YML102C-A CAC2(2,0) NUP188(7,0) MDM1(416,120) SEC65(0,4) URA5(0,4) YML107C YML108W ZDS2(8,7) COQ5(2,7) BUL2(2,11) CTK3(2,0) DAT1(5,2) TAF8(2,2) VAN1(1,2) ATR1(0,56) YML116W-A YML117W-A
Module genes		
YHR157W	REC104	Protein involved in early stages of meiotic recombination; required for meiotic crossing over; forms a complex with Rec102p and Spo11p necessary during the initiation of recombination
YLR058C	SHM2	serine hydroxymethyltransferase
YDR019C	GCV1	T subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm
YCL064C	CHA1	catabolism of hydroxy amino acids; catabolic serine (threonine) dehydratase
YGL255W	ZRT1	High-affinity zinc transporter of the plasma membrane, responsible for the majority of zinc uptake; transcription is induced under low-zinc conditions by the Zap1p transcription factor
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 seven zinc-finger domains
YHR111W	UBA4	Protein that activates Urm1p before its conjugation to proteins (urmylation); one target is the thioredoxin peroxidase Ahp1p,

		suggesting a role of urmylation in the oxidative stress response
YIL051C	MMF1	Maintenance of Mitochondrial Function; Maintenance of Mitochondrial DNA 1
YAL044C	GCV3	H subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm
YMR189W	GCV2	P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm
(5) MODULE 5		
Expression regulators		
YJR122W	CAF17	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins
YBR274W	CHK1	checkpoint kinase 1; homolog of the S. pombe and mammalian Chk1 checkpoint kinases; Protein kinase Chk1
YNL031C	HHT2	One of two identical histone H3 proteins (see also HHT1); core histone required for chromatin assembly, involved in heterochromatin-mediated telomeric and HM silencing; regulated by acetylation, methylation, and mitotic phosphorylation
YDR264C	AKR1	Negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; Ankyrin repeat-containing protein
Genotype regulators		
M12_659357_674651		YLR257W GSY2(1,6) HSP60(0,6) LCB5(10,6) VPS63(3,0) YPT6(0,13) RBF7 RED1(13,14) YLR264C-A RPS28B(0,5) NEJ1(7,0) PDR8(8,6) BOP2(4,6) SEC22(0,3) YLR269C DCS1(0,4) YLR271W
Module genes		
YGR209C	TRX2	thioredoxin
YGL179C	TOS3	Putative protein kinase, related to and redundant with Elm1p and Pak1p in activating the SNF1 complex
YOL101C	IZH4	Membrane protein involved in zinc metabolism, member of the four-protein IZH family, expression induced by fatty acids and altered zinc levels; deletion reduces sensitivity to excess zinc; possible role in sterol metabolism
YGR037C	ACB1	Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming processes
YDR213W	UPC2	involved in sterol uptake; zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
YDR518W	EUG1	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER
YOR092W	ECM3	Non-essential protein of unknown function
YLR255C	None	

YOR377W	ATF1	Alcohol acetyltransferase with potential roles in lipid and sterol metabolism; responsible for the major part of volatile acetate ester production during fermentation
YHR179W	OYE2	Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye3p with slight differences in ligand binding and catalytic properties; may be involved in sterol metabolism
YER011W	TIR1	Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins; expression is downregulated at acidic pH and induced by cold shock
YOR229W	WTM2	WD repeat containing transcriptional modulator 2; Transcriptional modulator
YOR321W	PMT3	Transfers mannose residues from dolichyl phosphate-D-mannose to specific serine/threonine residues of proteins in the secretory pathway; dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
YBR067C	TIP1	cold- and heat-shock induced protein of the Srp1p/Tip1p family of serine-alanine-rich proteins; cell wall mannoprotein
YLR244C	MAP1	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p
YOR175C	None	
YKL008C	LAC1	Ceramide synthase component, involved in synthesis of ceramide from C26(acyl)-coenzyme A and dihydrosphingosine or phytosphingosine, functionally equivalent to Lag1p
YIL121W	QDR2	Multidrug transporter responsible for resistance to quinidine and barban; member of a family of drug:proton antiporters; plasma membrane transporter
YLR265C	NEJ1	Nonhomologous End-Joining regulator 1; Repressed by MAT heterozygosity; Interacts with Lif1p in a yeast two-hybrid assay; Nonhomologous End-Joining regulator 1
YDR274C	None	
YDR297W	SUR2	Sphingosine hydroxylase; has a role in sphingolipid metabolism
YLR380W	CSR1	Phosphatidylinositol transfer protein with a potential role in lipid turnover; interacts specifically with thioredoxin peroxidase (Tsa2p) and may have a role in oxidative stress resistance
YDR044W	HEM13	Coproporphyrinogen III oxidase, an oxygen requiring enzyme that catalyzes the sixth step in the heme biosynthetic pathway; localizes to the mitochondrial inner membrane; transcription is repressed by oxygen and heme (via Rox1p and Hap1p)
YLR256W	HAP1	Heme-responsive zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type; redox sensing regulator of gene expression (activates CYC1, CYC7, CYP3, CYB2, CTT1, COR2, ROX1, ERG9, ERG11, SOD2 and YHB1; represses HEM13)
(6) MODULE 6		
Genotype regulators		
M11_643655_643655		UBP11(1,2) YKR099C-A BAS1(2,2) SKG1(5,0) SIR1(4,0) FLO10(878,496)
Module genes		

YKR103W	NFT1	ORFs YKR103W and YKR104W are merged in different strain backgrounds.
YKR105C	None	
YKR080W	MTD1	NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase, plays a catalytic role in oxidation of cytoplasmic one-carbon units; expression is regulated by Bas1p and Bas2p, repressed by adenine, and may be induced by inositol and choline
YKR104W	None	
YKR087C	OMA1	Metalloendopeptidase of the mitochondrial inner membrane, involved in turnover of membrane-embedded proteins; member of a family of predicted membrane-bound metallopeptidases in prokaryotes and higher eukaryotes
YKR102W	FLO10	Lectin-like protein with similarity to Flo1p, thought to be involved in flocculation
(7) MODULE 7		
Genotype regulators		
M15_1152_43217		CTR9(13,2) PSF3(1,1) PEX11(0,1) SPT20(4,15) DCP1(0,4) YOL150C GRE2(6,81) FRE7(38,11) YOL153C ZPS1(3,8) YOL155C YOL155W-A HXT11(6,53) YOL157C ENB1(5,8) YOL159C YOL159C-A YOL160W YOL161C YOL162W YOL163W YOL164W YOL164W-A AAD15(7,561) YOL166C YOL166W-A
Module genes		
YOL164W	None	
YOL152W	FRE7	Putative ferric reductase with similarity to Fre2p; expression induced by low copper levels but not by low iron levels
YOL162W	None	
YDL161W	ENT1	Epsin-like protein involved in endocytosis and actin patch assembly and functionally redundant with Ent2p; binds clathrin via a clathrin-binding domain motif at C-terminus
YOL163W	None	
(8) MODULE 9		
Expression regulators		
YER177W	BMH1	14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes including exocytosis and vesicle transport, Ras/MAPK signaling during pseudohyphal development, rapamycin-sentitive signaling, and others
YHR005C	GPA1	Alpha subunit of G protein coupled to mating factor receptors, involved in the mating pheromone signal transduction pathway; component of pheromone response pathway common to both a and alpha cells
YPL127C	HHO1	Histone H1, a linker histone required for nucleosome packaging at restricted sites; suppresses DNA repair involving homologous recombination; not required for telomeric silencing, basal transcriptional repression, or efficient sporulation
YDR461W	MFA1	a-factor mating pheromone precursor
Genotype regulators		
M14_206186_209852		URE2(0,3) ELA1(0,5) PDR16(0,0) CSL4(1,6) BNI4(12,1)

		YNL234W YNL235C SIN4(6,8) YTP1(33,1) KEX2(1,3) LAP3(0,0) NAR1(1,0) ZWF1(1,2)
Module genes		
YML123C	PHO84	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter; regulated by Pho4p and Spt7p; mutation confers resistance to arsenate; exit from the ER during maturation requires Pho86p
YJL012C	VTC4	Phosphate metabolism; transcription is regulated by PHO system; polyphosphate synthetase (putative)
YLR404W	None	
YGR233C	PHO81	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p-Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p
YCR098C	GIT1	Plasma membrane permease, mediates uptake of the phosphatidylinositol metabolite glycerophosphoinositol as a source of the nutrients inositol and phosphate; expression and transport rate are regulated by phosphate and inositol availability
YBR093C	PHO5	One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; induced by phosphate starvation and coordinately regulated by PHO4 and PHO2
YAR071W	PHO11	One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; induced by phosphate starvation and coordinately regulated by PHO4 and PHO2
YPL019C	VTC3	Phosphate metabolism; transcription is regulated by PHO system; polyphosphate synthetase (putative)
YLL052C	AQY2	Water channel that mediates the transport of water across cell membranes and may be involved in freeze tolerance; disrupted by a stop codon in many S. cerevisiae strains
YHR136C	SPL2	Protein with similarity to cyclin-dependent kinase inhibitors, overproduction suppresses a plc1 null mutation; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
YDR281C	PHM6	Protein of unknown function, expression is regulated by phosphate levels
YER072W	VTC1	Protein involved in vacuolar maintenance
YBR296C	PHO89	Na+/Pi cotransporter, active in early growth phase; similar to phosphate transporters of Neurospora crassa; transcription regulated by inorganic phosphate concentrations and Pho4p
YHR215W	PHO12	One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; nearly identical to Pho11p; upregulated by phosphate starvation
YBR092C	PHO3	Acid phosphatase, nearly identical to Pho5p; glycosylated; transported to cell surface by secretory pathway; expression is repressed by thiamine
(9) MODULE 10		
Expression regulators		
YHR005C	GPA1	Alpha subunit of G protein coupled to mating factor receptors, involved in the mating pheromone signal transduction pathway;

		component of pheromone response pathway common to both a and alpha cells
Genotype regulators		
M11_643655_643655		UBP11(1,2) YKR099C-A BAS1(2,2) SKG1(5,0) SIR1(4,0) FLO10(878,496)
Module genes		
YPR199C	ARR1	Transcriptional activator of the bZIP family, required for transcription of genes involved in resistance to arsenic compounds
YPR198W	SGE1	Member of drug-resistance protein family; multicopy suppressor of gal11 null mutation
YPR197C	None	
(10) MODULE 11		
Expression regulators		
YER040W	GLN3	Transcriptional activator of genes regulated by nitrogen catabolite repression (NCR), localization and activity regulated by quality of nitrogen source
YDR224C	HTB1	One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation
YDR264C	AKR1	Negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; Ankyrin repeat-containing protein
YOR178C	GAC1	Regulatory subunit for Glc7p (protein phosphatase I) for glycogen synthesis; regulatory role also predicted for glucose repression and ion homeostatis; potential Cdc28p substrate
YKR099W	BAS1	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways
YPR052C	NHP6A	Homologous to mammalian high mobility group proteins 1 and 2; functions redundantly with the highly homologous gene, NHP6B; high-mobility group non-histone chromatin protein; 11-kDa nonhistone chromosomal protein
YJL103C	None	
Module genes		
YDR425W	SNX41	Sorting nexin that mediates retrieval from endosomes
YOR316C	COT1	Vacuolar transporter that mediates zinc transport into the vacuole; overexpression confers resistance to cobalt and rhodium
YER055C	HIS1	ATP phosphoribosyltransferase, a hexameric enzyme, catalyzes the first step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control
YEL071W	DLD3	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and reduced in cells grown with glutamate as the sole nitrogen source, located in the cytoplasm
YBR249C	ARO4	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP)

		synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by tyrosine
YGL026C	TRP5	tryptophan synthetase
YER090W	TRP2	anthranilate synthase Component I
YNL229C	URE2	Nitrogen catabolite repression regulator that acts by inhibition of GLN3 transcription in good nitrogen source; altered form of Ure2p creates [URE3] prion
YKL033W-A	None	
YHR137W	ARO9	Aromatic aminotransferase, catalyzes the first step of tryptophan, phenylalanine, and tyrosine catabolism
YLL051C	FRE6	Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels
YPR005C	HAL1	Cytoplasmic protein involved in halotolerance; decreases intracellular Na+ (via Ena1p) and increases intracellular K+ by decreasing efflux; expression repressed by Ssn6p-Tup1p and Sko1p and induced by NaCl, KCl, and sorbitol through Gcn4p
YIL165C	None	
YGR204W	ADE3	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine
YBL029W	None	
YLR034C	SMF3	Putative metal transporter, Nramp homolog, homolog of SMF1 and SMF2
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 genes
YCR099C	None	
YGL162W	SUT1	Involved in sterol uptake; hypoxic gene family involved in sterol transport
YDR242W	AMD2	Putative amidase
YDR234W	LYS4	Homoaconitase, catalyzes the conversion of homocitrate to homoisocitrate, which is a step in the lysine biosynthesis pathway
YDR126W	SWF1	Spore Wall Formation
YDR408C	ADE8	Phosphoribosyl-glycinamide transformylase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway
YHL040C	ARN1	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores
YAR015W	ADE1	N-succinyl-5-aminoimidazole-4-carboxamide ribotide (SAICAR) synthetase, required for 'de novo' purine nucleotide biosynthesis; red pigment accumulates in mutant cells deprived of adenine
YBR104W	YMC2	Putative mitochondrial inner membrane transporter, member of the mitochondrial carrier (MCF) family
YDR531W	None	
YIL094C	LYS12	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine,

		in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate
YJL087C	TRL1	tRNA ligase
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
YNR065C	YSN1	Sortilin homolog, interacts with proteins of the endocytic machinery
YIL074C	SER33	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p
YNL129W	NRK1	Nicotinamide riboside kinase, catalyzes the synthesis of nicotinamide nucleotide (NMN) from nicotinamide riboside; involved in a salvage pathway for NAD+ biosynthesis
YPL212C	PUS1	Involved in tRNA biogenesis; intranuclear protein which exhibits a nucleotide-specific intron-dependent tRNA pseudouridine synthase activity
YMR300C	ADE4	Phosphoribosylpyrophosphate amidotransferase (PRPPAT; amidophosphoribosyltransferase), catalyzes first step of the 'de novo' purine nucleotide biosynthetic pathway
YHR122W	None	
YKL106W	AAT1	Mitochondrial aspartate aminotransferase, catalyzes the conversion of oxaloacetate to aspartate in aspartate and asparagine biosynthesis
YER061C	CEM1	homology with beta-keto-acyl synthases; Protein homologous to beta-keto-acyl synthase
YER045C	ACA1	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family, may regulate transcription of genes involved in utilization of non-optimal carbon sources
YIL173W	VTH1	vps ten homolog; potential membrane glycoprotein with strong similarity to Vth2 and Pep1/Vps10
YMR120C	ADE17	Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4-carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine
YMR063W	RIM9	Protein required for IME1 expression; involved in sporulation
YDR249C	None	
YOR363C	PIP2	peroxisome induction pathway 2 (PIP2); transcriptional activator of peroxisome proliferation; may form heterodimer with Oaf1 to activate oleate-inducible gene expression; activator of peroxisome proliferation
YPR058W	YMC1	Putative mitochondrial inner membrane transporter, member of the mitochondrial carrier (MCF) family
YMR019W	STB4	Protein that binds Sin3p in a two-hybrid assay
YDR380W	ARO10	Phenylpyruvate decarboxylase, catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in the Ehrlich pathway
YJL222W	VTH2	vps ten homolog; potential membrane glycoprotein with strong similarity to Vth1 and Pep1
YCL009C	ILV6	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances

		activity of the Ilv2p catalytic subunit, localizes to mitochondria
YNR066C	None	
YKR019C	IRS4	Protein involved in regulation of phosphatidylinositol 4,5-bisphosphate concentrations; Irs4p and Tax4p bind and activate the phosphatase Inp51p; mutation confers an increase in rDNA silencing
YBR035C	PDX3	Pyridoxine (pyridoxamine) phosphate oxidase, has homologs in E. coli and Myxococcus xanthus; transcription is under the general control of nitrogen metabolism
YGL148W	ARO2	Bifunctional chorismate synthase and flavin reductase, catalyzes the conversion of 5-enolpyruvylshikimate 3-phosphate (EPSP) to form chorismate, which is a precursor to aromatic amino acids
YLR303W	MET17	O-acetyl homoserine-O-acetyl serine sulfhydrylase, required for sulfur amino acid synthesis
YDR426C	None	
YER081W	SER3	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser33p
YDL171C	GLT1	NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with Gln1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source
YLR004C	None	
YNL240C	NAR1	Component of the cytosolic iron-sulfur (FeS) protein assembly machinery, required for maturation of cytosolic and nuclear FeS proteins; homologous to human Narf (Nuclear prelamin A Recognition Factor); Nuclear architecture related protein with homology to human Narf (Nuclear prelamin A Recognition Factor)
YIL046W	MET30	F-box protein containing five copies of the WD40 motif, controls cell cycle function, sulfur metabolism, and methionine biosynthesis as part of the ubiquitin ligase complex; interacts with and regulates Met4p, localizes within the nucleus
(11) MODULE 12		
Expression regulators		
YPL230W	None	
YNL173C	MDG1	Plasma membrane protein involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations
YPL230W	None	
YBL084C	CDC27	Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition
YGL121C	GPG1	Proposed gamma subunit of the heterotrimeric G protein that interacts with the receptor Grp1p; involved in regulation of pseudohyphal growth; requires Gpb1p or Gpb2p to interact with Gpa2p
YPR052C	NHP6A	Homologous to mammalian high mobility group proteins 1 and 2; functions redundantly with the highly homologous gene,

		NHP6B; high-mobility group non-histone chromatin protein; 11-kDa nonhistone chromosomal protein
Module genes		
YBR116C	None	
YPL134C	ODC1	Mitochondrial inner membrane transporter, exports 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol for use in lysine and glutamate biosynthesis and in lysine catabolism
YIL160C	POT1	3-ketoacyl-CoA thiolase with broad chain length specifity, cleaves 3-ketoacyl-CoA into acyl-CoA and acetyl-CoA during beta-oxidation of fatty acids
YPR192W	AQY1	Water channel that mediates the transport of water across cell membranes and may be involved in freeze tolerance
YGR256W	GND2	6-phosphogluconate dehydrogenase, decarboxylating; converts 6-phosphogluconate + NADP to ribulose-5-phosphate + NADPH + CO2; 6-phosphogluconate dehydrogenase
YMR102C	None	
YKL093W	MBR1	Protein involved in mitochondrial functions and stress response; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants
YJL144W	None	
YKL217W	JEN1	Lactate transporter, required for uptake of lactate and pyruvate; expression is derepressed by transcriptional activator Cat8p under nonfermentative growth conditions, and repressed in the presence of glucose, fructose, and mannose
YMR086W	None	
YDR034W-B	None	
YKR009C	FOX2	Multifunctional enzyme of the peroxisomal fatty acid beta-oxidation pathway; has 3-hydroxyacyl-CoA dehydrogenase and enoyl-CoA hydratase activities
YOR328W	PDR10	ABC (ATP-binding cassette) membrane pump involved in the pleiotropic drug resistance network, regulated by Pdr1p and Pdr3p, similar to Pdr5p
YNL194C	None	
YJL066C	MPM1	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches
YHR139C	SPS100	involved in spore development; sporulation-specific wall maturation protein
YPR012W	None	
YHL032C	GUT1	Glycerol kinase, converts glycerol to glycerol-3-phosphate; glucose repression of expression is mediated by Adr1p and Ino2p-Ino4p; derepression of expression on non-fermentable carbon sources is mediated by Opi1p and Rsf1p
YNL237W	YTP1	Probable type-III integral membrane protein of unknown function, has regions of similarity to mitochondrial electron transport proteins
YAL053W	None	
YLR174W	IDP2	Cytosolic NADP-specific isocitrate dehydrogenase, catalyzes oxidation of isocitrate to alpha-ketoglutarate; levels are elevated during growth on non-fermentable carbon sources and reduced

		during growth on glucose
YHR096C	HXT5	Hexose transporter with moderate affinity for glucose, may function in accumulation of reserve carbohydrates during stress, expression induced by a decrease in growth rate, contains an extended N-terminal domain relative to other HXTs
YMR175W	SIP18	Protein whose expression is induced by salt
YER096W	SHC1	Sporulation-specific activator of Chs3p (chitin synthase III), required for the synthesis of the chitosan layer of ascospores; has similarity to Skt5p, which activates Chs3p during vegetative growth; transcriptionally induced at alkaline pH
YNL117W	MLS1	carbon-catabolite sensitive malate synthase
YDR536W	STL1	sugar transporter-like protein
YMR107W	SPG4	Protein required for survival at high temperature during stationary phase
YKL163W	PIR3	Protein containing tandem internal repeats
YML054C	CYB2	Expression is repressed by glucose and anaerobic conditions, is induced by L-lactate and is regulated by GRR1, ROX3, HAP1, HXK2 and CYC8; Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]
YMR081C	ISF1	Serine-rich, hydrophilic protein with similarity to Mbr1p; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants; expression is under glucose control; cotranscribed with NAM7 in a cyp1 mutant
YDR534C	FIT1	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall
YIL055C	None	
YPR030W	CSR2	Nuclear protein with a potential regulatory role in utilization of galactose and nonfermentable carbon sources; overproduction suppresses the lethality at high temperature of a chs5 spa2 double null mutation; potential Cdc28p substrate
YOR348C	PUT4	proline-specific permease (also capable of transporting alanine and glycine); putative proline-specific permease
YBR114W	RAD16	Protein that recognizes and binds damaged DNA in an ATP-dependent manner (with Rad7p) during nucleotide excision repair; subunit of Nucleotide Excision Repair Factor 4 (NEF4); member of the SWI/SNF family
(12) MODULE 14		
Expression regulators		
YGL121C	GPG1	Proposed gamma subunit of the heterotrimeric G protein that interacts with the receptor Grp1p; involved in regulation of pseudohyphal growth; requires Gpb1p or Gpb2p to interact with Gpa2p
YLL019C	KNS1	Nonessential putative protein kinase of unknown cellular role; member of the LAMMER family of protein kinases, which are serine/threonine kinases also capable of phosphorylating tyrosine residues
YJR122W	CAF17	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial

		proteins
YGR200C	ELP2	Elongator protein, part of the six-subunit RNA polymerase II Elongator histone acetyltransferase complex; target of Kluyveromyces lactis zymocin
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. melanogaster shuttle craft and human NFX1
YBL052C	SAS3	Protein involved in silencing at HMR
Genotype regulators		
M12_659357_674651		YLR257W GSY2(1,6) HSP60(0,6) LCB5(10,6) VPS63(3,0) YPT6(0,13) RBF7 RED1(13,14) YLR264C-A RPS28B(0,5) NEJ1(7,0) PDR8(8,6) BOP2(4,6) SEC22(0,3) YLR269C DCS1(0,4) YLR271W
Module genes		
YOL132W	GAS4	Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall
YDR271C	None	
YPL194W	DDC1	DNA damage checkpoint protein, part of a PCNA-like complex required for DNA damage response, required for pachytene checkpoint to inhibit cell cycle in response to unrepaired recombination intermediates; potential Cdc28p substrate
YOR356W	None	
YDR270W	CCC2	copper-transporting P-type ATPase with similarity to human Menkes and Wilsons genes; Cu(2+)-transporting ATPase
YJL100W	LSB6	Protein of unknown function; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization
YPR065W	ROX1	Heme-dependent repressor of hypoxic genes; contains an HMG domain that is responsible for DNA bending activity
YJL049W	None	
YKR046C	PET10	Protein of unknown function that co-purifies with lipid particles; expression pattern suggests a role in respiratory growth; computational analysis of large-scale protein-protein interaction data suggests a role in ATP/ADP exchange
YLR231C	BNA5	Kynureninase, required for biosynthesis of nicotinic acid from tryptophan via kynurenine pathway
YDL174C	DLD1	D-lactate dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane
YAL039C	CYC3	Cytochrome c heme lyase (holocytochrome c synthase), attaches heme to apo-Cyc1p in the mitochondrial intermembrane space; human ortholog may have a role in microphthalmia with linear skin defects (MLS)
YEL039C	CYC7	Cytochrome c isoform 2, expressed under hypoxic conditions; electron carrier of the mitochondrial intermembrane space that transfers electrons from ubiquinone-cytochrome c oxidoreductase to cytochrome c oxidase during cellular respiration

YPR150W	None	
YHR008C	SOD2	Manganese-containing superoxide dismutase
YMR145C	NDE1	None
YBL043W	ECM13	Non-essential protein of unknown function
YNL328C	MDJ2	Protein of the mitochondrial inner membrane; function partially overlaps that of Mdj1p, which is a chaperone involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; member of the DnaJ family
YJL048C	UBX6	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p, transcription is repressed when cells are grown in media containing inositol and choline
YNL156C	NSG2	Protein of unknown function, potential homolog of mammalian Insig 1
YMR220W	ERG8	Phosphomevalonate kinase, an essential cytosolic enzyme that acts in the biosynthesis of isoprenoids and sterols, including ergosterol, from mevalonate
YER141W	COX15	Protein required for the hydroxylation of heme O to form heme A, which is an essential prosthetic group for cytochrome c oxidase
YBR183W	YPC1	Alkaline ceramidase that also has reverse (CoA-independent) ceramide synthase activity, catalyzes both breakdown and synthesis of phytoceramide; overexpression confers fumonisin B1 resistance
(13) MODULE 15		
Expression regulators		
YGL121C	GPG1	Proposed gamma subunit of the heterotrimeric G protein that interacts with the receptor Grp1p; involved in regulation of pseudohyphal growth; requires Gpb1p or Gpb2p to interact with Gpa2p
YJL141C	YAK1	Serine-threonine protein kinase
YJL005W	CYR1	Required for START A of cell cycle, and glucose and nitrogen repression of sporulation; adenylate cyclase
YCR091W	KIN82	Putative serine/threonine protein kinase, most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily
YIL119C	RPI1	Putative transcriptional regulator; overexpression suppresses the heat shock sensitivity of wild-type RAS2 overexpression and also suppresses the cell lysis defect of an mpk1 mutation
YPL026C	SKS1	multicopy suppressor of snf3 and grr1 mutants; serine/threonine protein kinase homologous to Ran1p
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; member of the Swi4p/Mbp1p family; potential Cdc28p substrate
Module genes		
YGR019W	UGA1	gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase)
YIL099W	SGA1	Intracellular sporulation-specific glucoamylase involved in glycogen degradation; induced during starvation of a/a diploids late in sporulation, but dispensable for sporulation

YLR252W	None	
YDR070C	FMP16	The authentic, non-tagged protein was localized to the mitochondria
YDR391C	None	
YML070W	DAK1	Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress adaptation
YNL200C	None	
YDL206W	None	
YBR169C	SSE2	HSP70 family member, highly homologous to Sse1p
YPR184W	GDB1	Glycogen debranching enzyme containing glucanotranferase and alpha-1,6-amyloglucosidase activities, required for glycogen degradation
YLR178C	TFS1	Carboxypeptidase Y inhibitor; (putative) lipid binding protein; supressor of a cdc25 mutation
YGR088W	CTT1	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide
YGR248W	SOL4	Protein with similarity to Sol3p
YHR104W	GRE3	Aldose reductase involved in methylglyoxal, d-xylose and arabinose metabolism; stress induced (osmotic, ionic, oxidative, heat shock, starvation and heavy metals); regulated by the HOG pathway
YLR297W	None	
YGR053C	None	
YMR251W-A	HOR7	Protein of unknown function; overexpression suppresses Ca2+ sensitivity of mutants lacking inositol phosphorylceramide mannosyltransferases Csg1p and Csh1p; transcription is induced under hyperosmotic stress and repressed by alpha factor
YML128C	MSC1	Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; msc1 mutants are defective in directing meiotic recombination events to homologous chromatids
YER150W	SPI1	Protein with similarity to Sed1p; strongly expressed during stationary phase, and trancription is dependent on Msn2p/Msn4p
YDL048C	STP4	Protein involved in pre-tRNA splicing and in uptake of branched-chain amino acids
YKR049C	FMP46	The authentic, non-tagged protein was localized to the mitochondria
YNL015W	PBI2	Cytosolic inhibitor of vacuolar proteinase B, required for efficient vacuole inheritance; with thioredoxin forms protein complex LMA1, which assists in priming SNARE molecules and promotes vacuole fusion
YNL305C	None	
YGR201C	None	
YPR160W	GPH1	Releases glucose-1-phosphate from glycogen; Glycogen phosphorylase
YPR098C	None	
YKL026C	GPX1	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative

		stress
YGR194C	XKS1	third enzyme in the xylose pathway; Xylulokinase
YLR177W	None	
YMR025W	CSI1	Subunit of the Cop9 signalosome, which is required for deneddylation, or removal of the ubiquitin-like protein Rub1p from Cdc53p (cullin); involved in adaptation to pheromone signaling
YLL019C	KNS1	Nonessential putative protein kinase of unknown cellular role; member of the LAMMER family of protein kinases, which are serine/threonine kinases also capable of phosphorylating tyrosine residues
YCL035C	GRX1	Hydroperoxide and superoxide-radical responsive heat-stable glutathione-dependent disulfide oxidoreductase with active site cysteine pair; protects cells from oxidative damage
YBR117C	TKL2	transketolase, homologous to tkl1
YEL011W	GLC3	Glycogen branching enzyme, involved in glycogen accumulation; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
YKR076W	ECM4	Non-essential protein of unknown function; similar to Ygr154cp
YGR052W	FMP48	The authentic, non-tagged protein was localized to the mitochondria
YPL223C	GRE1	Hydrophilin of unknown function; stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway
YLL023C	None	
YNR014W	None	
YNL160W	YGP1	may be involved in cellular adaptations prior to stationary phase; YGP1 encodes gp37, a glycoprotein synthesized in response to nutrient limitation which is homologous to the sporulation-specific SPS100 gene
YNL274C	None	
YPL123C	RNY1	RNAse; member of the T(2) family of endoribonucleases
YKL091C	None	
YMR090W	None	
YMR250W	GAD1	Glutamate decarboxylase, converts glutamate into gamma-aminobutyric acid (GABA) during glutamate catabolism; involved in response to oxidative stress
YDL130W-A	STF1	ATPase stabilizing factor
YDR074W	TPS2	Trehalose-6-phosphate phosphatase
YKL151C	None	
YBR285W	None	
YMR272C	SCS7	Required for the hydroxylation of the very long chain fatty acid (VLCFA), located in the endoplasmic reticulum; desaturase/hydroxylase enzyme
YPL230W	None	
YOR178C	GAC1	Regulatory subunit for Glc7p (protein phosphatase I) for glycogen synthesis; regulatory role also predicted for glucose repression and ion homeostatis; potential Cdc28p substrate

YJR096W	None	
YIL136W	OM45	Protein of unknown function, major constituent of the mitochondrial outer membrane; located on the outer (cytosolic) face of the outer membrane
YOR289W	None	
YJL161W	FMP33	The authentic, non-tagged protein was localized to the mitochondria
YMR252C	None	
YLR258W	GSY2	Glycogen synthase, similar to Gsy1p; expression induced by glucose limitation, nitrogen starvation, heat shock, and stationary phase; activity regulated by cAMP-dependent, Snf1p and Pho85p kinases as well as by the Gac1p-Glc7p phosphatase
YDR275W	BSC2	Protein of unknown function, ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression
YBR126C	TPS1	Probable regulator of glucose influx into the cell & into glycolytic pathway, indirectly regulating glucose-induced signalling (activation & inactivation) & initial step(s) of glucose metabolism. Homologue of E. coli otsA protein; 56 kD synthase subunit of trehalose-6-phosphate synthase/phosphatase complex
YBR230C	None	
YPR117W	None	
YAL061W	None	
YLR270W	DCS1	Non-essential hydrolase involved in mRNA decapping, may function in a feedback mechanism to regulate deadenylation, contains pyrophosphatase activity and a HIT (histidine triad) motif; interacts with neutral trehalase Nth1p
YMR056C	AAC1	Mitochondrial inner membrane ADP/ATP translocator, exchanges cytosolic ADP for mitochondrially synthesized ATP; Aac1p is a minor isoform while Pet9p is the major ADP/ATP translocator
YKL142W	MRP8	Putative mitochondrial ribosomal protein, has similarity to E. coli ribosomal protein S2
YGL006W	PMC1	May be involved in depleting cytosol of Ca2+ ions; putative vacuolar Ca2+ ATPase
YPL087W	YDC1	Yeast dihydro-ceramidase; alkaline dihydroceramidase with minor reverse activity.
YNL195C	None	
YJL017W	None	
YMR197C	VTI1	Involved in cis-Golgi membrane traffic; Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p
YDR171W	HSP42	Small cytosolic stress-induced chaperone that forms barrel-shaped oligomers and suppresses the aggregation of non-native proteins; oligomer dissociation is not required for function; involved in cytoskeleton reorganization after heat shock
YER053C	PIC2	Mitochondrial phosphate carrier, imports inorganic phosphate into mitochondria; functionally redundant with Mir1p but less abundant than Mir1p under normal conditions; expression is induced at high temperature
YDR533C	HSP31	Possible chaperone and cysteine protease with similarity to E.

		coli Hsp31 and S. cerevisiae Hsp32p, Hsp33p, and Sno4p; member of the DJ-1/ThiJ/PfpI superfamily, which includes human DJ-1 involved in Parkinson's disease; exists as a dimer
YDR453C	TSA2	Thioredoxin-peroxidase, reduces H2O2 and alkyl hydroperoxides with the use of hydrogens provided by thioredoxin, thioredoxin reductase, and NADPH; provides protection against oxidation systems that generate reactive oxygen and sulfur species
YDL204W	RTN2	reticulon gene member of the RTNLA (reticulon-like A) subfamily
YHR080C	None	
YBR286W	APE3	Vacuolar aminopeptidase Y, processed to mature form by Prb1p
YDR032C	PST2	Protein of unknown function with similarity to members of a family of flavodoxin-like proteins; induced by oxidative stress in a Yap1p dependent manner; GFP-fusion protein localizes to the cytoplasm in a punctate pattern
YMR169C	ALD3	Aldehyde dehydrogenase that uses NAD+ as the preferred coenzyme; expression is induced in response to heat shock, oxidative, and osmotic stress
YHR087W	None	
YGR043C	None	
YPL004C	LSP1	Long chain base-responsive inhibitor of protein kinases Phk1p and Phk2p, acts along with Pil1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p
YMR181C	None	
YMR196W	None	
YML100W	TSL1	123 kD regulatory subunit of trehalose-6-phosphate synthase/phosphatase complex; homologous to TPS3 gene product
YER158C	None	
YDL222C	FMP45	The authentic, non-tagged protein was localized to the mitochondria; cell cortex protein
YNL055C	POR1	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability
YOL048C	None	
YHR016C	YSC84	SH3 domain in C-terminus
YGR070W	ROM1	GDP/GTP exchange protein (GEP) for Rho1p; mutations are synthetically lethal with mutations in rom2, which also encodes a GEP
YFL030W	AGX1	Alanine : glyoxylate aminotransferase, catalyzes the synthesis of glycine from glyoxylate, which is one of three pathways for glycine biosynthesis in yeast; has similairty to mammalian and plant alanine : glyoxylate aminotransferases
YFL014W	HSP12	Plasma membrane localized protein that protects membranes from dessication; induced by heat shock, oxidative stress, osmostress, stationary phase entry, glucose depletion, oleate and alcohol; regulated by the HOG and Ras-Pka pathways

YNL115C	None	
YIL155C	GUT2	Mitochondrial glycerol-3-phosphate dehydrogenase; expression is repressed by both glucose and cAMP and derepressed by non-fermentable carbon sources in a Snf1p, Rsf1p, Hap2/3/4/5 complex dependent manner
YIL113W	SDP1	None
YPR026W	ATH1	Vacuolar acid trehalase, required for trehalose utilization
YOL083W	None	
YLR251W	SYM1	Protein homologous to mammalian peroxisomal membrane protein Mpv17; required for ethanol metabolismand induced by heat shock; localized to the inner mitochondrial membrane
YGL037C	PNC1	NAD(+) salvage pathway gene; pyrazinamidase and nicotinamidase
YMR148W	None	
YGL156W	AMS1	vacuolar alpha mannosidase
YER054C	GIP2	Putative regulatory subunit of the protein phosphatase Glc7p, proposed to be involved in glycogen metabolism; contains a conserved motif (GVNK motif) that is also found in Gac1p, Pig1p, and Pig2p
YMR041C	None	
YMR105C	PGM2	Phosphoglucomutase
YPL186C	UIP4	Protein of unknown function
YIR016W	None	
YMR297W	PRC1	Vacuolar carboxypeptidase Y (proteinase C), involved in protein degradation in the vacuole and required for full protein degradation during sporulation
YIL107C	PFK26	6-phosphofructo-2-kinase, inhibited by phosphoenolpyruvate and sn-glycerol 3-phosphate, has negligible fructose-2,6-bisphosphatase activity, transcriptional regulation involves protein kinase A
YGR044C	RME1	mediates cell type control of sporulation; negatively regulates IME1 and sporulation; zinc finger protein; negative regulator of meiosis; directly repressed by a1-a2 regulator
YOL085C	None	
YIR038C	GTT1	ER associated glutathione S-transferase capable of homodimerization; expression induced during the diauxic shift and throughout stationary phase; functional overlap with Gtt2p, Grx1p, and Grx2p
YOL053C-A	None	
YDL021W	GPM2	Similar to GPM1 (phosphoglycerate mutase); converts 3-phosphoglycerate to 2-phosphoglycerate in glycolysis; phosphoglycerate mutase, involved in glycolysis
YDL223C	HBT1	Substrate of the Hub1p ubiquitin-like protein that localizes to the shmoo tip (mating projection); mutants are defective for mating projection formation, thereby implicating Hbt1p in polarized cell morphogenesis
YGR008C	STF2	ATPase stabilizing factor
YOL153C	None	
YGR143W	SKN1	Involved in (1->6)-beta-glucan biosynthesis; encodes a predicted

		type II membrane protein highly homologous to Kre6p
YDR001C	NTH1	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be phosphorylated by Cdc28p
YPL154C	PEP4	Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; synthesized as a zymogen, self-activates
YMR170C	ALD2	Cytosolic aldeyhde dehydrogenase that uses NAD+ as the preferred coenzyme; expression is induced in response to high osmotic stress
(14) MODULE 16		
Expression regulators		
YIR017C	MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism
YFR009W	GCN20	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA
YNL305C	None	
YLR150W	STM1	Protein that binds quadruplex nucleic acids; multicopy suppressor of tom1 and pop2 mutations; acts with Cdc13p to maintain telomere structure
YDR277C	MTH1	Negative regulator of the glucose-sensing signal transduction pathway, required for repression of transcription by Rgt1p; interacts with Rgt1p and the Snf3p and Rgt2p glucose sensors; phosphorylated by Yck1p, triggering Mth1p degradation
YGR123C	PPT1	Protein serine/threonine phosphatase with similarity to human phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth
YGR070W	ROM1	GDP/GTP exchange protein (GEP) for Rho1p; mutations are synthetically lethal with mutations in rom2, which also encodes a GEP
Module genes		
YNL010W	None	
YPR069C	SPE3	biosynthesis of spermidine; putrescine aminopropyltransferase (spermidine synthase)
YMR012W	CLU1	CLU1 is similar to the Dictyostelium cluA gene; translation initiation factor eIF3 subunit
YDL096C	None	
YOR239W	ABP140	Nonessential protein that binds actin filaments and localizes to actin patches and cables, has similarity to S-adenosylmethionine (AdoMet)-dependent methyltransferases
YER043C	SAH1	Putative S-adenosyl-L-homocysteine hydrolase with a probable role in S-adenosylhomocysteine catabolism and/or methionine degradation
YER003C	PMI40	catalyzes the interconversion of fructose-6-P and mannose-6-P; mannose-6-phosphate isomerase
YMR186W	HSC82	constitutively expressed heat shock protein
YAL005C	SSA1	Stress-seventy subfamily A; Heat shock protein of HSP70 family, cytoplasmic
YOR198C	BFR1	Component of mRNP complexes associated with

		polyribosomes; implicated in secretion and nuclear segregation; multicopy suppressor of BFA (Brefeldin A) sensitivity
YIL076W	SEC28	Part of a heptameric protein complex that regulates retrograde Golgi-to-ER protein traffic in eukaryotic cells; coatomer forms the COP I vesicle coat whose functions are essential; epsilon-COP coatomer subunit Sec28p
YAL004W	None	
YLR301W	None	
YOL141W	PPM2	Putative carboxyl methyl transferase, has similarity to Ppm1p but biochemical activity not yet demonstrated
YFL037W	TUB2	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules
YNR016C	ACC1	Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids
YDL084W	SUB2	Suppresses the cold-sensitive snRNP biogenesis brr1-1 mutation; RNA helicase
YGR087C	PDC6	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and ethanol-dependent, involved in amino acid catabolism
YPL240C	HSP82	Cytoplasmic chaperone (Hsp90 family) required for pheromone signaling and negative regulation of Hsf1p; docks with the mitochondrial import receptor Tom70p for preprotein delivery; interacts with co-chaperones Cns1p, Cpr6p, Cpr7p, and Sti1p
YLL024C	SSA2	member of 70 kDa heat shock protein family
YJL105W	SET4	None
YHR042W	NCP1	NADP-cytochrome P450 reductase
YMR307W	GAS1	Beta-1.3-glucanosyltransferase, required for cell wall assembly; localizes to the cell surface via a glycosylphosphatidylinositol (GPI) anchor
YOR181W	LAS17	Actin assembly factor, activates the Arp2/3 protein complex that nucleates branched actin filaments; localizes with the Arp2/3 complex to actin patches; homolog of the human Wiskott-Aldrich syndrome protein (WASP)
YER087C-A	None	
YLR134W	PDC5	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and ethanol-dependent, repressed by thiamine, involved in amino acid catabolism
YMR215W	GAS3	Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall
YHR183W	GND1	6-phosphogluconate dehydrogenase, decarboxylating; converts 6-phosphogluconate + NADP to ribulose-5-phosphate + NADPH + CO2; Phosphogluconate Dehydrogenase (Decarboxylating)
YGL077C	HNM1	Choline transporter (permease) that also controls the uptake of nitrogen mustard; expression is co-regulated with phospholipid biosynthetic genes and negatively regulated by choline and myo-inositol

YAL023C	PMT2	Transfers mannosyl residues from dolichyl phosphate-D-mannose to seryl and threonyl residues in proteins; acts in complex with Pmt1p; dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
YAL038W	CDC19	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration
YGR240C	PFK1	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes
YJR105W	ADO1	adenosine kinase
YDR502C	SAM2	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p)
YJR143C	PMT4	Transfers mannose residues from dolichyl phosphate-D-mannose to specific serine/threonine residues of proteins in the secretory pathway; dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
YLR378C	SEC61	membrane component of ER protein translocation apparatus
(15) MODULE 17		
Expression regulators		
YMR001C	CDC5	Polo-like kinase with similarity to Xenopus Plx1 and S. pombe Plo1p; found at bud neck, nucleus and SPBs; has multiple functions in mitosis and cytokinesis through phosphorylation of substrates; may be a Cdc28p substrate
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 following phosphorylation by Ime2p
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation; shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
Module genes		
YLR286C	CTS1	Endochitinase, required for cell separation after mitosis; transcriptional activation during late G and early M cell cycle phases is mediated by transcription factor Ace2p
YJR160C	MPH3	Alpha-glucoside permease, transports maltose, maltotriose, alpha-methylglucoside, and turanose; identical to Mph2p; encoded in a subtelomeric position in a region likely to have undergone duplication
YJR159W	SOR1	Sorbitol dehydrogenase; expression is induced in the presence of sorbitol
YDL247W	MPH2	Alpha-glucoside permease, transports maltose, maltotriose, alpha-methylglucoside, and turanose; identical to Mph3p; encoded in a subtelomeric position in a region likely to have undergone duplication
YLR339C	None	
YGL035C	MIG1	Transcription factor involved in glucose repression; C2H2 zinc

		finger protein which resembles the mammalian Egr and Wilms tumour proteins
YJL217W	None	
YML093W	UTP14	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YDR280W	RRP45	Ribosomal RNA Processing; Putative 3'->5' exoribonuclease; component of exosome complex of 3'->5' exonucleases
(16) MODULE 18		
Expression regulators		
YBL084C	CDC27	Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition
YDL064W	UBC9	SUMO-conjugating enzyme involved in the Smt3p conjugation pathway; nuclear protein required for S- and M-phase cyclin degradation and mitotic control; involved in proteolysis mediated by the anaphase-promoting complex cyclosome (APCC)
YDR277C	MTH1	Negative regulator of the glucose-sensing signal transduction pathway, required for repression of transcription by Rgt1p; interacts with Rgt1p and the Snf3p and Rgt2p glucose sensors; phosphorylated by Yck1p, triggering Mth1p degradation
YMR036C	MIH1	S. pombe cdc25+ homolog; homolog of S. pombe cdc25
Module genes		
YNR033W	ABZ1	Para-aminobenzoate (PABA) synthase, has similarity to Escherichia coli PABA synthase components PabA and PabB
YDR193W	None	
YBR277C	None	
YPL046C	ELC1	Elongin C, forms heterodimer with Ela1p that participates in transcription elongation; expression dramatically upregulated during sporulation; widely conserved among eukaryotes
YGL230C	None	
YHR032W	None	
YIR033W	MGA2	ER membrane protein involved, with its homolog Spt23p, in regulation of OLE1 transcription; inactive ER form dimerizes and one subunit is then activated by ubiquitin/proteasome-dependent processing followed by nuclear targeting
YJR156C	THI11	Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family including THI5, THI11, THI12, and THI13
YML013C-A	None	
YFR032C	None	
YDL163W	None	
YGR113W	DAM1	Component of the DASH complex, localized to intranuclear spindles and spindle pole bodies; interacts with Duo1p and Mps1p; key Ipl1p target for regulating kinetochore-microtubule attachments
YJL091C	GWT1	Protein involved in the inositol acylation of glucosaminyl

		phosphatidylinositol (GlcN-PI) to form glucosaminyl(acyl)phosphatidylinositol (GlcN(acyl)PI), an intermediate in the biosynthesis of glycosylphosphatidylinositol (GPI) anchors
YKL076C	PSY1	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 69% of ORF overlaps the uncharacterized ORF YKL075C
(17) MODULE 20		
Expression regulators		
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
YIR026C	YVH1	nitrogen starvation-induced protein phosphatase
YGL248W	PDE1	Low-affinity cyclic AMP phosphodiesterase, controls glucose and intracellular acidification-induced cAMP signaling, target of the cAMP-protein kinase A (PKA) pathway; glucose induces transcription and inhibits translation
YPL203W	TPK2	Involved in nutrient control of cell growth and division; cAMP-dependent protein kinase catalytic subunit
YGL158W	RCK1	Serine/threonine protein kinase
YNR054C	ESF2	Protein required for cell viability
YDR496C	PUF6	member of the PUF protein family; YDR496C
Module genes		
YOR106W	VAM3	Syntaxin-related protein; required for vacuolar assembly; PEP12 homolog; member of the syntaxin family of proteins; predicted C-terminal TMD
YNL303W	None	
YDR339C	None	
YDR161W	None	
YDR179C	CSN9	Subunit of the Cop9 signalosome, which is required for deneddylation, or removal of the ubiquitin-like protein Rub1p from Cdc53p (cullin); involved in adaptation to pheromone signaling
YGL029W	CGR1	Coiled-coil protein that may contribute to compartmentalization of nucleolar constituents; expression is growth-regulated
YPL266W	DIM1	Essential 18S rRNA dimethylase, responsible for conserved m6(2)Am6(2)A dimethylation in 3'-terminal loop of 18 S rRNA, part of 90S and 40S pre-particles in nucleolus, involved in pre-ribosomal RNA processing
YIL149C	MLP2	Mlp proteins restrict telomere length by influencing the Rif1-Tel1 pathway of telomerase regulation; also involved in the translocation of macromolecules between the nucleoplasm and the NPC; colied-coil protein (putative), similar to myosin and TPR
YKL110C	KTI12	Protein assoctiated with the RNA polymerase II Elongator complex; involved in sensitivity to G1 arrest induced by Kluyveromyces lactis toxin, zymocin
YDR334W	SWR1	Swi2/Snf2-related ATPase, component of the SWR1 complex; required for the incorporation of Htz1p into chromatin

YIL092W	None	
YOL095C	HMI1	Mitochondrial inner membrane localized ATP-dependent DNA helicase, required for the maintenance of the mitochondrial genome; not required for mitochondrial transcription
YDR527W	RBA50	Protein required for cell viability
YLR002C	NOC3	Protein that forms a nuclear complex with Noc2p that binds to 66S ribosomal precursors to mediate their intranuclear transport; also binds to chromatin to promote the association of DNA replication factors and replication initiation
YIL064W	None	
YHR066W	SSF1	putative involvement in mating; homologous to Ssf2p
YDR195W	REF2	RNA-binding protein involved in the cleavage step of mRNA 3'-end formation prior to polyadenylation; also involved in snoRNA maturation
YOR342C	None	
YMR014W	BUD22	Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern
YDR110W	FOB1	Nucleolar protein required for DNA replication fork blocking and recombinational hotspot activities; binds to the replication fork barrier site in the rDNA region; related to retroviral integrases
YER161C	SPT2	Protein involved in negative regulation of transcription, exhibits regulated interactions with both histones and SWI-SNF components, has similarity to mammalian HMG1 proteins
YDL121C	None	
YAL033W	POP5	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends
YDR075W	PPH3	Catalytic subunit of protein phosphatase; involved in activation of Gln3p, which is a transcription factor with a role in nitrogen utilization
YML060W	OGG1	Mitochondrial glycosylase/lyase that specifically excises 7,8-dihydro-8-oxoguanine residues located opposite cytosine or thymine residues in DNA, repairs oxidative damage to mitochondrial DNA
YDL166C	FAP7	Essential nuclear protein, involved in the oxidative stress response
YDL158C	None	
YHR144C	DCD1	Deaminase required for dCTP and dTTP synthesis; expression is cell cycle regulated
YLR003C	None	
YNL186W	UBP10	Ubiquitin-specific protease that deubiquitinates ubiquitin-protein moieties; may regulate silencing by acting on Sir4p; involved in posttranscriptionally regulating Gap1p and possibly other transporters; primarily located in the nucleus
YNL231C	PDR16	Phosphatidylinositol transfer protein (PITP) controlled by the multiple drug resistance regulator Pdr1p, localizes to lipid particles and microsomes, controls levels of various lipids, may regulate lipid synthesis, homologous to Pdr17p
YGR272C	None	

YPL111W	CAR1	arginase
YDL129W	None	
YDR045C	RPC11	RNA polymerase III subunit C11; mediates pol III RNA cleavage activity and is important for termination of transcription
YDR526C	None	
YHL012W	None	
YDR412W	None	
YCL036W	GFD2	Protein of unknown function, identified as a high-copy suppressor of a dbp5 mutation
YNL150W	None	
YHR184W	SSP1	Protein involved in the control of meiotic nuclear division and spore formation
YOR051C	None	
YGR251W	None	
YPR143W	RRP15	Essential protein involved in pre-rRNA processing
YNL191W	None	
YHR041C	SRB2	RNA polymerase II holoenzyme/mediator subunit
(18) MODULE 21		
Expression regulators		
YPL153C	RAD53	Protein kinase, required for cell-cycle arrest in response to DNA damage; activated by trans autophosphorylation when interacting with hyperphosphorylated Rad9p
YMR001C	CDC5	Polo-like kinase with similarity to Xenopus Plx1 and S. pombe Plo1p; found at bud neck, nucleus and SPBs; has multiple functions in mitosis and cytokinesis through phosphorylation of substrates; may be a Cdc28p substrate
YDL101C	DUN1	Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and Sml1p, and transient G2/M arrest after DNA damage; also regulates postreplicative DNA repair
Module genes		
YPL233W	NSL1	Essential component of the MIND kinetochore complex (Mtw1p Including Nnf1p-Nsl1p-Dsn1p) which joins kinetochore subunits contacting DNA to those contacting microtubules; required for accurate chromosome segregation
YPR194C	OPT2	Oligopeptide transporter; member of the OPT family, with potential orthologs in S. pombe and C. albicans
YCL074W	None	
YIL057C	None	
YJL154C	VPS35	Protein involved in vacuolar sorting; retromer complex component
YCR022C	None	
YML111W	BUL2	a homologue of BUL1; (putative) ubiquitin-mediated protein degradation
YPL164C	MLH3	Mutl Homolog; MutL Homolog
YML061C	PIF1	involved in repair and recombination of mitochondrial DNA;

		also plays a role in (nuclear) chromosomal telomere formation and elongation; 5' to 3' DNA helicase
YHR056C	RSC30	RSC complex component
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 DNA; mediates aerobic transcriptional repression of COX5b
YJL179W	PFD1	Subunit of heterohexameric prefoldin, which binds cytosolic chaperonin and transfers target proteins to it; involved in the biogenesis of actin and of alpha- and gamma-tubulin
YDR514C	None	
YPL204W	HRR25	Similar to YCK1 and YCK2, two other casein kinase I isoforms; found primarily in nucleus; may be involved in DNA-damage repair; casein kinase I isoform
(19) MODULE 22		
Expression regulators		
YFR009W	GCN20	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation; shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
YOR337W	TEA1	Mutants are defective in Ty1 Enhancer-mediated Activation; Ty1 enhancer activator
YGR156W	PTI1	Pta1p Interacting protein
YDR283C	GCN2	Protein kinase, phosphorylates the alpha-subunit of translation initiation factor eIF2 (Sui2p) in response to starvation; activated by uncharged tRNAs and the Gcn1p-Gcn20p complex
YBR073W	RDH54	genetic interaction with DMC1; Putative helicase similar to RAD54
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
Module genes		
YCR088W	ABP1	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization
YPR035W	GLN1	Glutamine synthetase (GS), synthesizes glutamine from glutamate and ammonia; with Glt1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source and by amino acid limitation
YGL012W	ERG4	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants are viable, but lack ergosterol
YFR006W	None	
YFR044C	None	
YCR013C	None	
YDL160C	DHH1	Cytoplasmic DExD/H-box helicase, stimulates mRNA decapping, coordinates distinct steps in mRNA function and

		decay, interacts with both the decapping and deadenylase complexes, may have a role in mRNA export and translation
YNL088W	TOP2	Essential type II topoisomerase, catalyzes topology changes in DNA via transient breakage and rejoining of phosphodiester bonds in the DNA backbone; localizes to axial cores in meiosis
YKL153W	None	
YIL123W	SIM1	(putative) invovled in control of DNA replication
YCR012W	PGK1	3-phosphoglycerate kinase
YHL030W	ECM29	Major component of the proteasome; tethers the proteasome core particle to the regulatory particle, and enhances the stability of the proteasome
YDL100C	ARR4	ATPase, involved in resistance to heat and metal stress, active as a dimer; normally localized to the cytosol, but appears to localize to late endosomes under stress conditions
YML085C	TUB1	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules
YKL182W	FAS1	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities
YJR103W	URA8	Last step in pyrimidine biosynthesis pathway; CTP synthase
YOL002C	IZH2	Membrane protein involved in zinc metabolism, member of the four-protein IZH family, direct target of the Zap1p transcription factor, expression induced by zinc deficiency and fatty acids, deletion increases sensitivity to elevated zinc
YNL058C	None	
YMR076C	PDS5	Protein required for establishment and maintenance of sister chromatid condensation and cohesion, colocalizes with cohesin on chromosomes in an interdependent manner, may function as a protein-protein interaction scaffold
YGL195W	GCN1	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate Gcn2p activation by an uncharged tRNA
YER023W	PRO3	Delta 1-pyrroline-5-carboxylate reductase, catalyzes the last step in proline biosythesis
YNL057W	None	
YLR460C	None	
YMR323W	None	
YJR116W	None	
YDR388W	RVS167	BAR adaptor protein, subunit of a complex (Rvs161p-Rvs167p) that regulates actin, endocytosis, and viability following starvation or osmotic stress
YKL152C	GPM1	converts 3-phosphoglycerate to 2-phosphoglycerate in glycolysis; Phosphoglycerate mutase
YPL231W	FAS2	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities
YOR153W	PDR5	Short-lived membrane ABC (ATP-binding cassette) transporter, actively exports various drugs, expression regulated by Pdr1p; also involved in steroid transport, cation resistance, and cellular

		detoxification during exponential growth
YDL185W	TFP1	Vacuolar ATPase V1 domain subunit A; protein precursor is spliced to yield the extein Tfp1p and the intein Vde (PI-SceI), which is a site-specific endonuclease
YDR261C	EXG2	Exo-1,3-beta-glucanase, involved in cell wall beta-glucan assembly; may be anchored to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor
YGL173C	KEM1	5'-3' exonuclease involved in mRNA decay, evolutionarily conserved component of cytoplasmic processing (P) bodies, plays a role in microtubule-mediated processes, filamentous growth, and ribosomal RNA maturation
YMR276W	DSK2	Nuclear-enriched ubiquitin-like polyubiquitin-binding protein, required for spindle pole body (SPB) duplication and for transit through the G2/M phase of the cell cycle, involved in proteolysis, interacts with the proteasome
YBR127C	VMA2	Vacuolar H+ ATPase regulatory subunit (subunit B) of the catalytic (V1) sector
YNL262W	POL2	Catalytic subunit of DNA polymerase epsilon, one of the major chromosomal DNA replication polymerases characterized by processivity and proofreading exonuclease activity; also involved in DNA synthesis during DNA repair
YFL006W	None	
YKL127W	PGM1	phosphoglucomutase, minor isoform
YNL035C	None	
YGR180C	RNR4	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits
YPL048W	CAM1	Calcium and phospholipid binding protein homologous to translation elongation factor 1-gamma (EF-1gamma)
YGL060W	YBP2	Protein with a role in resistance to oxidative stress; has similarity to Ybp1p, which is involved in regulation of the transcription factor Yap1p via oxidation of specific cysteine residues
YFL007W	BLM3	Protein involved in assembly of proteasomal core particles in the nucleus; required for normal resistance to bleomycin, may be involved in protection against oxidative damage
(20) MODULE 23		
Expression regulators		
YDR043C	NRG1	Transcriptional repressor that recruits the Cyc8p-Tup1p complex to promoters; mediates glucose repression and negatively regulates a variety of processes including filamentous growth and alkaline pH response
YPR070W	MED1	Subunit 1 of the Mediator complex essential for transcriptional regulation
YDR496C	PUF6	member of the PUF protein family; YDR496C
YGL035C	MIG1	Transcription factor involved in glucose repression; C2H2 zinc finger protein which resembles the mammalian Egr and Wilms tumour proteins
YJR122W	CAF17	Mitochondrial protein that interacts with Ccr4p in the two-

		hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins
Module genes		
YDL027C	None	
YMR173W-A	None	
YMR302C	PRP12	Integral inner mitochondrial membrane protein with similarity to exonucleases; prp12 mutants exhibit an increased rate of mt DNA escape
YMR173W	DDR48	DNA damage-responsive protein, expression is increased in response to heat-shock stress or treatments that produce DNA lesions; contains multiple repeats of the amino acid sequence NNNDSYGS
YLR121C	YPS3	Aspartic protease, attached to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor
YLR194C	None	
YOR227W	None	
YNL208W	None	
YGR032W	GSC2	Catalytic subunit of 1,3-beta-glucan synthase, has similarity to an alternate catalytic subunit, Fks1p (Gsc1p); Rho1p encodes the regulatory subunit; involved in cell wall synthesis and maintenance
YGR250C	None	
YBR182C	SMP1	Transcription factor of the MADS (Mcm1p, Agamous, Deficiens, SRF) box family; closely related to RLM1; Probable DNA-binding transcription factor, Homolog to SRF/SL-2
YMR023C	MSS1	May play a part in mitochondrial translation; putative mitochondrial GTPase
YMR280C	CAT8	Zinc-cluster protein involved in activating gluconeogenic genes; related to Gal4p
YPL054W	LEE1	Protein of unknown function
YHL008C	None	
YOR385W	None	
YOR220W	None	
YNL093W	YPT53	Involved in vacuolar protein sorting and endocytosis; GTP-binding protein of the rab family
YMR030W	RSF1	Protein localized to both the nucleus and mitochondrion; mutant displays decreased transcription of specific nuclear and mitochondrial genes whose products are involved in respiratory growth
YMR191W	SPG5	Protein required for survival at high temperature during stationary phase
YOR306C	MCH5	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma membrane; mutant is not deficient in monocarboxylate transport
YKR061W	KTR2	Mannosyltransferase involved in N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family
YDL032W	None	

YKR013W	PRY2	Protein of unknown function, has similarity to Pry1p and Pry3p and to the plant PR-1 class of pathogen related proteins
YMR305C	SCW10	Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on mutant phenotype and its regulation by Ste12p
YMR068W	AVO2	Component of a complex containing the Tor2p kinase and other proteins, which may have a role in regulation of cell growth
YJR061W	None	
YOL016C	CMK2	Calmodulin-dependent protein kinase
YER130C	None	
YMR040W	YET2	Endoplasmic reticulum transmembrane protein, homolog of human BAP31 protein
(21) MODULE 24		
Expression regulators		
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 seven zinc-finger domains
YGL254W	FZF1	Transcription factor involved in sulfite resistance; contains five zinc-fingers; activates SSU1 transcription
Module genes		
YOL086C	ADH1	Alcohol dehydrogenase, involved in the production of certain carboxylate esters
YMR303C	ADH2	Glucose-repressible alcohol dehydrogenase II, involved in the production of certain carboxylate esters
YLR130C	ZRT2	Low-affinity zinc transporter of the plasma membrane; transcription is induced under low-zinc conditions by the Zap1p transcription factor
YMR083W	ADH3	Alcohol dehydrogenase isoenzyme III, shows a high affinity for alcohols with a double bond conjugated to the alcohol group
YDR235W	PRP42	U1 snRNP protein involved in splicing, required for U1 snRNP biogenesis; contains multiple tetriatricopeptide repeats
YIL027C	KRE27	Protein of unknown function; null mutant shows K1 killer toxin resistance
(22) MODULE 25		
Expression regulators		
YBR125C	PTC4	Phosphatase type Two C; Type 2C protein phosphatase
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 DNA; mediates aerobic transcriptional repression of COX5b
YLL019C	KNS1	Nonessential putative protein kinase of unknown cellular role; member of the LAMMER family of protein kinases, which are serine/threonine kinases also capable of phosphorylating tyrosine residues
Module genes		
YFR012W	None	
(23) MODULE 26		

Expression regulators		
YGR123C	PPT1	Protein serine/threonine phosphatase with similarity to human phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth
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 responsive genes, inducing gene expression
YOR337W	TEA1	Mutants are defective in Ty1 Enhancer-mediated Activation; Ty1 enhancer activator
Genotype regulators		
M1_51324_52943		YAL042C-A ERV46(1,0) PTA1(4,0) YAL043C-A GCV3(3,4) YAL044W-A YAL045C YAL046C SPC72(6,3) YAL047W-A GEM1(1,1) YAL049C OAF1(6,1) YAL053W ACS1(2,7) PEX22(3,3)
Module genes		
YAL049C	None	
YGL205W	POX1	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the peroxisomal matrix
YOL147C	PEX11	May promote peroxisomal proliferation by participating in peroxisomal elongation or fission or segregation of peroxisomes to daughter cells; Peroxisomal membrane protein
YER015W	FAA2	Long chain fatty acyl-CoA synthetase; accepts a wider range of acyl chain lengths than Faa1p, preferring C9:0-C13:0; involved in the activation of endogenous pools of fatty acids
YPR128C	ANT1	adenine nucleotide transporter; Adenine Nucleotide Transporter
(24) MODULE 27		
Expression regulators		
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation; shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
YOL100W	PKH2	Pkb-activating Kinase Homologue; Ser/Thr protein kinase
YDL064W	UBC9	SUMO-conjugating enzyme involved in the Smt3p conjugation pathway; nuclear protein required for S- and M-phase cyclin degradation and mitotic control; involved in proteolysis mediated by the anaphase-promoting complex cyclosome (APCC)
YGR108W	CLB1	Involved in mitotic induction; G(sub)2-specific B-type cyclin
YDR296W	MHR1	Protein involved in mitochondrial homologous DNA recombination and in transcription regulation; binds to activation domains of acidic activators; presence in RNA pol II holoenzyme may help recruit an Ssn3p-active form of the holoenzyme to target promoters
Genotype regulators		
M5_99004_99004		RIP1(1,5) YEL025C SNU13(0,1) CUP5(0,0) YEL028W BUD16(0,2) YEL030C-A ECM10(2,0) SPF1(1,0)
Module genes		
YJR036C	HUL4	Protein with similarity to hect domain E3 ubiquitin-protein

		ligases, not essential for viability
YML020W	None	
YLR377C	FBP1	Fructose-1,6-bisphosphatase, required for glucose metabolism
YPL280W	HSP32	Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp31p, Hsp33p, and Sno4p; member of the DJ-1/ThiJ/PfpI superfamily, which includes human DJ-1 involved in Parkinson's disease
YBR250W	None	
YNL295W	None	
(25) MODULE 28		
Expression regulators		
YDR496C	PUF6	member of the PUF protein family; YDR496C
Genotype regulators		
M12_450041_508029		YLR149C-A STM1(0,0) PCD1(0,2) YLR152C ACS2(2,0) RNH203(0,3) YLR154C-G YLR154C-H TAR1(0,0) YLR154W-B YLR154W-C YLR154W-E YLR154W-F ASP3-1(193,529) YLR156C-A YLR156W ASP3-2(193,524) YLR157C-C YLR157W-A YLR157W-C ASP3-3(193,529) YLR159C-A YLR159W ASP3-4(193,529) YLR161W YLR162W YLR162W-A YLR162W- MAS1(3,5) YLR163W-A YLR164W PUS5(3,1) SEC10(7,11) RPS31(0,11) YLR168C YLR169W APS1(1,2) YLR171W DPH5(0,5) YLR173W IDP2(0,3) CBF5(1,2) RFX1(13,11) YLR177W TFS1(1,3) YLR179C SAM1(0,10) VTA1(4,4)
Module genes		
YLR156W	None	
YLR158C	ASP3-3	Cell-wall L-asparaginase II, involved in asparagine catabolism; expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C
YLR161W	None	
YLR155C	ASP3-1	Cell-wall L-asparaginase II, involved in asparagine catabolism; expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C
YCL073C	None	
YLR160C	ASP3-4	Cell-wall L-asparaginase II, involved in asparagine catabolism; expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C
YLR159W	None	
YLR157C	ASP3-2	Cell-wall L-asparaginase II, involved in asparagine catabolism; expression is induced during nitrogen starvation; four copies of ASP3 are present in the genome reference strain S288C
(26) MODULE 29		
Expression regulators		
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 following phosphorylation by Ime2p
YDR277C	MTH1	Negative regulator of the glucose-sensing signal transduction

		pathway, required for repression of transcription by Rgt1p; interacts with Rgt1p and the Snf3p and Rgt2p glucose sensors; phosphorylated by Yck1p, triggering Mth1p degradation
YPL016W	SWI1	Global transcription activator that acts in complex with Snf2p, Snf5p, Snf6p, and Swi3p to assist gene-specific activators; involved in the regulation of expression of many genes, including ADH1, ADH2, GAL1, HO, INO1 and SUC2; Zinc-finger transcription factor
Module genes		
YCR101C	None	
YGR156W	PTI1	Pta1p Interacting protein
YOR392W	None	
YGL091C	NBP35	NBP35 encodes an essential evolutionary conserved protein with homology to bacterial partitioning ATPases; 35 kDa nucleotide binding protein
YPR116W	None	
YGR226C	None	
YJL038C	None	
YMR042W	ARG80	Regulator of arginine-responsive genes with ARG81 and ARG82; transcription factor
YPR014C	None	
YIL060W	None	
YHL037C	None	
YOR173W	DCS2	Non-essential protein containing a HIT (histidine triad) motif; regulated by Msn2p, Msn4p, and the Ras-cAMP-cAPK signalling pathway, transcript accumulates under glucose limitation, similar to Dcs1p
YNL054W	VAC7	Integral vacuolar membrane protein; may function to regulate Fab1p kinase activity
YPR067W	ISA2	Protein required for maturation of mitochondrial and cytosolic Fe/S proteins, localizes to the mitochondrial intermembrane space, overexpression of ISA2 suppresses grx5 mutations
YMR326C	None	
(27) MODULE 30		
Expression regulators		
YOL100W	PKH2	Pkb-activating Kinase Homologue; Ser/Thr protein kinase
YJL005W	CYR1	Required for START A of cell cycle, and glucose and nitrogen repression of sporulation; adenylate cyclase
YDR195W	REF2	RNA-binding protein involved in the cleavage step of mRNA 3'-end formation prior to polyadenylation; also involved in snoRNA maturation
YGL071W	RCS1	Transcription factor that binds the consensus site PyPuCACCCPu, involved in iron homeostasis and cell size regulation; activates the expression of target genes in response to low-iron conditions
YPL016W	SWI1	Global transcription activator that acts in complex with Snf2p, Snf5p, Snf6p, and Swi3p to assist gene-specific activators; involved in the regulation of expression of many genes, including ADH1, ADH2, GAL1, HO, INO1 and SUC2; Zinc-

		finger transcription factor
YNL031C	HHT2	One of two identical histone H3 proteins (see also HHT1); core histone required for chromatin assembly, involved in heterochromatin-mediated telomeric and HM silencing; regulated by acetylation, methylation, and mitotic phosphorylation
Genotype regulators		
M12_1056097_1056103		FMP27(8,6) YLR455W YLR456W NBP1(2,5) YLR458W GAB1(1,5) YLR460C PAU4(1,435)
Module genes		
YPR203W	None	
YFL068W	None	
YER190W	YRF1-2	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p
YJL225C	None	
YLR434C	None	
YPL283C	YRF1-7	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p
YLL067C	None	
YEL076W-C	None	
YEL077C	None	
YIL177C	None	
YFL066C	None	
YLR463C	None	
YBL109W	None	
YDR544C	None	
YLR466W	YRF1-4	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p
YJR115W	None	
YLR462W	None	
YEL076C-A	None	
YHR218W	None	
YML133C	None	
YBL111C	None	
YHL049C	None	
YNL339C	YRF1-6	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p
YLR467W	YRF1-5	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p
YEL075C	None	
YNL338W	None	
YHR219W	None	

YER189W	None	
YFL064C	None	
YBL112C	None	
YLR465C	BSC3	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 100% of YLR465C overlaps the uncharacterized ORF YLR464W and 86% of YLR465C overlaps the verified gene YRF1-4
YPR202W	None	
YEL074W	None	
YFL067W	None	
YLR464W	None	
YLL066C	None	
YHL050C	None	
YDR545W	YRF1-1	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p
YEL076C	None	
YFL065C	None	
YBL113C	None	
YGR296W	YRF1-3	Helicase encoded by the Y' element of subtelomeric regions, highly expressed in the mutants lacking the telomerase component TLC1; potentially phosphorylated by Cdc28p
(28) MODULE 31		
Expression regulators		
YGL229C	SAP4	Protein required for function of the Sit4p protein phosphatase, member of a family of similar proteins that form complexes with Sit4p, including Sap155p, Sap185p, and Sap190p
YIL033C	BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation
YDR523C	SPS1	dispensable for mitosis, involved in middle/late stage of meiosis, required for spore wall formation; serine/threonine kinase homologous to Ste20p; expressed in middle/late meiosis
YGR156W	PTI1	Pta1p Interacting protein
YMR179W	SPT21	Protein required for normal transcription at several loci including HTA2-HTB2 and HHF2-HHT2, but not required at the other histone loci; functionally related to Spt10p
YNL030W	HHF2	One of two identical histone H4 proteins (see also HHF1); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity
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 principal activation function of the complex
Module genes		
YMR325W	None	

YIL175W	None	
YIR041W	None	
YLR461W	PAU4	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme
YDR542W	None	
YLL064C	None	
YIR040C	None	
YGR294W	None	
YJL223C	PAU1	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme
YCR103C	None	
YOR394W	None	
YGL261C	None	
YKL223W	None	
YAL068C	None	
YHL046C	None	
YGL260W	None	
YIL174W	None	
YPL282C	None	
YIL176C	None	
YOL161C	None	
(29) MODULE 33		
Expression regulators		
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation; shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
YCL026C-A	FRM2	Protein of unknown function, involved in the integration of lipid signaling pathways with cellular homeostasis
YDL064W	UBC9	SUMO-conjugating enzyme involved in the Smt3p conjugation pathway; nuclear protein required for S- and M-phase cyclin degradation and mitotic control; involved in proteolysis mediated by the anaphase-promoting complex cyclosome (APCC)
YPL026C	SKS1	multicopy suppressor of snf3 and grr1 mutants; serine/threonine protein kinase homologous to Ran1p
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; expression is induced in G1 by bound SBF
YDL101C	DUN1	Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and Sml1p, and transient G2/M arrest after DNA damage; also regulates postreplicative DNA

		repair
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
Module genes		
YDL218W	None	
YOL156W	HXT11	Putative hexose transporter that is nearly identical to Hxt9p, has similarity to major facilitator superfamily (MFS) transporters and is involved in pleiotropic drug resistance
YMR034C	None	
YGR213C	RTA1	involved in 7-aminocholesterol resistance
YCR021C	HSP30	Hydrophobic plasma membrane localized, stress-responsive protein that negatively regulates the H(+)-ATPase Pma1p; induced by heat shock, ethanol treatment, weak organic acid, glucose limitation, and entry into stationary phase
YGR286C	BIO2	Biotin synthase, catalyzes the conversion of dethiobiotin to biotin, which is the last step of the biotin biosynthesis pathway; complements E. coli bioB mutant
YLR445W	None	
YLL063C	AYT1	Acetyltransferase; catalyzes trichothecene 3-O-acetylation, suggesting a possible role in trichothecene biosynthesis
YNL336W	COS1	Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins
YPL163C	SVS1	Cell wall and vacuolar protein, required for wild-type resistance to vanadate
YIR043C	None	
YAR060C	None	
YIL085C	KTR7	Putative mannosyltransferase involved in protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family
YBR045C	GIP1	Meiosis-specific protein proposed to be a regulatory subunit of the protein phosphatase Glc7p, required for spore wall formation and proper septin organization
YNL289W	PCL1	Pho85 cyclin of the Pcl1,2-like subfamily, involved in entry into the mitotic cell cycle and regulation of morphogenesis, localizes to sites of polarized cell growth
YDR276C	PMP3	plasma membrane protein involved in salt tolerance; hypothetical transmembrane protein
YDR540C	None	
YML131W	None	
YNL334C	SNO2	Protein of unknown function, nearly identical to Sno3p; expression is induced before the diauxic shift and also in the absence of thiamin
YGR295C	COS6	Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins
YMR206W	None	
YPL272C	None	
YJR161C	COS5	Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins
YDL248W	COS7	Protein of unknown function, member of a family of conserved,

		often subtelomerically-encoded proteins
YLR235C	None	
YGR259C	None	
YIR044C	None	
YDR419W	RAD30	DNA polymerase eta, involved in the predominantly error-free bypass replication of DNA lesions; homolog of human XPV and bacterial DinB proteins
YBR302C	COS2	Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins
YLL047W	None	
YIL120W	QDR1	Quinidine Resistance; MFS-MDR transporter
YKL003C	MRP17	Mitochondrial ribosomal protein of the small subunit; MRP17 exhibits genetic interactions with PET122, encoding a COX3-specific translational activator
YEL049W	PAU2	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme
YOL146W	PSF3	Subunit of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which binds to DNA replication origins and facilitates assembly of the DNA replication machinery
YML132W	COS3	Protein involved in salt resistance; interacts with sodium:hydrogen antiporter Nha1p; member of a family of conserved, often subtelomerically-encoded proteins
YFL062W	COS4	Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins
YPL089C	RLM1	serum response factor-like protein that may function downstream of MPK1 (SLT2) MAP-kinase pathway; serum response factor-like protein
YPL281C	ERR2	Protein of unknown function, has similarity to enolases
YHL048W	COS8	Nuclear membrane protein, member of a family of conserved, often subtelomerically-encoded proteins; regulation suggests a potential role in the unfolded protein response
YPR054W	SMK1	Mitogen-activated protein kinase required for spore morphogenesis that is expressed as a middle sporulation-specific gene
YNR074C	None	
YPL096W	PNG1	de-N-glycosylation enzyme; peptide:N-glycanase
YEL070W	DSF1	None
YDR400W	URH1	uridine nucleosidase (uridine ribohydrolase); EC 3.2.2.3
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
YIL162W	SUC2	None
YGR189C	CRH1	Putative glycosidase of the cell wall, may have a role in cell wall architecture
YOR302W	None	
YOR222W	ODC2	Mitochondrial inner membrane transporter, exports 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol

		for use in lysine and glutamate biosynthesis and in lysine catabolism
YNL014W	HEF3	Translational elongation factor EF-3; paralog of YEF3 and member of the ABC superfamily; stimulates EF-1 alpha-dependent binding of aminoacyl-tRNA by the ribosome; normally expressed in zinc deficient cells
YOL065C	INP54	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase with a role in secretion, localizes to the endoplasmic reticulum via the C-terminal tail; lacks the Sac1 domain and proline-rich region found in the other 3 INP proteins
(30) MODULE 35		
Expression regulators		
YIL033C	BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation
YMR228W	MTF1	Mitochondrial RNA polymerase sigma-like specificity factor required for promoter recognition, interacts with mitochondrial core polymerase Rpo41p, imported into mitochondria via a novel process requiring most of the Mtf1p sequence
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)-Cys(6) binuclear cluster domain type
YHR136C	SPL2	Protein with similarity to cyclin-dependent kinase inhibitors, overproduction suppresses a plc1 null mutation; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
Module genes		
YLR308W	CDA2	Required for proper formation of the ascospore wall; Chitin Deacetylase
YBR051W	None	
YKL205W	LOS1	Nuclear pore protein involved in nuclear export of pre-tRNA
YPR179C	HDA3	Subunit of a possibly tetrameric trichostatin A-sensitive class II histone deacetylase complex that contains an Hda1p homodimer and an Hda2p-Hda3p heterodimer; required for the activity of the complex; has similarity to Hda2p
YMR018W	None	
YBR018C	GAL7	Galactose-1-phosphate uridyl transferase, synthesizes glucose-1-phosphate and UDP-galactose from UDP-D-glucose and alpha-D-galactose-1-phosphate in the second step of galactose catabolism
YMR265C	None	
YPL209C	IPL1	Aurora kinase involved in regulating kinetochore-microtubule attachments, associates with Sli5p, which stimulates Ipl1p kinase activity and promotes its association with the mitotic spindle, potential Cdc28p substrate
YIR001C	SGN1	Cytoplasmic RNA-binding protein, contains an RNA recognition motif (RRM); may have a role in mRNA translation, as suggested by genetic interactions with genes encoding

		proteins involved in translational initiation
(31) MODULE 36		
Expression regulators		
YIR017C	MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism
YDR225W	HTA1	One of two nearly identical (see also HTA2) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p
YMR019W	STB4	Protein that binds Sin3p in a two-hybrid assay
YJL187C	SWE1	Protein kinase that regulates the G2/M transition by inhibition of Cdc28p kinase activity; localizes to the nucleus and to the daughter side of the mother-bud neck; homolog of S. pombe Wee1p; potential Cdc28p substrate
YHR005C	GPA1	Alpha subunit of G protein coupled to mating factor receptors, involved in the mating pheromone signal transduction pathway; component of pheromone response pathway common to both a and alpha cells
Genotype regulators		
M4_1022764_1039379		PMP3(0,3) MTH1(0,5) YDR278C RNH202(0,2) RRP45(0,0) PHM6(0,2) YDR282C GCN2(2,0) DPP1(0,0) ZIP1(0,0) YDR286C YDR287W NSE3(1,0) RTT103(2,0) YDR290W YDR291W SRP101(1,1) SSD1(0,0)
Module genes		
YOR202W	HIS3	Imidazoleglycerol-phosphate dehydratase, catalyzes the sixth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control via Gcn4p
YIL164C	NIT1	Nitrilase, member of the widely found nitrilase branch (EC:3.5.5.1) of the nitrilase superfamily
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)-Cys(6) binuclear cluster domain type
YDL066W	IDP1	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes
YBR147W	None	
YLR092W	SUL2	High affinity sulfate permease; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates
YMR062C	ECM40	Mitochondrial ornithine acetyltransferase, catalyzes the fifth step in arginine biosynthesis; also possesses acetylglutamate synthase activity, regenerates acetylglutamate while forming ornithine
YCL030C	HIS4	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis

YJR111C	None	
YNL104C	LEU4	Alpha-isopropylmalate synthase (2-isopropylmalate synthase); the main isozyme responsible for the first step in the leucine biosynthesis pathway
YFR030W	MET10	Subunit alpha of assimilatory sulfite reductase, which is responsible for the conversion of sulfite into sulfide
YBR047W	FMP23	The authentic, non-tagged protein was localized to the mitochondria
YKL218C	SRY1	3-hydroxyaspartate dehydratase, deaminates L-threo-3-hydroxyaspartate to form oxaloacetate and ammonia; required for survival in the presence of hydroxyaspartate
YJL088W	ARG3	Ornithine carbamoyltransferase (carbamoylphosphate:L-ornithine carbamoyltransferase), catalyzes the sixth step in the biosynthesis of the arginine precursor ornithine
YDR034C	LYS14	Transcriptional activator involved in regulation of genes of the lysine biosynthesis pathway; requires 2-aminoadipate semialdehyde as co-inducer
YOL140W	ARG8	Acetylornithine aminotransferase, catalyzes the fourth step in the biosynthesis of the arginine precursor ornithine
YMR095C	SNO1	Protein of unconfirmed function, involved in pyridoxine metabolism; expression is induced during stationary phase; forms a putative glutamine amidotransferase complex with Snz1p, with Sno1p serving as the glutaminase
YGL125W	MET13	Isozyme of methylenetetrahydrofolate reductase, catalyzes the reduction of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate in the methionine biosynthesis pathway
YGL117W	None	
YOR303W	CPA1	Small subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; translationally regulated by an attenuator peptide encoded by YOR302W within the CPA1 mRNA 5'-leader
YFR055W	None	
YHR018C	ARG4	Argininosuccinate lyase, catalyzes the final step in the arginine biosynthesis pathway
YDR354W	TRP4	anthranilate phosphoribosyl transferase
YOR203W	None	
YJR155W	AAD10	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role
YOL118C	None	
YMR094W	CTF13	Subunit of the CBF3 complex, which binds to the CDE III element of centromeres, bending the DNA upon binding, and may be involved in sister chromatid cohesion during mitosis
YDR158W	HOM2	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis
YOR184W	SER1	phosphoserine transaminase
YHR017W	YSC83	similar to S. douglasii YSD83
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation;

		shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
YER052C	HOM3	Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis
YOR221C	MCT1	Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid synthase that produces intermediates for phospholipid remodeling
YIL003W	CFD1	Highly conserved, putative P-loop ATPase localized in the cytoplasm; has a potential role in assembly of iron-sulfur clusters in proteins
YDL131W	LYS21	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p
YNL036W	NCE103	Protein with a carbonic anhydrase activity, involved in non-classical protein export pathway
YNL277W	MET2	L-homoserine-O-acetyltransferase, catalyzes the conversion of homoserine to O-acetyl homoserine which is the first step of the methionine biosynthetic pathway
YGL184C	STR3	Cystathionine beta-lyase, converts cystathionine into homocysteine
YJR137C	ECM17	Sulfite reductase beta subunit, involved in amino acid biosynthesis, transcription repressed by methionine
YFR025C	HIS2	Histidinolphosphatase, catalyzes the eighth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control
YIL056W	None	
YBR218C	PYC2	converts pyruvate to oxaloacetate; pyruvate carboxylase
YPR145W	ASN1	Asparagine synthetase, isozyme of Asn2p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway
YKL211C	TRP3	anthranilate synthase Component II and indole-3-phosphate (multifunctional enzyme)
YGR267C	FOL2	GTP-cyclohydrolase I, catalyzes the first step in the folic acid biosynthetic pathway
YHR162W	None	
YGL202W	ARO8	Aromatic aminotransferase, expression is regulated by general control of amino acid biosynthesis
YDR106W	ARP10	Actin-related protein
YGL114W	None	
YNR069C	BSC5	Protein of unknown function, ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression
YJR109C	CPA2	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor

YOR044W	None	
YOR108W	LEU9	Alpha-isopropylmalate synthase II (2-isopropylmalate synthase), catalyzes the first step in the leucine biosynthesis pathway; the minor isozyme, responsible for the residual alpha-IPMS activity detected in a leu4 null mutant
YJR148W	BAT2	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase
YIL116W	HIS5	Histidinol-phosphate aminotransferase, catalyzes the seventh step in histidine biosynthesis; responsive to general control of amino acid biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts
YDL198C	GGC1	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family; (putative) mitochondrial carrier protein
YPR167C	MET16	3'-phosphoadenylsulfate reductase, reduces 3'-phosphoadenylyl sulfate to adenosine-3',5'-bisphosphate and free sulfite using reduced thioredoxin as cosubstrate, involved in sulfate assimilation and methionine metabolism
YOL119C	MCH4	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma membrane; mutant is not deficient in monocarboxylate transport
YKR069W	MET1	S-adenosyl-L-methionine uroporphyrinogen III transmethylase, involved in sulfate assimilation, methionine metabolism, and siroheme biosynthesis
YJL213W	None	
YGR239C	PEX21	Peroxin; Pex18p and Pex21p are partially functionally redundant
YGR029W	ERV1	Flavin-linked sulfhydryl oxidase localized to the mitochondrial intermembrane space, has a role in the maturation of cytosolic iron-sulfur proteins; ortholog of human hepatopoietin (ALR)
YGL224C	SDT1	Pyrimidine nucleotidase; overexpression suppresses the 6-AU sensitivity of transcription elongation factor S-II, as well as resistance to other pryimidine derivatives
YDR481C	PHO8	Repressible alkaline phosphatase, a glycoprotein localized to the vacuole; regulated by levels of inorganic phosphate and by a system consisting of Pho4p, Pho9p, Pho80p, Pho81p and Pho85p; dephosphorylates phosphotyrosyl peptides
YDL025C	None	
YOR337W	TEA1	Mutants are defective in Ty1 Enhancer-mediated Activation; Ty1 enhancer activator
YPR059C	None	
YLR027C	AAT2	Cytosolic aspartate aminotransferase, involved in nitrogen metabolism; localizes to peroxisomes in oleate-grown cells
YBR145W	ADH5	alcohol dehydrogenase isoenzyme V
YOL058W	ARG1	Arginosuccinate synthetase, catalyzes the formation of L-argininosuccinate from citrulline and L-aspartate in the arginine biosynthesis pathway; potential Cdc28p substrate
YLL027W	ISA1	Mitochondrial matrix protein involved in biogenesis of the iron-

		sulfur (Fe/S) cluster of Fe/S proteins, isa1 deletion causes loss of mitochondrial DNA and respiratory deficiency; depletion reduces growth on nonfermentable carbon sources
YGL059W	None	
YML116W	ATR1	Multidrug efflux pump of the major facilitator superfamily, required for resistance to aminotriazole and 4-nitroquinoline-N-oxide
YCR023C	None	
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 genes
YPL135W	ISU1	Conserved protein of the mitochondrial matrix, performs a scaffolding function during assembly of iron-sulfur clusters, interacts physically and functionally with yeast frataxin (Yfh1p); isu1 isu2 double mutant is inviable
YMR097C	MTG1	Peripheral GTPase of the mitochondrial inner membrane, essential for respiratory competence, likely functions in assembly of the large ribosomal subunit, has homologs in plants and animals
YDR127W	ARO1	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids
YOR130C	ORT1	Ornithine transporter of the mitochondrial inner membrane, exports ornithine from mitochondria as part of arginine biosynthesis; human ortholog is associated with hyperammonaemia-hyperornithinaemia-homocitrullinuria (HHH) syndrome
YER128W	None	
YLR267W	BOP2	Protein of unknown function, overproduction suppresses a pam1 slv3 double null mutation
YDR035W	ARO3	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by phenylalanine
YPL188W	POS5	Mitochondrial NADH kinase, phosphorylates NADH; also phosphorylates NAD(+) with lower specificity; required for the response to oxidative stress
YDL054C	MCH1	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma membrane; mutant is not deficient in monocarboxylate transport
YNL311C	None	
YEL063C	CAN1	arginine permease
YOL064C	MET22	Bisphosphate-3'-nucleotidase, involved in salt tolerance and methionine biogenesis; dephosphorylates 3'-phosphoadenosine-5'-phosphate and 3'-phosphoadenosine-5'-phosphosulfate, intermediates of the sulfate assimilation pathway
YHR071W	PCL5	Cyclin, interacts with Pho85p cyclin-dependent kinase (Cdk), induced by Gcn4p at level of transcription, specifically required for Gcn4p degradation, may be sensor of cellular protein biosynthetic capacity

YMR096W	SNZ1	Snooze: stationary phase-induced gene family; involved in cellular response to nutrient limitation and growth arrest; encodes highly conserved 35 kDa protein that shows increased expression after entry into stationary phase
YJR130C	STR2	Cystathionine gamma-synthase, converts cysteine into cystathionine
YER024W	YAT2	Carnitine acetyltransferase; has similarity to Yat1p, which is a carnitine acetyltransferase associated with the mitochondrial outer membrane
YER040W	GLN3	Transcriptional activator of genes regulated by nitrogen catabolite repression (NCR), localization and activity regulated by quality of nitrogen source
YDL057W	None	
YBR043C	QDR3	Protein of unknown function, may have a role in drug resistance
YFL028C	CAF16	CCR4 associated factor; ABC ATPase
YCL026C-A	FRM2	Protein of unknown function, involved in the integration of lipid signaling pathways with cellular homeostasis
YPL092W	SSU1	putative sulfite pump; major facilitator superfamily protein
YGL180W	ATG1	Protein serine/threonine kinase, required for autophagy and for the cytoplasm-to-vacuole targeting (Cvt) pathway
YER069W	ARG5,6	Bifunctional enzyme with N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate kinase activities, catalyzes the second and third steps in the biosynthesis of the arginine precursor ornithine; forms a complex with Arg2p
YBR248C	HIS7	Imidazole glycerol phosphate synthase (glutamine amidotransferase:cyclase), catalyzes the fifth and sixth steps of histidine biosynthesis and also produces 5-aminoimidazole-4-carboxamide ribotide (AICAR), a purine precursor
YBR256C	RIB5	Riboflavin synthase; catalyzes the last step of the riboflavin biosynthesis pathway
YLR089C	ALT1	putative alanine transaminase (glutamyc pyruvic transaminase)
YPL033C	None	
YGL186C	TPN1	Pyridoxine transporter
YCR100C	None	
YHR029C	None	
YDR487C	RIB3	3,4-dihydroxy-2-butanone-4-phosphate synthase (DHBP synthase), required for riboflavin biosynthesis from ribulose-5-phosphate, also has an unrelated function in mitochondrial respiration
YER175C	TMT1	Trans-aconitate methyltransferase
YJL200C	None	
YDL182W	LYS20	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p
YJL071W	ARG2	Acetylglutamate synthase (glutamate N-acetyltransferase), mitochondrial enzyme that catalyzes the first step in the biosynthesis of the arginine precursor ornithine; forms a complex with Arg5,6p

YPL250C	ICY2	Protein that interacts with the cytoskeleton and is involved in chromatin organization and nuclear transport, interacts genetically with TCP1 and ICY1; potential Cdc28p substrate
YIR034C	LYS1	Saccharopine dehydrogenase (NAD+, L-lysine-forming), catalyzes the conversion of saccharopine to L-lysine, which is the final step in the lysine biosynthesis pathway
YGR288W	MAL13	MAL-activator protein, part of complex locus MAL1; nonfunctional in genomic reference strain S288C
(32) MODULE 37		
Expression regulators		
YBL066C	SEF1	Suppressor of Essential Function; putative transcription factor
YPL075W	GCR1	Transcriptional activator of genes involved in glycolysis, functions and interacts with Gcr2p
YAL017W	PSK1	One of two (see also PSK2) PAS domain containing S/T protein kinases; coordinately regulates protein synthesis and carbohydrate metabolism and storage in response to a unknown metabolite that reflects nutritional status
YJR127C	ZMS1	Zinc-finger protein that localizes to the nucleus, putative transcriptional regulator of ALD6
YJR147W	HMS2	Protein with similarity to heat shock transcription factors; overexpression suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 homozygous null mutant
YKR099W	BAS1	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways
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 utilizing Ire1p, Trl1p and Ada5p facilitates efficient Hac1p synthesis
Module genes		
YML090W	None	
YLR294C	None	
YDR501W	PLM2	Plasmid Maintenance; PLasmid Maintenance
YBR039W	ATP3	Gamma subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
YGL187C	COX4	Subunit IV of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; N-terminal 25 residues of precursor are cleaved during mitochondrial import
YKL085W	MDH1	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle
YJR080C	FMP26	The authentic, non-tagged protein was localized to the mitochondria
YLR395C	COX8	Subunit VIII of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain
YML002W	None	

YDR178W	SDH4	Membrane anchor subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone
YNL037C	IDH1	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle
YLR038C	COX12	Subunit VIb of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; required for assembly of fully active cytochrome c oxidase but not required for activity after assembly
YGR174C	CBP4	Essential for the expression and activity of ubiquinol-cytochrome c reductase; ubiquinol--cytochrome-c reductase assembly factor
YGR182C	None	
YBL030C	PET9	Major ADP/ATP carrier of the mitochondrial inner membrane, exchanges cytosolic ADP for mitochondrially synthesized ATP; Pet9p and Sal1p have an overlapping function critical for viability
YLR295C	ATP14	Subunit h of the F0 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
YKL141W	SDH3	Cytochrome b subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone
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 principal activation function of the complex
YML120C	NDI1	NADH:ubiquinone oxidoreductase, transfers electrons from NADH to ubiquinone in the respiratory chain but does not pump protons, in contrast to the higher eukaryotic multisubunit respiratory complex I which is absent in S. cerevisiae
YGL188C	None	
YJR077C	MIR1	Mitochondrial phosphate carrier, imports inorganic phosphate into mitochondria; functionally redundant with Pic2p but more abundant than Pic2 under normal conditions
YPR020W	ATP20	Subunit g of the mitochondrial F1F0 ATP synthase, which is a large enzyme complex required for ATP synthesis; associated only with the dimeric form of ATP synthase
YNL052W	COX5A	Subunit Va of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; predominantly expressed during aerobic growth while its isoform Vb (Cox5Bp) is expressed during anaerobic growth
YMR256C	COX7	Subunit VII of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain
YFR033C	QCR6	ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa)
YKR016W	FMP13	The authentic, non-tagged protein was localized to the mitochondria
YEL024W	RIP1	oxidizes ubiquinol at center P in the protonmotive Q cycle mechanism, transferring one electron to cytochrome c1 and

		generating a low-potential ubisemiquinone anion which reduces the low-potential cytochrome b-566 heme group; Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex
YDR148C	KGD2	Dihydrolipoyl transsuccinylase, a component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to succinyl-CoA
YML081C-A	ATP18	Subunit of the mitochondrial F1F0 ATP synthase, which is a large enzyme complex required for ATP synthesis; termed subunit I or subunit j; does not correspond to known ATP synthase subunits in other organisms
YGR183C	QCR9	7.3 kDa subunit 9 of the ubiquinol cytochrome c oxidoreductase complex
YBR085W	AAC3	Mitochondrial inner membrane ADP/ATP translocator, exchanges cytosolic ADP for mitochondrially synthesized ATP; expressed under anaerobic conditions; similar to Pet9p and Aac1p; has roles in maintenance of viability and in respiration
YPL271W	ATP15	Epsilon subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
YGL191W	COX13	Subunit VIa of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; not essential for cytochrome c oxidase activity but may modulate activity in response to ATP
YMR002W	None	
YKL148C	SDH1	Flavoprotein subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone
YLR299W	ECM38	Gamma-glutamyltranspeptidase, major glutathione-degrading enzyme; expression induced mainly by nitrogen starvation
YBL099W	ATP1	Alpha subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
YHR001W-A	QCR10	8.5 kDa subunit of the ubiqunol-cytochrome c oxidoreductase complex
YLR168C	None	
YJL166W	QCR8	Ubiquinol cytochrome-c reductase subunit 8 (11 kDa protein)
YJR120W	None	
YOR065W	CYT1	Cytochrome c1
YDL004W	ATP16	Delta subunit of the central stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
YIL125W	KGD1	Component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a key step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA
YJL103C	None	
YDL181W	INH1	Protein that inhibits ATP hydrolysis by the F1F0-ATP synthase, inhibitory function is enhanced by stabilizing proteins Stf1p and

		Stf2p; has similarity to Stf1p and both Inh1p and Stf1p exhibit the potential to form coiled-coil structures
YLR304C	ACO1	Mitochondrial aconitase, required for the tricarboxylic acid (TCA) cycle; mutation leads to glutamate auxotrophy
YKL016C	ATP7	Subunit d of the stator stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
YLL041C	SDH2	Iron-sulfur protein subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer of electrons to ubiquinone
YDR298C	ATP5	Subunit 5 of the stator stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis; homologous to bovine subunit OSCP (oligomycin sensitivity-conferring protein)
YDR322C-A	TIM11	Protein associated with mitochondrial ATP synthase; essential for dimeric state of ATP synthase. ; subunit e of mitochondrial F1F0-ATPase
YBL100C	None	
YHR051W	COX6	Subunit VI of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; expression is regulated by oxygen levels
YJL102W	MEF2	mitochondrial elongation factor G-like protein
YPR191W	QCR2	40 kDa ubiquinol cytochrome-c reductase core protein 2
YCL058C	FYV5	Protein of unknown function, required for survival upon exposure to K1 killer toxin; involved in ion homeostasis
YJR121W	ATP2	Beta subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
YDR377W	ATP17	Subunit f of the F0 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
YDL067C	COX9	Subunit VIIa of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain
YBL045C	COR1	Core subunit of the ubiquinol-cytochrome c reductase complex (bc1 complex), which is a component of the mitochondrial inner membrane electron transport chain
YPL078C	ATP4	Subunit b of the stator stalk of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis
(33) MODULE 38		
Expression regulators		
YOR304W	ISW2	Member of the imitation-switch (ISWI) class of ATP-dependent chromatin remodeling complexes; ATPase component that, with Itc1p, forms a complex required for repression of a-specific genes, INO1, and early meiotic genes during mitotic growth
YIL147C	SLN1	Histidine kinase osmosensor that regulates a MAP kinase cascade; transmembrane protein with an intracellular kinase domain that signals to Ypd1p and Ssk1p, thereby forming a phosphorelay system similar to bacterial two-component regulators

YIL147C	SLN1	Histidine kinase osmosensor that regulates a MAP kinase cascade; transmembrane protein with an intracellular kinase domain that signals to Ypd1p and Ssk1p, thereby forming a phosphorelay system similar to bacterial two-component regulators
YIL147C	SLN1	Histidine kinase osmosensor that regulates a MAP kinase cascade; transmembrane protein with an intracellular kinase domain that signals to Ypd1p and Ssk1p, thereby forming a phosphorelay system similar to bacterial two-component regulators
YOR230W	WTM1	WD repeat containing transcriptional modulator 1; Transcriptional modulator
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 responsive genes, inducing gene expression
Genotype regulators		
M4_85846_106892		ARF1(0,3) YDL193W SNF3(12,2) SEC31(6,4) YDL196W ASF2(9,4) GGC1(0,4) YDL199C MGT1(3,0) TRM8(0,4) MRPL11(0,4) YDL203C RTN2(0,5) HEM3(0,5) YDL206W GLE1(4,5) NHP2(1,2) CWC2(1,2) UGA4(1,9) YDL211C SHR3(1,3) NOP6(0,3)
Module genes		
YFL002W-A	None	
YBL005W-B	None	
YBL101W-B	None	
YMR046C	None	
YLR035C-A	None	
YHR214C-B	None	
YFL035C-A	None	
YDL230W	PTP1	phosphotyrosine-specific protein phosphatase
YBL107W-A	None	
YMR050C	None	
YDR283C	GCN2	Protein kinase, phosphorylates the alpha-subunit of translation initiation factor eIF2 (Sui2p) in response to starvation; activated by uncharged tRNAs and the Gcn1p-Gcn20p complex
YCR018C-A	None	
YJR026W	None	
YEL069C	HXT13	Protein of unknown function with similarity to hexose transporter family members, expression is induced by low levels of glucose and repressed by high levels of glucose
YLR334C	None	
YMR158C-B	None	
YCR032W	BPH1	Protein homologous to human Chediak-Higashi syndrome protein and murine beige gene, which are implicated in disease syndromes due to defective lysosomal trafficking
YDR170W-A	None	
YDR034C-A	None	

YER160C	None	
YML039W	None	
YJR039W	None	
YAL001C	TFC3	transcription factor tau (TFIIIC) subunit 138
YER138W-A	None	
YJR027W	None	
YBR013C	None	
YKL215C	None	
YBR012W-B	None	
YBL005W-A	None	
YML049C	RSE1	RNA splicing and ER to Golgi transport; involved in secretion and RNA splicing
YMR046W-A	None	
YMR308C	PSE1	Karyopherin/importin that interacts with the nuclear pore complex; acts as the nuclear import receptor for specific proteins, including Pdr1p, Yap1p, Ste12p, and Aft1p
YAR009C	None	
YGR122C-A	None	
YCL019W	None	
YDL246C	SOR2	Protein of unknown function, computational analysis of large-scale protein-protein interaction data suggests a possible role in fructose or mannose metabolism
YIL015C-A	None	
YHR102W	KIC1	Protein kinase of the PAK/Ste20 kinase family, required for cell integrity possibly through regulating 1,6-beta-glucan levels in the wall; physically interacts with Cdc31p (centrin), which is a component of the spindle pole body
YML040W	None	
YOL106W	None	
YJL007C	None	
YMR176W	ECM5	Non-essential protein of unknown function, contains ATP/GTP-binding site motif A; null mutant exhibits cellular volume up to four times greater than wild-type, also large drooping buds with elongated necks
YER138C	None	
YMR045C	None	
YML045W	None	
YJR029W	None	
YAR029W	None	
YMR128W	ECM16	Essential DEAH-box ATP-dependent RNA helicase specific to the U3 snoRNP, predominantly nucleolar in distribution, required for 18S rRNA synthesis
YDL243C	AAD4	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase, involved in the oxidative stress response
YAL002W	VPS8	involved in vacuolar protein sorting; required for localization and trafficking of the CPY sorting receptor; Vps8p is a

		membrane-associated hydrophilic protein which contains a C-terminal cysteine-rich region that conforms to the H2 variant of the RING finger Zn2+ binding motif.
YOL051W	GAL11	Component of the Mediator complex; interacts with RNA polymerase II and the general transcription factors to form the RNA polymerase II holoenzyme; affects transcription by acting as target of activators and repressors
YGL094C	PAN2	Essential subunit of the Pan2p-Pan3p poly(A)-ribonuclease complex, which acts to control poly(A) tail length and regulate the stoichiometry and activity of postreplication repair complexes
YHL045W	None	
YCL069W	None	
YLR225C	None	
YPR002C-A	None	
(34) MODULE 39		
Expression regulators		
YBR274W	CHK1	checkpoint kinase 1; homolog of the S. pombe and mammalian Chk1 checkpoint kinases; Protein kinase Chk1
YHL027W	RIM101	Transcriptional activator required for entry into meiosis, has similarity to the Aspergillus Phenotype-response regulator PacC and the Yarrowia proteinase YlRim1010p; Meiotic regulatory protein; Cys-His zinc fingers
YAL017W	PSK1	One of two (see also PSK2) PAS domain containing S/T protein kinases; coordinately regulates protein synthesis and carbohydrate metabolism and storage in response to a unknown metabolite that reflects nutritional status
YDR034C	LYS14	Transcriptional activator involved in regulation of genes of the lysine biosynthesis pathway; requires 2-aminoadipate semialdehyde as co-inducer
YDR496C	PUF6	member of the PUF protein family; YDR496C
YNL180C	RHO5	Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, likely involved in protein kinase C (Pkc1p)-dependent signal transduction pathway that controls cell integrity
Module genes		
YBR140C	IRA1	GTPase-activating protein that negatively regulates RAS by converting it from the GTP- to the GDP-bound inactive form, required for reducing cAMP levels under nutrient limiting conditions, mediates membrane association of adenylate cyclase
YBR036C	CSG2	Endoplasmic reticulum membrane protein, required for mannosylation of inositolphosphorylceramide and for growth at high calcium concentrations
YBR171W	SEC66	glycoprotein complexed with Sec62p and Sec63p in the Sec63 complex, an integral endoplasmic reticulum membrane protein complex required for translocation of presecretory proteins
YBR235W	None	
YBL101C	ECM21	Non-essential protein of unknown function; promoter contains several Gcn4p binding elements
YBL094C	None	

YBR008C	FLR1	Plasma membrane multidrug transporter, member of the major facilitator superfamily; involved in efflux of fluconazole, diazaborine, benomyl, methotrexate, and other drugs
YBR151W	APD1	Protein of unknown function, required for normal localization of actin patches and for normal tolerance of sodium ions and hydrogen peroxide; localizes to both cytoplasm and nucleus
YBR071W	None	
YBL066C	SEF1	Suppressor of Essential Function; putative transcription factor
YBL074C	AAR2	Component of the U5 snRNP, required for splicing of U3 precursors; originally described as a splicing factor specifically required for splicing pre-mRNA of the MATa1 cistron
YBL089W	AVT5	Putative transporter, member of a family of seven S. cerevisiae genes (AVT1-7) related to vesicular GABA-glycine transporters
YBR173C	UMP1	Involved in ubiquitin-mediated proteolysis; 20S proteasome maturation factor
YBR096W	None	
YBR221C	PDB1	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria
YBL022C	PIM1	mitochondrial ATP-dependent protease
YBR136W	MEC1	Central regulator of the Mec1p/Tel1p signaling network; required for mitotic growth, DNA repair and mitotic recombination, regulates phosphorylation of Rad53p, required for dmc1 arrest and meiotic recombination; similar to phosphatidylinositol(PI)3-kinases required for DNA damage induced checkpoint responses in G1, S/M, intra S, and G2/M in mitosis
YBR297W	MAL33	MAL-activator protein, part of complex locus MAL3; nonfunctional in genomic reference strain S288C
YBL098W	BNA4	Kynurenine 3-mono oxygenase, required for biosynthesis of nicotinic acid from tryptophan via kynurenine pathway
YBR108W	None	
YBR212W	NGR1	negative growth regulatory protein
YBR086C	IST2	Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomysin-driven process
YBR293W	None	
YBL047C	EDE1	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins
YDR264C	AKR1	Negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; Ankyrin repeat-containing protein
YBR138C	None	
YBR170C	NPL4	Endoplasmic reticulum and nuclear membrane protein, forms a complex with Cdc48p and Ufd1p that recognizes ubiquitinated proteins in the endoplasmic reticulum and delivers them to the proteasome for degradation

YBR234C	ARC40	Arp2/3 complex subunit, 40 kilodalton; component of Arp2/Arp3 protein complex
YBR016W	None	
YBL107C	None	
YPL148C	PPT2	Phosphopantetheine:protein transferase (PPTase), activates mitochondrial acyl carrier protein (Acp1p) by phosphopantetheinylation
YBR020W	GAL1	Galactokinase, phosphorylates alpha-D-galactose to alpha-D-galactose-1-phosphate in the first step of galactose catabolism; expression regulated by Gal4p
YBR222C	PCS60	Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase
YBL007C	SLA1	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin dynamics and with proteins required for endocytosis
YBR291C	CTP1	Mitochondrial inner membrane citrate transporter, member of the mitochondrial carrier family
YBR225W	None	
YBL084C	CDC27	Subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition
YBL102W	SFT2	similar to mammalian syntaxin 5
YOR275C	RIM20	Regulator of IME2
YBR041W	FAT1	Fatty acid transporter and very long-chain fatty acyl-CoA synthetase, may form a complex with Faa1p or Faa4p that imports and activates exogenous fatty acids
YBR059C	AKL1	Serine-threonine protein kinase, member (with Ark1p and Prk1p) of the Ark kinase family
YBR223C	TDP1	Tyrosine-DNA Phosphodiesterase
YBR055C	PRP6	Splicing factor, component of the U4/U6-U5 snRNP complex
YBR005W	RCR1	Endoplasmic reticulum membrane protein whose overproduction confers resistance to Congo Red
YBR019C	GAL10	UDP-glucose-4-epimerase, catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism; also catalyzes the conversion of alpha-D-glucose or alpha-D-galactose to their beta-anomers
YBR211C	AME1	associated with microtubules and essential; regulator of microtubule stability
YJR037W	None	
YBR111C	YSA1	Protein with weak similarity to D. melanogaster serendipity protein and X. laevis basis fibroblast growth factor
YBR007C	DSF2	None
YBR038W	CHS2	Chitin synthase II, requires activation from zymogenic form in order to catalyze the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for the synthesis of chitin in the primary septum during cytokinesis

YBR295W	PCA1	P-type metal-transporting ATPase with a role in copper and iron homeostasis; R970G-substitution in the C-terminal region confers cadmium resistance
YBR287W	ZSP1	None
YJR091C	JSN1	Member of the Puf family of RNA-binding proteins, interacts with mRNAs encoding membrane-associated proteins; overexpression suppresses a tub2-150 mutation and causes increased sensitivity to benomyl in wild-type cells
YPR002W	PDH1	Mitochondrial protein that participates in respiration, induced by diauxic shift; homologous to E. coli PrpD, may take part in the conversion of 2-methylcitrate to 2-methylisocitrate
YBR255W	None	
YBL033C	RIB1	GTP cyclohydrolase II; catalyzes the first step of the riboflavin biosynthesis pathway
YBL017C	PEP1	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles between the late-Golgi and prevacuolar endosome-like compartments
(35) MODULE 40		
Expression regulators		
YGL180W	ATG1	Protein serine/threonine kinase, required for autophagy and for the cytoplasm-to-vacuole targeting (Cvt) pathway
YOR224C	RPB8	RNA polymerase subunit, found in RNA polymerase complexes I, II, and III
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 genes
YCL055W	KAR4	Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation; shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
YCL055W	KAR4	Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
YJR122W	CAF17	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins
Module genes		
YBR010W	HHT1	One of two identical histone H3 proteins (see also HHT2); core histone required for chromatin assembly, involved in heterochromatin-mediated telomeric and HM silencing; regulated by acetylation, methylation, and mitotic phosphorylation
YNL024C	None	

YBR177C	EHT1	Possible serine hydrolase, may be involved in lipid metabolism, null mutant slightly temperature sensitive at 37C
YGL225W	VRG4	May regulate Golgi function and glycosylation in Golgi; Golgi GDP-mannose transporter
YDR225W	HTA1	One of two nearly identical (see also HTA2) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p
YER070W	RNR1	Ribonucleotide-diphosphate reductase (RNR), large subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits
YLR112W	None	
YPL127C	HHO1	Histone H1, a linker histone required for nucleosome packaging at restricted sites; suppresses DNA repair involving homologous recombination; not required for telomeric silencing, basal transcriptional repression, or efficient sporulation
YBR009C	HHF1	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity
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; expression is cell cycle-regulated; potential Cdc28p substrate
YDR222W	None	
YMR199W	CLN1	role in cell cycle START; G(sub)1 cyclin
YBR070C	None	
YDR224C	HTB1	One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation
YIL016W	SNL1	Integral membrane protein containing a Bag domain; suppressor of nup116-C lethal
YBL003C	HTA2	One of two nearly identical (see also HTA1) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p
YML052W	SUR7	Multicopy suppressor of rvs167 mutation; putative integral membrane protein
YOL007C	None	
YCR034W	FEN1	Fatty acid elongase, involved in sphingolipid biosynthesis; acts on fatty acids of up to 24 carbons in length; mutations have regulatory effects on 1,3-beta-glucan synthase, vacuolar ATPase, and the secretory pathway
YBL002W	HTB2	One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation

YMR292W	GOT1	Golgi Transport; membrane protein
YOR045W	TOM6	involved in supporting the cooperativity between receptors and the general insertion pore and facilitating the release of preproteins from import components; outer mitochondrial membrane protein, component of the mitochondiral protein translocation complex, associates with TOM40
YOR067C	ALG8	adds glucose to the dolichol-linked oligosaccharide precursor prior to transfer to protein; glycosyl transferase
YMR003W	None	
YOR101W	RAS1	ras proto-oncogene homolog
YNL031C	HHT2	One of two identical histone H3 proteins (see also HHT1); core histone required for chromatin assembly, involved in heterochromatin-mediated telomeric and HM silencing; regulated by acetylation, methylation, and mitotic phosphorylation
YHR153C	SPO16	Protein of unknown function, required for spore formation
YPL144W	None	
YPR052C	NHP6A	Homologous to mammalian high mobility group proteins 1 and 2; functions redundantly with the highly homologous gene, NHP6B; high-mobility group non-histone chromatin protein; 11-kDa nonhistone chromosomal protein
YMR318C	ADH6	NADPH-dependent alcohol dehydrogenase
YNL030W	HHF2	One of two identical histone H4 proteins (see also HHF1); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity
(36) MODULE 41		
Genotype regulators		
M1_184243_187272		YAR019W-A PAU7(0,2) YAR023C UIP3(9,133) YAR028W YAR029W YAR030C PRM9(60,6) MST28(5,7) YAR035C-A YAT1(2,63) SWH1(10,11) YAR044W
Module genes		
YAR027W	UIP3	Putative integral membrane protein of unknown function; interacts with Ulp1p at the nuclear periphery; member of DUP240 gene family
YAR028W	None	
(37) MODULE 42		
Genotype regulators		
M16_533282_555416		HAT1(2,2) SNF8(0,2) ULA1(2,0) LSP1(0,0) AEP3(2,0) NCR1(0,3) TFC8(1,3) CHL1(2,1) YPL009C RET3(1,2) TAF3(1,2) RRP12(5,1) MRPS16(0,1) YPL014W HST2(1,2) CIT3(0,23) YPR002C-A PDH1(0,0) YPR003C YPR004C
Module genes		
YPL002C	SNF8	appears to be functionally related to SNF7; involved in glucose derepression
YPR006C	ICL2	2-methylisocitrate lyase of the mitochondrial matrix, functions in the methylcitrate cycle to catalyze the conversion of 2-methylisocitrate to succinate and pyruvate; ICL2 transcription is repressed by glucose and induced by ethanol

(38) MODULE 43		
Expression regulators		
YDR043C	NRG1	Transcriptional repressor that recruits the Cyc8p-Tup1p complex to promoters; mediates glucose repression and negatively regulates a variety of processes including filamentous growth and alkaline pH response
YGR014W	MSB2	Protein that functions as an osmosensor in parallel to the Sho1p-mediated pathway, multicopy suppressor of a temperature-sensitive mutation in CDC24, potential Cdc28p substrate
Genotype regulators		
M2_562409_570229		ICS2(1,5) AMN1(3,17) YBR159W CDC28(0,5) CSH1(0,3) TOS1(2,3) YSY6(1,3) DEM1(6,5) ARL1(0,5) UBS1(0,5) TYR1(7,5) POP7(1,4) PEX32(4,4) SSE2(4,7) NPL4(2,1) SEC66(0,1)
Module genes		
YNR067C	DSE4	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother
YBR132C	AGP2	Plasma membrane carnitine transporter, expression is down-regulated by osmotic stress; also functions as a low-affinity amino acid permease
YJL078C	PRY3	Protein of unknown function, has similarity to Pry1p and Pry2p and to the plant PR-1 class of pathogen related proteins
YOR264W	DSE3	Daughter cell-specific protein, may help establish daughter fate
YER124C	DSE1	Daughter cell-specific protein, may participate in pathways regulating cell wall metabolism; deletion affects cell separation after division and sensitivity to drugs targeted against the cell wall
YGR041W	BUD9	Protein involved in bud-site selection; diploid mutants display a unipolar budding pattern instead of the wild-type bipolar pattern, and bud at the distal pole
YGL028C	SCW11	Cell wall protein with similarity to glucanases; may play a role in conjugation during mating based on its regulation by Ste12p
YMR285C	NGL2	RNase required for correct 3'-end formation of 5.8S rRNA at site E; has similarity to Ngl1p and Ngl3p and to drosophila Angelgene
YKL132C	RMA1	probable folyl-polyglutamate synthetase
YOR263C	None	
YNL078W	NIS1	None
YBR158W	AMN1	Involved in daughter cell separation and Chromosome STability; Chromosome STability
YHR143W	DSE2	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate from mother; expression is repressed by cAMP
YPR106W	ISR1	Predicted protein kinase, overexpression causes sensitivity to staurosporine, which is a potent inhibitor of protein kinase C
YNL066W	SUN4	Protein involved in the aging process; related to glucanases
YNL327W	EGT2	Glycosylphosphatidylinositol (GPI)-anchored cell wall endoglucanase required for proper cell separation after

		cytokinesis, expression is activated by Swi5p and tightly regulated in a cell cycle-dependent manner
(39) MODULE 44		
Expression regulators		
YGL208W	SIP2	Member of a family of proteins, including Sip1p and Gal83p, that interact with Snf1p and Snf4p and are involved in the response to glucose starvation; component of Snf1 protein complex involved in response to glucose starvation
YOR337W	TEA1	Mutants are defective in Ty1 Enhancer-mediated Activation; Ty1 enhancer activator
YOR101W	RAS1	ras proto-oncogene homolog
YPL230W	None	
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 principal activation function of the complex
YFR009W	GCN20	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA
YIL033C	BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation
Module genes		
YOL092W	None	
YMR038C	CCS1	Copper chaperone for superoxide dismutase Sod1p, involved in oxidative stress protection; Met-X-Cys-X2-Cys motif within the N-terminal portion is involved in insertion of copper into Sod1p under conditions of copper deprivation
YDR046C	BAP3	Amino acid permease involved in the uptake of cysteine, leucine, isoleucine and valine
YER086W	ILV1	Threonine deaminase, catalyzes the first step in isoleucine biosynthesis; expression is under general amino acid control; ILV1 locus exhibits highly positioned nucleosomes whose organization is independent of known ILV1 regulation
YGR061C	ADE6	Formylglycinamidine-ribonucleotide (FGAM)-synthetase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway
YHR020W	None	
YDR037W	KRS1	Lysyl-tRNA synthetase; also identified as a negative regulator of general control of amino acid biosynthesis
YNR046W	None	
YPR033C	HTS1	Cytoplasmic and mitochondrial histidine tRNA synthetase; encoded by a single nuclear gene that specifies two messages; efficient mitochondrial localization requires both a presequence and an amino-terminal sequence
YOL046C	None	
YGR124W	ASN2	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway

YHR025W	THR1	homoserine kinase
YGL234W	ADE5,7	Bifunctional enzyme of the 'de novo' purine nucleotide biosynthetic pathway, contains aminoimidazole ribotide synthetase and glycinamide ribotide synthetase activities
YHR047C	AAP1'	Arginine/alanine aminopeptidase, overproduction stimulates glycogen accumulation
YHR063C	PAN5	2-dehydropantoate 2-reductase, part of the pantothenic acid pathway, structurally homologous to E. coli panE
YCR053W	THR4	threonine synthase
YLR331C	JIP3	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 98% of ORF overlaps the verified gene MID2
YNL095C	None	
YHR014W	SPO13	Meiosis-specific protein of unknown function, involved in maintaining sister chromatid cohesion during meiosis I as well as promoting proper attachment of kinetochores to the spindle during meiosis I and meiosis II
YLR359W	ADE13	Adenylosuccinate lyase, catalyzes two steps in the 'de novo' purine nucleotide biosynthetic pathway
YGL071W	RCS1	Transcription factor that binds the consensus site PyPuCACCCPu, involved in iron homeostasis and cell size regulation; activates the expression of target genes in response to low-iron conditions
YGL039W	None	
YDR341C	None	
YOR323C	PRO2	Gamma-glutamyl phosphate reductase, catalyzes the second step in proline biosynthesis
YOR262W	None	
YPL160W	CDC60	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA
YKR099W	BAS1	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways
YKL072W	STB6	binds Sin3p in two-hybrid assay; involved in transcription
(40) MODULE 46		
Expression regulators		
YGR070W	ROM1	GDP/GTP exchange protein (GEP) for Rho1p; mutations are synthetically lethal with mutations in rom2, which also encodes a GEP
YGL248W	PDE1	Low-affinity cyclic AMP phosphodiesterase, controls glucose and intracellular acidification-induced cAMP signaling, target of the cAMP-protein kinase A (PKA) pathway; glucose induces transcription and inhibits translation
YCR091W	KIN82	Putative serine/threonine protein kinase, most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily
YOL113W	SKM1	Serine/threonine protein kinase with similarity to Ste20p and Cla4p
YGR200C	ELP2	Elongator protein, part of the six-subunit RNA polymerase II Elongator histone acetyltransferase complex; target of

		Kluyveromyces lactis zymocin
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
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; member of the Swi4p/Mbp1p family; potential Cdc28p substrate
Module genes		
YDR058C	TGL2	Triglyceride Lipase
YOR228C	None	
YEL060C	PRB1	Vacuolar proteinase B (yscB), a serine protease of the subtilisin family; involved in protein degradation in the vacuole and required for full protein degradation during sporulation
YKR067W	GPT2	Glycerol-3-phosphate acyltransferase located in both lipid particles and the ER; involved in the stepwise acylation of glycerol-3-phosphate and dihydroxyacetone, which are intermediate steps in lipid biosynthesis
YBR269C	FMP21	The authentic, non-tagged protein was localized to the mitochondria
YLR164W	None	
YMR020W	FMS1	Polyamine oxidase, converts spermine to spermidine, which is required for the essential hypusination modification of translation factor eIF-5A; also involved in pantothenic acid biosynthesis
YCR068W	ATG15	Lipase, required for intravacuolar lysis of autophagic bodies; located in the endoplasmic reticulum membrane and targeted to intravacuolar vesicles during autophagy via the multivesicular body (MVB) pathway
YBL078C	ATG8	Forms a protein complex with Aut2p to mediate attachment of autophagosomes to microtubules. Defective in maturation of the vacuolar protein, aminopeptidase I; Aut7p has homology to LC3, a microtubule-associated protein from rat.
YMR279C	None	
YER039C	HVG1	Protein of unknown function, has homology to Vrg4p
YOR152C	None	
YML118W	NGL3	DNase/RNase (putative); CCR4 C-terminal homolog; displays homology to drosophila Angel gene; homolog to ngl1 and ngl2
YNL223W	ATG4	Anchor protein involved in autophagy and required for sporulation; interacts with Tub1p and Tub2p and forms a complex with Aut7p; mediates attachment of autophagosomes to microtubules
YJL057C	None	
YLR080W	EMP46	Integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles, which function in ER to Golgi transport
YHR138C	None	
YDR018C	None	
YML042W	CAT2	Carnitine O-acetyltransferase, peroxisomal and mitochondrial

YGR045C	None	
YJL141C	YAK1	Serine-threonine protein kinase
YPL247C	None	
YDR358W	GGA1	Golgi-localized protein with homology to gamma-adaptin, interacts with and regulates Arf1p and Arf2p in a GTP-dependent manner in order to facilitate traffic through the late Golgi
YDL072C	YET3	Endoplasmic reticulum transmembrane protein, homolog of human BAP31 protein
YBR241C	None	
YDR059C	UBC5	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins, central component of the cellular stress response; expression is heat inducible
YBL049W	MOH1	Protein of unknown function, has homology to kinase Snf7p
YIL077C	None	
YJL132W	None	
YAL028W	FRT2	Tail-anchored endoplasmic reticulum membrane protein, interacts with homolog Frt1p but is not a substrate of calcineurin (unlike Frt1p), promotes growth in conditions of high Na+, alkaline pH, or cell wall stress; potential Cdc28p substrate
YPL166W	None	
YMR262W	None	
YOR137C	SIA1	Suppressor of eIF5A; High-copy suppressor of temperature-sensitive tif51A-1
YER079W	None	
YDL169C	UGX2	Protein of unknown function
YGR066C	None	
YFL042C	None	
YKL121W	None	
YGR281W	YOR1	Plasma membrane transporter of the ATP-binding cassette (ABC) family, mediates export of many different organic anions including oligomycin
YDR043C	NRG1	Transcriptional repressor that recruits the Cyc8p-Tup1p complex to promoters; mediates glucose repression and negatively regulates a variety of processes including filamentous growth and alkaline pH response
YIR018W	YAP5	bZIP transcription factor
YNL116W	DMA2	Protein involved in regulating spindle position and orientation, functionally redundant with Dma1p; homolog of S. pombe Dma1 and H. sapiens Chfr
YJL070C	None	
YAL054C	ACS1	one of 2 acetyl-coA synthetases in yeast; inducible acetyl-coenzyme A synthetase
YPL222W	FMP40	The authentic, non-tagged protein was localized to the mitochondria.
YOR121C	None	
YIL017C	VID28	Vacuole import and degradation

YFR017C	None	
YBR001C	NTH2	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses
YAL034C	FUN19	Protein of unknown function
YPL018W	CTF19	Outer kinetochore protein, required for accurate mitotic chromosome segregation; forms a complex with Mcm21p and Okp1p that binds to centromeres via the CBF3 complex
YKL188C	PXA2	Homolog of the human adrenoleukodystrophy transporter; forms a heterodimer with Pxa1p of two half ATP-binding cassette transporters in the peroxisome membrane; peroxisomal ABC transporter 2
YMR291W	None	
YMR195W	ICY1	Protein that interacts with the cytoskeleton and is involved in chromatin organization and nuclear transport, interacts genetically with TCP1 and ICY2, required for viability in rich media of cells lacking mitochondrial DNA
YER035W	EDC2	RNA-binding protein, activates mRNA decapping directly by binding to the mRNA substrate and enhancing the activity of the decapping proteins Dcp1p and Dcp2p
YHL027W	RIM101	Transcriptional activator required for entry into meiosis, has similarity to the Aspergillus Phenotype-response regulator PacC and the Yarrowia proteinase YlRim1010p; Meiotic regulatory protein; Cys-His zinc fingers
YBR046C	ZTA1	Zeta-crystallin homolog, found in the cytoplasm and nucleus; has similarity to E. coli quinone oxidoreductase and to human zeta-crystallin, which has quinone oxidoreductase activity
YJL079C	PRY1	Protein of unknown function, has similarity to Pry2p and Pry3p and to the plant PR-1 class of pathogen related proteins
YKL103C	LAP4	Vacuolar aminopeptidase, often used as a marker protein in studies of autophagy and cytosol to vacuole targeting (CTV) pathway
YPL006W	NCR1	A transmembrane glycoprotein that is homologous to human Niemann-Pick Type C (NPC) gene; involved in sphingolipid metabolism; predicted transmembrane protein
YLL040C	VPS13	homologous to human COH1; component of peripheral vacuolar membrane protein complex
YOR040W	GLO4	Mitochondrial glyoxalase II, catalyzes the hydrolysis of S-D-lactoylglutathione into glutathione and D-lactate
YOR120W	GCY1	Putative NADP(+) coupled glycerol dehydrogenase, proposed to be involved in an alternative pathway for glycerol catabolism
YPR155C	NCA2	Regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase; Regulates expression of mitochondrial ATP synthase
YJL163C	None	
YGR067C	None	
YMR251W	None	
YDR525W-A	SNA2	Protein of unknown function, has similarity to Pmp3p, which is involved in cation transport; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern

YPL177C	CUP9	Homeodomain-containing transcriptional repressor of PTR2, which encodes a major peptide transporter; imported peptides activate ubiquitin-dependent proteolysis, resulting in degradation of Cup9p and de-repression of PTR2 transcription
YLR375W	STP3	Protein involved in pre-tRNA splicing and in uptake of branched-chain amino acids
YDR055W	PST1	Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts; up-regulated by activation of the cell integrity pathway, as mediated by Rlm1p; upregulated by cell wall damage via disruption of FKS1
YJR008W	None	
YIL042C	None	
YOR347C	PYK2	Pyruvate kinase, glucose-repressed isoform; pyruvate kinase
YMR261C	TPS3	115 kD regulatory subunit of trehalose-6-phosphate synthase/phosphatase complex
YMR253C	None	
YPL165C	SET6	None
YHR171W	ATG7	autophagy; similar to ubiquitin-activating enzymes, involved in autophagy
YHL021C	FMP12	The authentic, non-tagged protein was localized to the mitochondria
YDL085W	NDE2	None
YDL199C	None	
YLR312C	None	
YPR003C	None	
YOR186W	None	
YNL242W	ATG2	Defective in autophagy; required for sporulation; Required for sporulation.
YKR058W	GLG1	Self-glucosylating initiator of glycogen synthesis, also glucosylates n-dodecyl-beta-D-maltoside; similar to mammalian glycogenin
YJL210W	PEX2	C3HC4 zinc-binding integral peroxisomal membrane protein; Pex2p, Pex10p, and Pex12p together make up the RING finger complex of the peroxisomal import machinery
YMR053C	STB2	Protein that binds Sin3p in a two-hybrid assay and is part of a large protein complex with Sin3p and Stb1p
YOR215C	None	
YFR047C	BNA6	Quinolinate phosphoribosyl transferase, required for biosynthesis of nicotinic acid from tryptophan via kynurenine pathway
YBR214W	SDS24	Nuclear protein with similarity to S. pombe Sds23, suppresses dis2 mutations
YBR280C	None	
YPL017C	None	
YKL129C	MYO3	One of two class-I myosins; localizes to actin cortical patches; deletion of MYO3 has little affect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeletion organization; myosin I
YKL065C	YET1	Endoplasmic reticulum transmembrane protein, homolog of

		human BAP31 protein
YGL121C	GPG1	Proposed gamma subunit of the heterotrimeric G protein that interacts with the receptor Grp1p; involved in regulation of pseudohyphal growth; requires Gpb1p or Gpb2p to interact with Gpa2p
YMR304W	UBP15	Ubiquitin-specific protease that may play a role in ubiquitin precursor processing
YDR530C	APA2	Diadenosine 5',5''-P1,P4-tetraphosphate phosphorylase II (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa1p
YNL011C	None	
YFR043C	None	
YJL116C	NCA3	With NCA2, regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase; involved in regulating expression of F0F1 ATPase subunits
YLR356W	None	
YDR204W	COQ4	Protein with a role in ubiquinone (Coenzyme Q) biosynthesis, possibly functioning in stabilization of Coq7p; located on the matrix face of the mitochondrial inner membrane
YCL038C	ATG22	Autophagy gene essential for breakdown of autophagic vesicles in the vacuole
YER037W	PHM8	Protein of unknown function, expression is induced by low phosphate levels and by inactivation of Pho85p
YOR134W	BAG7	Rho GTPase activating protein (RhoGAP), stimulates the intrinsic GTPase activity of Rho1p, which plays a role in actin cytoskeleton organization and control of cell wall synthesis; structurally and functionally related to Sac7p
YBR006W	UGA2	involved in utilization of GABA as a nitrogen source; succinate semialdehyde dehydrogenase
YPR127W	None	
YMR322C	SNO4	Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp31p, Hsp32p, and Hsp33p; member of the DJ-1/ThiJ/PfpI superfamily; may have a role in pyridoxine metabolism
YNR002C	FUN34	Putative transmembrane protein, involved in ammonia production; member of the TC 9.B.33 YaaH family; homolog of Ady2p and Y. lipolytica Gpr1p
(41) MODULE 48		
Expression regulators		
YIR017C	MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism
YOR178C	GAC1	Regulatory subunit for Glc7p (protein phosphatase I) for glycogen synthesis; regulatory role also predicted for glucose repression and ion homeostatis; potential Cdc28p substrate
YJL164C	TPK1	putative catalytic subunit of cAMP-dependent protein kinase
YJL157C	FAR1	Cyclin-dependent kinase inhibitor that mediates cell cycle arrest in response to pheromone; also forms a complex with Cdc24p, Ste4p, and Ste18p that may specify the direction of polarized growth during mating; potential Cdc28p substrate
YJL103C	None	

YER054C	GIP2	Putative regulatory subunit of the protein phosphatase Glc7p, proposed to be involved in glycogen metabolism; contains a conserved motif (GVNK motif) that is also found in Gac1p, Pig1p, and Pig2p
YER054C	GIP2	Putative regulatory subunit of the protein phosphatase Glc7p, proposed to be involved in glycogen metabolism; contains a conserved motif (GVNK motif) that is also found in Gac1p, Pig1p, and Pig2p
Module genes		
YDR402C	DIT2	Sporulation-specific enzyme required for spore wall maturation, involved in the production of a soluble LL-dityrosine-containing precursor of the spore wall, homologous to cytochrome P-450s
YPL265W	DIP5	Dicarboxylic amino acid permease, mediates high-affinity and high-capacity transport of L-glutamate and L-aspartate; also a transporter for Gln, Asn, Ser, Ala, and Gly
YER091C	MET6	Cobalamin-independent methionine synthase, involved in amino acid biosynthesis; also called N5-methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyltriglutamate homocysteine methyltransferase
YJR146W	None	
YKL001C	MET14	Adenylylsulfate kinase, required for sulfate assimilation and involved in methionine metabolism
YGL153W	PEX14	Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins; component of peroxisomal import machinery
YDL114W	None	
YOL158C	ENB1	Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment
YHR046C	INM1	Inositol monophosphatase, involved in biosynthesis of inositol and in phosphoinositide second messenger signalling; INM1 expression increases in the presence of inositol and decreases upon exposure to antibipolar drugs lithium and valproate
YPR048W	TAH18	Protein with a potential role in DNA replication; displays synthetic lethal genetic interaction with the pol3-13 allele of POL3, which encodes DNA polymerase delta
YNR034W	SOL1	Multicopy Suppressor Of los1; shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains; homologous to Sol2p and Sol3p
YJR010W	MET3	ATP sulfurylase, catalyzes the primary step of intracellular sulfate activation, essential for assimilatory reduction of sulfate to sulfide, involved in methionine metabolism
YLR302C	None	
YDR384C	ATO3	Plasma membrane protein, regulation pattern suggests a possible role in export of ammonia from the cell; member of the TC 9.B.33 YaaH family of putative transporters
YIL168W	None	
YEL072W	RMD6	Protein required for sporulation

YLR355C	ILV5	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA
YMR058W	FET3	Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases
YNL318C	HXT14	Protein of unknown function with similarity to hexose transporter family members, expression is induced by low levels of glucose and repressed by high levels of glucose
YIL105C	SLM1	Protein of unknown function; mutation is synthetically lethal with an mss4 mutation
YEL008W	None	
YPL130W	SPO19	Meiosis-specific protein of unknown function, involved in completion of nuclear divisions; identified as a weak high-copy suppressor of the spo1-1 ts mutation; putative GPI-dependent cell-wall protein
YPL080C	None	
YEL065W	SIT1	Ferrioxamine B transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; transcription is induced during iron deprivation and diauxic shift; potentially phosphorylated by Cdc28p
YJL127C	SPT10	Putative histone acetylase, required for transcriptional regulation at core promoters, functions at or near the TATA box
YIL053W	RHR2	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress
YIL163C	None	
YNL276C	None	
YOL059W	GPD2	Involved in glycerol production via conversion of glyerol-3-phosphate and NAD+ to glycerol phosphate and NADH; Glycerol-3-phosphate dehydrogenase (NAD+)
YLR307W	CDA1	Required for proper formation of the ascospore wall; Chitin Deacetylase
YDL059C	RAD59	Protein involved in the repair of double-strand breaks in DNA during vegetative growth via recombination and single-strand annealing; anneals complementary single-stranded DNA; homologous to Rad52p
YJL212C	OPT1	Plasma membrane transporter that transports tetra- and pentapeptides and glutathione; member of the OPT family
YPL058C	PDR12	Plasma membrane weak-acid-inducible ATP-binding cassette (ABC) transporter, required for weak organic acid resistance, strongly induced by sorbate and benzoate, regulated by War1p, mutants exhibit sorbate hypersensitivity
(42) MODULE 49		
Expression regulators		
YOL113W	SKM1	Serine/threonine protein kinase with similarity to Ste20p and Cla4p
YIL147C	SLN1	Histidine kinase osmosensor that regulates a MAP kinase cascade; transmembrane protein with an intracellular kinase

		domain that signals to Ypd1p and Ssk1p, thereby forming a phosphorelay system similar to bacterial two-component regulators
Genotype regulators		
M13_905780_922268		YMR310C GLC8(0,3) ELP6(1,3) TGL3(1,5) PRE5(0,5) YMR315W YMR315W-A YMR316C-A YMR316C-B DIA1(1,4) YMR317W ADH6(0,8) FET4(1,8) YMR320W YMR321C SNO4(1,20) ERR3 YMR324C YMR325W YMR326C
Module genes		
YPL273W	SAM4	S-adenosylmethionine-homocysteine methyltransferase, functions along with Mht1p in the conversion of S-adenosylmethionine (AdoMet) to methionine to control the methionine/AdoMet ratio
YPL279C	None	
YPL274W	SAM3	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-methylmethionine permease Mmp1p
YOR389W	None	
YPL277C	None	
YOR390W	None	
YMR321C	None	
YPL278C	None	
(43) MODULE 50		
Expression regulators		
YBR158W	AMN1	Involved in daughter cell separation and Chromosome STability; Chromosome STability
YOR047C	STD1	Protein that interacts with the Snf1p protein kinase and Spt15p in two-hybrid and in in vitro binding studies
YGR108W	CLB1	Involved in mitotic induction; G(sub)2-specific B-type cyclin
YBL066C	SEF1	Suppressor of Essential Function; putative transcription factor
YPR013C	None	
Module genes		
YAL020C	ATS1	Protein with a potential role in regulatory interactions between microtubules and the cell cycle, as suggested by genetic and physical interactions with Nap1p and genetic interactions with TUB1
YGR203W	None	
YLR414C	None	
YCR073W-A	SOL2	multicopy suppressor of los1-1; shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains; homologous to Sol1p and Sol3p
YNL241C	ZWF1	Glucose-6-phosphate dehydrogenase
YPL067C	None	
YBR148W	YSW1	Protein expressed specifically in spores
YLR042C	None	
YLR099C	ICT1	Protein of unknown function, null mutation leads to an increase in sensitivity to Calcofluor white; expression of the gene is

		induced in the presence of isooctane
YOR084W	None	
YNL300W	None	
YNL322C	KRE1	Cell wall glycoprotein involved in beta-glucan assembly; serves as a K1 killer toxin membrane receptor
YCL044C	None	
YBR150C	TBS1	Probable Zn-finger protein
YIL153W	RRD1	Resistant to Rapamycin Deletion
YOL110W	SHR5	Subunit of a palmitoyltransferase, composed of Shr5p and Erf2p, that adds a palmitoyl lipid moiety to Ras2p through a thioester linkage; palmitoylation is required for Ras2p localization to the plasma membrane
YER004W	FMP52	The authentic, non-tagged protein was localized to the mitochondria
YDR156W	RPA14	RNA polymerase I subunit A14
YGR014W	MSB2	Protein that functions as an osmosensor in parallel to the Sho1p-mediated pathway, multicopy suppressor of a temperature-sensitive mutation in CDC24, potential Cdc28p substrate
YLR337C	VRP1	Involved in cytoskeletal organization and cellular growth; Proline-rich protein verprolin
YER018C	SPC25	Spindle pole body (SPB) component, localizes to the nuclear side of spindle pole; interacts with Nuf2p, Ndc80p, and Spc24p at the kinetochore; has a putative role in spindle checkpoint control and centromere clustering at spindle pole
YFR051C	RET2	Delta subunit of the coatomer complex (COPI), which coats Golgi-derived transport vesicles; involved in retrograde transport between Golgi and ER
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 utilizing Ire1p, Trl1p and Ada5p facilitates efficient Hac1p synthesis
(44) MODULE 51		
Expression regulators		
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
YHR030C	SLT2	Suppressor of lyt2; serine/threonine MAP kinase
YJL164C	TPK1	putative catalytic subunit of cAMP-dependent protein kinase
YCR091W	KIN82	Putative serine/threonine protein kinase, most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily
YJL164C	TPK1	putative catalytic subunit of cAMP-dependent protein kinase

Module genes		
YMR185W	None	
YOR340C	RPA43	RNA polymerase I subunit A43
YOR195W	SLK19	Kinetochore-associated protein required for normal segregation of chromosomes in meiosis and mitosis; component of the FEAR regulatory network, which promotes Cdc14p release from the nucleolus during anaphase; potential Cdc28p substrate
YNL075W	IMP4	Component of the SSU processome, which is required for pre-18S rRNA processing; interacts with Mpp10p; member of a superfamily of proteins that contain a sigma(70)-like motif and associate with RNAs
YGR245C	SDA1	Severe Depolymerization of Actin
YKL021C	MAK11	Protein essential for cell growth and replication of M dsRNA virus; contains four beta-transducin repeats
YBR155W	CNS1	cyclophilin seven suppressor; component of Hsp90p chaperone machinery
YAL019W	FUN30	Protein whose overexpression affects chromosome stability, potential Cdc28p substrate; homolog of Snf2p
YMR310C	None	
YPL012W	RRP12	Protein required for normal pre-rRNA Processing; member of a group of seven genes whose expression is repressed during growth on glucose before and during the diauxic shift
YLR068W	FYV7	Protein of unknown function, required for survival upon exposure to K1 killer toxin; involved in processing the 35S rRNA primary transcript to generate the 20S and 27SA2 pre-rRNA transcripts
YHR052W	CIC1	Core interacting component 1; ribosome biogenesis protein
YMR093W	UTP15	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YPL093W	NOG1	Putative GTPase that associates with free 60S ribosomal subunits in the nucleolus and is required for 60S ribosomal subunit biogenesis; member of the ODN family of nucleolar G-proteins
YHR197W	RIX1	RIbosome eXport; Protein required for cell viability
YDR165W	TRM82	Subunit of a tRNA methyltransferase complex composed of Trm8p and Trm82p that catalyzes 7-methylguanosine modification of tRNA
YOR144C	ELG1	Protein required for S phase progression and telomere homeostasis, forms an alternative replication factor C complex important for DNA replication and genome integrity; mutants are sensitive to DNA damage
YOR048C	RAT1	RNA trafficking protein; transcription activator
YKR024C	DBP7	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis
YDL150W	RPC53	RNA polymerase III subunit C53
YOL041C	NOP12	Nucleolar protein, required for pre-25S rRNA processing; contains an RNA recognition motif (RRM) and has similarity to Nop13p, Nsr1p, and putative orthologs in Drosophila and S. pombe

YNL207W	RIO2	Protein required for cell viability
YGR103W	NOP7	Nucleolar protein involved in rRNA processing and 60S ribosomal subunit biogenesis; constituent of several different pre-ribosomal particles
YOL144W	NOP8	Nucleolar protein required for 60S ribosomal subunit biogenesis
YKL082C	RRP14	Required for normal pre-rRNA Processing; Protein required for cell viability
YLR449W	FPR4	Nuclear protein, putative peptidyl-prolyl cis-trans isomerase (PPIase) with similarity to Fpr3p; overproduction suppresses the growth defect resulting from the absence of E3 ubiquitin-protein ligase Tom1p
YHR169W	DBP8	Putative ATP-dependent RNA helicase of the DEAD-box family involved in biogenesis of the 40S ribosomal subunit
YJR003C	None	
YCL059C	KRR1	Essential nucleolar protein required for the synthesis of 18S rRNA and for the assembly of 40S ribosomal subunit
YFL034C-A	RPL22B	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl22Ap and to rat L22 ribosomal protein
YDL148C	NOP14	Nucleolar protein, forms a complex with Noc4p that mediates maturation and nuclear export of 40S ribosomal subunits; also present in the small subunit processome complex, which is required for processing of pre-18S rRNA
YOR091W	None	
YJL109C	UTP10	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YNL292W	PUS4	catalyzes formation of Psi55 (modified uridine) in mitochondrial and cytoplasmic tRNAs; Pseudouridine synthase
YGR228W	None	
YJL148W	RPA34	RNA polymerase I subunit A34.5
YMR239C	RNT1	RNAase III; cleaves a stem-loop structure at the 3' end of U2 snRNA to ensure formation of the correct U2 3' end
YHR085W	IPI1	Protein of unknown function, essential for viability, may be involved in rRNA processing
YDR496C	PUF6	member of the PUF protein family; YDR496C
YKR081C	RPF2	None
YAL025C	MAK16	Essential nuclear protein required for normal concentration of free 60S ribosomal subunits; required for maintenance of M1 satellite double-stranded RNA of the L-A virus
YLR074C	BUD20	Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern
YCR016W	None	
YNR003C	RPC34	RNA polymerase III subunit C34; interacts with TFIIIB70 and is a key determinant in pol III recruitment by the preinitiation complex
YHR081W	LRP1	Protein involved in homologous recombination and in non-homologous DNA end joining; homolog of mammalian C1D, which is a nuclear matrix protein involved in regulation of DNA repair and recombination

YJR002W	MPP10	Component of the SSU processome, which is required for pre-18S rRNA processing, interacts with and controls the stability of Imp3p and Imp4p, essential for viability
YIL020C	HIS6	Phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase, catalyzes the fourth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts
YDL036C	None	
YIL019W	FAF1	Protein required for pre-rRNA processing and 40S ribosomal subunit assembly
YLR222C	UTP13	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YGR140W	CBF2	Essential kinetochore protein, component of the CBF3 multisubunit complex that binds to the CDEIII region of the centromere; Cbf2p also binds to the CDEII region possibly forming a different multimeric complex, ubiquitinated in vivo
YKL014C	URB1	Nucleolar protein required for the normal accumulation of 25S and 5.8S rRNAs, associated with the 27SA2 pre-ribosomal particle; proposed to be involved in the biogenesis of the 60S ribosomal subunit
YLR287C	None	
YDR021W	FAL1	Nucleolar protein required for maturation of 18S rRNA, member of the eIF4A subfamily of DEAD-box ATP-dependent RNA helicases
YER006W	NUG1	GTPase that associates with nuclear 60S pre-ribosomes, required for export of 60S ribosomal subuits from the nucleus
YCL054W	SPB1	Suppressor of PaB1 mutant; encodes a S-adenosylmethionine-dependent methyltransferase; involved in 60S ribosomal subunit biogenesis and rRNA processing; Putative methyltransferase
YOR145C	PNO1	Partner of Nob1; Protein required for cell viability
YDR399W	HPT1	enzyme involved in de novo purine biosynthesis; hypoxanthine guanine phosphoribosyltransferase
YKR056W	TRM2	tRNA methyltransferase, 5-methylates the uridine residue at position 54 of tRNAs and may also have a role in tRNA stabilization or maturation; previously thought to be an endo-exonuclease
YLR106C	MDN1	Midasin, pseudo-hexameric assembly of AAA protomers associated with a C-terminal MIDAS-containing M-domain, associated with 60S pre-ribosomes (large subunit precursor) and their export from the nucleus
YLR129W	DIP2	Nucleolar protein, specifically associated with the U3 snoRNA, part of the large ribonucleoprotein complex known as the small subunit (SSU) processome, required for 18S rRNA biogenesis, part of the active pre-rRNA processing complex
YMR131C	RRB1	RiboSome Assembly 2
YKL009W	MRT4	Protein involved in mRNA turnover and ribosome assembly, localizes to the nucleolus
YDR299W	BFR2	Essential protein possibly involved in secretion; multicopy suppressor of sensitivity to Brefeldin A
YOR252W	None	

YOL022C	None	
YNL166C	BNI5	Protein involved in organization of septins at the mother-bud neck, may interact directly with the Cdc11p septin, localizes to bud neck in a septin-dependent manner
YNL182C	IPI3	Protein required for cell viability; computational analysis of large-scale protein-protein interaction data suggests a possible role in assembly of the ribosomal large subunit
YNL132W	KRE33	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance
YKR060W	UTP30	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data
YOL109W	ZEO1	Peripheral membrane protein of the plasma membrane that interacts with Mid2p; regulates the cell integrity pathway mediated by Pkc1p and Slt2p
YGR173W	RBG2	Protein with similarity to mammalian developmentally regulated GTP-binding protein
YPL126W	NAN1	part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); Net1-Associated Nucleolar protein 1; Net1-Associated Nucleolar protein 1
YKL078W	DHR2	Predominantly nucleolar DEAH-box RNA helicase, required for 18S rRNA synthesis
YDR184C	ATC1	Nuclear protein, possibly involved in regulation of cation stress responses and/or in the establishment of bipolar budding pattern
YER127W	LCP5	Essential protein involved in maturation of 18S rRNA; depletion leads to inhibited pre-rRNA processing and reduced polysome levels; localizes primarily to the nucleolus
YDL031W	DBP10	Essential protein involved in ribosome biogenesis; putative ATP-dependent RNA helicase of the DEAD-box protein family
YDL153C	SAS10	part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); Something About Silencing 10; nuclear protein involved in silencing
YNL112W	DBP2	Essential ATP-dependent RNA helicase of the DEAD-box protein family, involved in nonsense-mediated mRNA decay and rRNA processing
YFL002C	SPB4	involved in the maturation of 25S ribosomal RNA; ATP-dependent RNA helicase
YLR009W	RLP24	Ribosomal Like Protein 24
YGR187C	HGH1	Protein of unknown function with similarity to human HMG1 and HMG2; localizes to the cytoplasm
YGR145W	ENP2	Essential protein of unknown function
YHR154W	RTT107	Regulator of Ty1 Transposition; Establishes Silent Chromatin; involved in silencing
YHR170W	NMD3	putative Upf1p-interacting protein; cytoplasmic factor required for a late cytoplasmic assembly step of the 60S subunit
YDR324C	UTP4	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YMR179W	SPT21	Protein required for normal transcription at several loci including HTA2-HTB2 and HHF2-HHT2, but not required at the other histone loci; functionally related to Spt10p

YGL099W	LSG1	Putative GTPase involved in 60S ribosomal subunit biogenesis; localized to the cytoplasm
YDL213C	NOP6	Protein with similarity to hydrophilins, which are involved in the adaptive response to hyperosmotic conditions; computational analysis of large-scale protein-protein interaction data suggests a possible role in rRNA processing
YPR110C	RPC40	RNA polymerase subunit, common to RNA polymerase I and III
YBL054W	None	
YPL239W	YAR1	YAR1 encodes a 200-amino-acid protein with two ANK repeat motifs and an acidic C terminus rich in PEST-like sequences
YDR465C	RMT2	Arginine methyltransferase; ribosomal protein L12 is a substrate
YDR449C	UTP6	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YNL114C	None	
YJL010C	None	
YDL208W	NHP2	HMG-like nuclear protein
YPR163C	TIF3	Suppressor of translation mutants; Translation initiation factor eIF-4B
YLR051C	None	
YJL033W	HCA4	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis
YGR083C	GCD2	Delta subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression
YPL044C	None	
YLR276C	DBP9	ATP-dependent RNA helicase of the DEAD-box family involved in biogenesis of the 60S ribosomal subunit
YNR053C	NOG2	Putative GTPase that associates with pre-60S ribosomal subunits in the nucleolus and is required for their nuclear export and maturation
YDR365C	ESF1	Nucleolar protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels
YGL171W	ROK1	ATP-dependent RNA helicase of the DEAD box family; required for 18S rRNA synthesis
YDR083W	RRP8	None
YOR004W	None	
YOR310C	NOP58	Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA
YNL022C	None	
YNL110C	NOP15	Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis; localizes to both nucleolus and cytoplasm
YDL060W	TSR1	Protein required for processing of 20S pre-rRNA in the cytoplasm, associates with pre-40S ribosomal particles

YOR287C	None	
YOR341W	RPA190	RNA polymerase I subunit alpha; largest subunit of RNA polymerase I
YNL061W	NOP2	Probable RNA m(5)C methyltransferase, essential for processing and maturation of 27S pre-rRNA and large ribosomal subunit biogenesis; localized to the nucleolus
YLR103C	CDC45	DNA replication initiation factor; recruited to MCM pre-RC complexes at origins of replication; promotes disengagement of MCM from its anchor, Mcm10p, and recruits elongation machinery
YKR079C	TRZ1	Protein required for cell viability
YBR247C	ENP1	Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and 40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the nucleolus
YLR336C	SGD1	Suppressor of Glycerol Defect; may be involved in high osmolarity signaling pathway
YDR120C	TRM1	tRNA methyltransferase, localizes to both the nucleus and mitochondrion to produce the modified base N2,N2-dimethylguanosine in tRNAs in both compartments
YKL191W	DPH2	Protein of unknown function, involved in diphtheria toxicity and diphthamide biosynthesis, not essential for viability
YDR097C	MSH6	Protein required for mismatch repair in mitosis and meiosis, forms a complex with Msh2p to repair both single-base & insertion-deletion mispairs; potentially phosphorylated by Cdc28p
YDR361C	BCP1	Essential protein involved in nuclear export of Mss4p, which is a lipid kinase that generates phosphatidylinositol 4,5-biphosphate and plays a role in actin cytoskeleton organization and vesicular transport
YNL002C	RLP7	Significant sequence similarity to RPL7B, but neither can functionally replace the other. Does not correspond to any ribosomal component identified so far, based on its biochemical features; Protein with similarity to ribosomal proteins including Rpl6p
YDL112W	TRM3	2'-O-ribose methyltransferase, catalyzes the ribose methylation of the guanosine nucleotide at position 18 of tRNAs
YNL227C	JJJ1	Protein that may function as a cochaperone, as suggested by the presence of a DnaJ-like domain
YNL113W	RPC19	RNA polymerase subunit, common to RNA polymerases I and III
YGR123C	PPT1	Protein serine/threonine phosphatase with similarity to human phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth
YGR162W	TIF4631	also called eIF4 (eIF-4) gamma; mRNA cap-binding protein (eIF-4F), 150K subunit , highly homologous to Tif4632p, homologs of mammalian p220
YBL028C	None	
YMR229C	RRP5	Part of small ribosomal subunit (SSU) processosome containing U3 snoRNA); required for the synthesis of both 18S and 5.8S rRNAs
YPL043W	NOP4	Nucleolar protein, essential for processing and maturation of

		27S pre-rRNA and large ribosomal subunit biogenesis; contains four RNA recognition motifs (RRMs)
YLR435W	TSR2	Protein with a potential role in pre-rRNA processing
YMR309C	NIP1	Protein required for nuclear import with some similarity to Nsr1p, another protein involved in nuclear transport; ~100 kDa cytoplasmic protein
YLL011W	SOF1	Nucleolar protein, part of the small (ribosomal) subunit (SSU) processosome that contains U3 snoRNA; has similarity to beta subunits of G-proteins and the splicing factor Prp4p
YKL083W	None	
YDR211W	GCD6	Catalytic epsilon subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression
YNL151C	RPC31	RNA polymerase III subunit C31; contains HMG-like C-terminal domain
YOR294W	RRS1	Essential protein that binds ribosomal protein L11 and is required for nuclear export of the 60S pre-ribosomal subunit during ribosome biogenesis; mouse homolog shows altered expression in Huntington's disease model mice
YNL174W	None	
YGR280C	PXR1	Protein with a role in maturation of rRNAs and small nucleolar RNAs; Protein required for cell viability
YGR264C	MES1	Methionyl-tRNA synthetase, forms a complex with glutamyl-tRNA synthetase (Ygl245wp) and Arc1p, which increases the catalytic efficiency of both tRNA synthetases; also has a role in nuclear export of tRNAs
YCR072C	None	
YPL217C	BMS1	GTP-binding protein required for processing of 35S pre-rRNA at sites A0,
YMR049C	ERB1	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; homologous to mammalian Bop1
YLR175W	CBF5	major low affinity 55 kDa Centromere/microtubule binding protein
YKL143W	LTV1	Protein required for growth at low temperature
YGL111W	NSA1	Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis
YMR290W-A	None	
YML018C	None	
YER082C	UTP7	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YDL050C	None	
YOR243C	PUS7	pseudouridylates U2 snRNA at position 35
YIL091C	None	
YPR018W	RLF2	Chromatin Assembly Complex, subunit 1: largest (p90) subunit of three-subunit protein complex (yeast CAF-I) involved in DNA-replication-linked nucleosome assembly. Homol. to p150 subunit human Chromatin Assembly Factor-I (CAF-I); p90 subunit of yeast Chromatin Assembly Factor-I (CAF-I)

YOL124C	None	
YOL010W	RCL1	RNA terminal phosphate cyclase-like protein involved in rRNA processing at sites A0, A1, and A2; does not possess detectable RNA cyclase activity
YJL122W	None	
YJL050W	MTR4	Dead-box family ATP dependent helicase required for mRNA export from the nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA
YNL299W	TRF5	TRF4 homolog; TRF4/5 function is required for proper mitosis; exhibits homology to Trf4p and Top1p
YHR149C	SKG6	Protein of unknown function found in the bud tip and bud neck, potential Cdc28p substrate
YNR054C	ESF2	Protein required for cell viability
YHR196W	UTP9	Nucleolar protein, component of the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YER126C	NSA2	Constituent of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis
YOR047C	STD1	Protein that interacts with the Snf1p protein kinase and Spt15p in two-hybrid and in in vitro binding studies
YOR119C	RIO1	Essential protein that plays a role in cell cycle progression, has similarity to C. elegans ZK632.3 protein
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. melanogaster shuttle craft and human NFX1
YIL127C	None	
YDL167C	NRP1	Protein of unknown function, rich in asparagine residues
YPR136C	None	
YPR144C	NOC4	Nucleolar protein, forms a complex with Nop14p that mediates maturation and nuclear export of 40S ribosomal subunits
YOR094W	ARF3	GTP-binding ADP-ribosylation factor
YOR078W	BUD21	Component of small ribosomal subunit (SSU) processosome that contains U3 snoRNA; originally isolated as bud-site selection mutant that displays a random budding pattern
YNL248C	RPA49	RNA polymerase I subunit A49
YGR128C	UTP8	Nucleolar protein required for export of tRNAs from the nucleus; also copurifies with the small subunit (SSU) processome containing the U3 snoRNA that is involved in processing of pre-18S rRNA
YLR063W	None	
YOL097C	WRS1	Cytoplasmic tryptophanyl-tRNA synthetase, aminoacylates tryptophanyl-tRNA
YLR409C	UTP21	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data
YHR065C	RRP3	Required for maturation of the 35S primary transcript of pre-rRNA and is required for cleavages leading to mature 18S RNA; RRP3 is a DEAD box gene homologous to eIF-4a which encodes an RNA-dependent ATPase possessing helicase activity

		which is not specific for RNA
YMR290C	HAS1	Putative ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions
YHR088W	RPF1	Nucleolar protein involved in the assembly of the large ribosomal subunit; contains a sigma(70)-like motif, which is thought to bind RNA
YLL008W	DRS1	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits
YDR312W	SSF2	high copy suppressor of G beta subunit temperature sensitive mutation; possibly involved in mating
YDR152W	GIR2	RWD domain containing protein of unknown function
YOR001W	RRP6	Exonuclease component of the nuclear exosome; contributes to the quality-control system that retains and degrades aberrant mRNAs in the nucleus
YER049W	None	
YFR001W	LOC1	Nuclear protein involved in asymmetric localization of ASH1 mRNA; binds double-stranded RNA in vitro
YOR146W	None	
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
YNL308C	KRI1	Essential nucleolar protein required for 40S ribosome biogenesis; physically and functionally interacts with Krr1p
YNL164C	IBD2	Component of the BUB2-dependent spindle checkpoint pathway, interacts with Bfa1p and functions upstream of Bub2p and Bfa1p
YKR092C	SRP40	Suppressor of mutant AC40 subunit of RNA polymerase I and III; nucleolar protein that is immunologically and structurally related to rat Nopp140, a nonribosomal protein of the nucleolus and coiled bodies.
YAL036C	RBG1	GTPase, interacts with ribosomes, has similarity to Xenopus GTP-binding protein DRG
YGR155W	CYS4	Cystathionine beta-synthase, catalyzes the first committed step of transsulfuration in cysteine biosynthesis
YDR101C	ARX1	None
YBR267W	REI1	Protein of unknown function involved in bud growth in the mitotic signaling network; proposed negative regulator of Swe1p and Gin4p; contains dispersed C2H2 zinc finger domains
YAL059W	ECM1	Protein of unknown function, localized in the nucleoplasm and the nucleolus, genetically interacts with MTR2 in 60S ribosomal protein subunit export
YLR196W	PWP1	Protein with periodic trytophan residues that resembles members of beta-transducin superfamily because of presence of WD-40 repeats; similar to beta-transducin superfamily
YPL158C	None	
YPL086C	ELP3	Histone acetyltransferase subunit of the Elongator complex, which is a component of the RNA polymerase II holoenzyme; activity is directed specifically towards histones H3 and H4; disruption confers resistance to K. lactis zymotoxin

YIR012W	SQT1	Protein involved in a late step of 60S ribosomal subunit assembly or modification; contains multiple WD repeats; interacts with Qsr1p in the two-hybrid system
YHR148W	IMP3	Component of the SSU processome, which is required for pre-18S rRNA processing, essential protein that interacts with Mpp10p and mediates interactions of Imp4p and Mpp10p with U3 snoRNA
YKL172W	EBP2	Essential protein required for the maturation of 25S rRNA and 60S ribosomal subunit assembly, localizes to the nucleolus
YDR060W	MAK21	Protein required for large (60S) ribosomal subunit biogenesis; involved in nuclear export of pre-ribosomes; required for maintenance of dsRNA virus; homolog of human CAATT-binding protein
YGL078C	DBP3	Putative ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis
YMR269W	None	
YDL063C	None	
YPR112C	MRD1	Essential conserved protein that associates with 35S precursor rRNA and is required for its initial processing at the A(0)-A(2) cleavage sites, shows partial nucleolar localization, contains five consensus RNA-binding domains
YOR206W	NOC2	Protein that forms a nucleolar complex with Mak21p that binds to 90S and 66S pre-ribosomes, as well as a nuclear complex with Noc3p that binds to 66S pre-ribosomes; both complexes mediate intranuclear transport of ribosomal precursors
YGR200C	ELP2	Elongator protein, part of the six-subunit RNA polymerase II Elongator histone acetyltransferase complex; target of Kluyveromyces lactis zymocin
YIL096C	None	
YOR359W	VTS1	None
YLR401C	DUS3	Dihydrouridine synthase, member of a widespread family of conserved proteins including Smm1p, Dus1p, and Dus4p; contains a consensus oleate response element (ORE) in its promoter region
YKL113C	RAD27	5' to 3' exonuclease, 5' flap endonuclease, required for Okazaki fragment processing and maturation as well as for long-patch base-excision repair; member of the S. pombe RAD2/FEN1 family
YCR057C	PWP2	part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); Eight WD-repeats with homology with G protein beta subunits flanked by nonhomologous N-terminal and C-terminal extensions; regulatory protein
YFL023W	BUD27	Protein involved in bud-site selection, nutrient signaling, and gene expression controlled by the TOR kinase; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern
YPL146C	None	
YIR026C	YVH1	nitrogen starvation-induced protein phosphatase
YLL034C	RIX7	Putative ATPase of the AAA family, required for export of pre-ribosomal large subunits from the nucleus; distributed between

		the nucleolus, nucleoplasm, and nuclear periphery depending on growth conditions
(45) MODULE 52		
Expression regulators		
YHR030C	SLT2	Suppressor of lyt2; serine/threonine MAP kinase
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)-Cys(6) binuclear cluster domain type
Genotype regulators		
M10_22213_34098		NUC1(1,2) CBP1(6,3) PEX2(1,6) YJL211C OPT1(3,6) YJL213W HXT8(93,12) YJL215C YJL216C YJL217W YJL218W HXT9(12,50) YJL220W FSP2(4,32) VTH2(323,435)
M6_38648_48224		TUB2(1,1) YPT1(0,1) ACT1(3,5) YFL040W FET5(4,1) YFL041W-A YFL042C YFL043C YOD1(1,0) SEC53(0,2) FMP32(1,3) RGD2(5,3) EMP47(4,3) YFL049W ALR2(19,15) YFL051C YFL052W
Module genes		
YFL052W	None	
YFL054C	None	
YFL053W	DAK2	Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress adaptation
YDL244W	THI13	Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family including THI5, THI11, THI12, and THI13
YNL331C	AAD14	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role
YFL056C	AAD6	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase, involved in the oxidative stress response
YFL055W	AGP3	Low-affinity amino acid permease, may act to supply the cell with amino acids as nitrogen source in nitrogen-poor conditions; transcription is induced under conditions of sulfur limitation
(46) MODULE 53		
Expression regulators		
YPL230W	None	
YLL019C	KNS1	Nonessential putative protein kinase of unknown cellular role; member of the LAMMER family of protein kinases, which are serine/threonine kinases also capable of phosphorylating tyrosine residues
YPL230W	None	
YOL113W	SKM1	Serine/threonine protein kinase with similarity to Ste20p and Cla4p
YLR150W	STM1	Protein that binds quadruplex nucleic acids; multicopy suppressor of tom1 and pop2 mutations; acts with Cdc13p to maintain telomere structure
YLL019C	KNS1	Nonessential putative protein kinase of unknown cellular role; member of the LAMMER family of protein kinases, which are

		serine/threonine kinases also capable of phosphorylating tyrosine residues
Module genes		
YOL084W	PHM7	Protein of unknown function, expression is regulated by phosphate levels; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery and vacuole
YHR140W	None	
YDL046W	NPC2	Putative homolog of human NPC2/He1, which is a cholesterol-binding protein whose deficiency causes Niemann-Pick type C2 disease involving retention of cholesterol in lysosomes
YLR289W	GUF1	Mitochondrial GTPase of unknown function, similar to E. coli elongation factor-type GTP-binding protein LepA and to LK1236.1 from Caenorhabditis elegans
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
YNL173C	MDG1	Plasma membrane protein involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations
YHR034C	PIH1	Protein possibly involved in protein synthesis
YGR086C	PIL1	Long chain base-responsive inhibitor of protein kinases Phk1p and Phk2p, acts along with Lsp1p to down-regulate heat stress resistance via regulation of the Pkc1p and Ypk1p pathways; phosphorylated by Phk1p and Phk2p
YDR406W	PDR15	ATP binding cassette (ABC) transporter of the plasma membrane; general stress response factor implicated in cellular detoxification; target of Pdr1p, Pdr3p and Pdr8p transcription regulators; promoter contains a PDR responsive element
YOR031W	CRS5	Copper-binding metallothionein, required for wild-type copper resistance
YOR161C	PNS1	Protein of unknown function; has similarity to Torpedo californica tCTL1p, which is postulated to be a choline transporter, neither null mutation nor overexpression affects choline transport
YJL016W	None	
YHR033W	None	
YNR036C	None	
YGL226W	None	
YOR125C	CAT5	may encode a protein involved in one or more monoxygenase or hydroxylase steps of ubiquinone biosynthesis
YPR149W	NCE102	involved in secretion of proteins that lack classical secretory signal sequences; Involved in secretion of proteins that lack classical secretory signal sequences
YOL053W	None	
YMR031C	None	
YDL049C	KNH1	Protein with similarity to Kre9p, which is involved in cell wall beta 1,6-glucan synthesis; overproduction suppresses growth defects of a kre9 null mutant
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; member of the Swi4p/Mbp1p family; potential Cdc28p substrate
YNL100W	None	
YOL047C	None	
YKL150W	MCR1	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis
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 responsive genes, inducing gene expression
YLL020C	None	
YOR062C	None	
YMR244C-A	None	
YBR091C	MRS5	Essential protein of the inner mitochondrial membrane, peripherally localized; component of the TIM22 complex, which is a a twin-pore translocase that mediates insertion of numerous multispanning inner membrane proteins
YHR044C	DOG1	2-deoxyglucose-6-phosphate phosphatase, similar to Dog2p, member of a family of low molecular weight phosphatases; confers 2-deoxyglucose resistance when overexpressed, in vivo substrate has not yet been identified
YIL087C	None	
YGR230W	BNS1	Protein with some similarity to Spo12p; overexpression bypasses need for Spo12p, but not required for meiosis
YPL161C	BEM4	Protein involved in establishment of cell polarity and bud emergence; interacts with the Rho1p small GTP-binding protein and with the Rho-type GTPase Cdc42p
YHL024W	RIM4	Regulator of IMe2 expression; RNA-binding protein of the RRM class (putative)
YER097W	None	
YNL234W	None	
YCR083W	TRX3	mitochondrial thioredoxin
YMR031W-A	None	
YER062C	HOR2	One of two redundant DL-glycerol-3-phosphatases (RHR2/GPP1 encodes the other) involved in glycerol biosynthesis; induced in response to hyperosmotic stress and oxidative stress, and during the diauxic transition
YGL208W	SIP2	Member of a family of proteins, including Sip1p and Gal83p, that interact with Snf1p and Snf4p and are involved in the response to glucose starvation; component of Snf1 protein complex involved in response to glucose starvation
YDR216W	ADR1	Positive transcriptional regulator, controls the expression of ADH2, peroxisomal protein genes, and genes required for ethanol, glycerol, and fatty acid utilization
YGR243W	FMP43	The authentic, non-tagged protein was localized to mitochondria
YMR254C	None	
YJR127C	ZMS1	Zinc-finger protein that localizes to the nucleus, putative transcriptional regulator of ALD6
YJR119C	None	

(47) MODULE 54		
Expression regulators		
YGR233C	PHO81	Cyclin-dependent kinase (CDK) inhibitor, regulates Pho80p-Pho85p and Pcl7p-Pho85p cyclin-CDK complexes in response to phosphate levels; required for derepression of PHO5; transcriptionally regulated by Pho4p and Pho2p
YOL113W	SKM1	Serine/threonine protein kinase with similarity to Ste20p and Cla4p
YER177W	BMH1	14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes including exocytosis and vesicle transport, Ras/MAPK signaling during pseudohyphal development, rapamycin-sentitive signaling, and others
YBR083W	TEC1	transcription factor of the TEA/ATTS DNA-binding domain family, regulator of Ty1 expression
YDL230W	PTP1	phosphotyrosine-specific protein phosphatase
Genotype regulators		
M13_27644_28694		YML116W-A NAB6(7,1) YML117W-A NGL3(3,3) YML119W NDI1(1,1) GTR1(0,50) YML122C PHO84(2,48) TUB3(8,0) YML125C ERG13(0,0) RSC9(0,0)
Module genes		
YFR042W	None	
YKR091W	SRL3	Cytoplasmic protein that, when overexpressed, suppresses the lethality of a rad53 null mutation; potential Cdc28p substrate
YMR245W	None	
YDL118W	None	
YBR193C	MED8	Member of RNA Polymerase II transcriptional regulation mediator; Stoichiometric member of mediator complex
YAL064W	None	
YJL032W	None	
YOL133W	HRT1	RING finger containing subunit of Skp1-Cullin-F-box ubiquitin protein ligases (SCF); required for Gic2p, Far1p, Sic1p and Cln2p degradation; may tether Cdc34p (a ubiquitin conjugating enzyme or E2) and Cdc53p (a cullin) subunits of SCF
YKL158W	None	
YDR256C	CTA1	Catalase A, breaks down hydrogen peroxide in the peroxisomal matrix formed by acyl-CoA oxidase (Pox1p) during fatty acid beta-oxidation
YPR130C	None	
YGR137W	None	
YDR327W	None	
YOR024W	None	
YIR020C	None	
YJL119C	None	
YPL169C	MEX67	Involved in nuclear mRNA export, binds both poly(A); a poly(A)+RNA binding protein
YDR223W	CRF1	Protein of unknown function, potentially phosphorylated by Cdc28p

YGR188C	BUB1	checkpoint gene involved in permitting entry into mitosis depending upon the assembly state of microtubules; Serine/threonine protein kinase required for cell cycle arrest in response to loss of microtubule function
YNL238W	KEX2	Subtilisin-like protease (proprotein convertase), a calcium-dependent serine protease involved in the activation of proproteins of the secretory pathway
YCL001W-A	None	
YNL211C	None	
YOR190W	SPR1	Sporulation regulated genes; sporulation-specific exo-1,3-beta-glucanase
YJL022W	None	
YFL020C	PAU5	Part of 23-member seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by anaerobiosis, negatively regulated by oxygen, repressed by heme
YPL200W	CSM4	Protein required for accurate chromosome segregation during meiosis
(48) MODULE 55		
Expression regulators		
YDR195W	REF2	RNA-binding protein involved in the cleavage step of mRNA 3'-end formation prior to polyadenylation; also involved in snoRNA maturation
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 utilizing Ire1p, Trl1p and Ada5p facilitates efficient Hac1p synthesis
YGL037C	PNC1	NAD(+) salvage pathway gene; pyrazinamidase and nicotinamidase
YJL103C	None	
Module genes		
YNL140C	None	
YPR111W	DBF20	Ser/Thr kinase involved in late nuclear division, one of the mitotic exit network (MEN) proteins; necessary for the execution of cytokinesis
YFL033C	RIM15	RIM15 is glucose-repressed; RIM15 is required for IME2 expression; Trehalose-associated protein kinase related to S. pombe cek1+
YAL029C	MYO4	Required for mother-specific HO expression, for the bud tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p; myosin
YLR124W	None	
YDR219C	None	
YML124C	TUB3	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p
YGL178W	MPT5	Protein that specifically binds to mRNAs encoding chromatin modifiers and spindle pole body components; has roles in longevity, in maintenance of cell wall integrity, and in

		sensitivity to and recovery from pheromone arrest
YER056C	FCY2	Purine-cytosine permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine accumulation
YGL166W	CUP2	Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated copper concentrations
YNL128W	TEP1	Similar to human tumor suppressor gene known as TEP1, MMAC1 and PTEN1; Putative protein tyrosine phosphatase
YJL097W	None	
YKL147C	None	
YOR213C	SAS5	Protein involved in silencing at telomeres, HML, and HMR
YHR021W-A	ECM12	Non-essential protein of unknown function
YLR422W	None	
YDR431W	None	
YOR237W	HES1	Protein implicated in the regulation of ergosterol biosynthesis; one of a seven member gene family with a common essential function and non-essential unique functions; similar to human oxysterol binding protein (OSBP)
YNR025C	None	
YNR072W	HXT17	Protein of unknown function with similarity to hexose transporter family members, expression is repressed by high levels of glucose
YEL017W	GTT3	Protein of unknown function with a possible role in glutathione metabolism, as suggested by computational analysis of large-scale protein-protein interaction data; GFP-fusion protein localizes to the nuclear periphery
YEL041W	None	
YLR411W	CTR3	High-affinity copper transporter of the plasma membrane, acts as a trimer; gene is disrupted by a Ty2 transposon insertion in many laboratory strains of S. cerevisiae
YMR228W	MTF1	Mitochondrial RNA polymerase sigma-like specificity factor required for promoter recognition, interacts with mitochondrial core polymerase Rpo41p, imported into mitochondria via a novel process requiring most of the Mtf1p sequence
YKR015C	None	
YJL216C	None	
YDR370C	None	
YIL170W	None	
YMR013C	SEC59	Membrane protein that catalyzes the CTP-mediated phosphorylation of dolichol, the terminal step in dolichyl monophosphate (Dol-P) biosynthesis; required for viability, normal rates of lipid intermediate synthesis, and protein N-glycosylation
YPL132W	COX11	Mitochondrial membrane protein required for assembly of active cytochrome c oxidase, probably involved in insertion of Cu(B) and magnesium
YGL132W	None	
YBR240C	THI2	Zinc finger protein of the Zn(II)2Cys6 type, probable transcriptional activator of thiamine biosynthetic genes

(49) MODULE 56		
Expression regulators		
YCL055W	KAR4	Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
YGR156W	PTI1	Pta1p Interacting protein
Genotype regulators		
M9_214482_254745		NEO1(0,4) DFG10(4,6) PCL7(1,2) MMF1(1,2) RPL34B(13,11) RHR2(0,7) YIL054W YIL055C YIL056W YIL057C YIL058W YIL059C YIL060W SNP1(3,132) ARC15(0,2) YRB2(3,1) YIL064W FIS1(0,1) RNR3(2,6) YIL066W-A YIL067C SEC6(0,0) YIL068W-A RPS24B(1,2) MAM33(0,0) PCI8(0,0) YIL071W-A HOP1(1,9) SPO22(218,0) SER33(1,0) RPN2(0,0) SEC28(0,4) YIL077C THS1(2,4) AIR1(3,4) YIL080W YIL082W YIL082W-A
Module genes		
YIL080W	None	
YIL082W-A	None	
YIL049W	DFG10	Protein of unknown function, involved in filamentous growth
YIL082W	None	
(50) MODULE 57		
Expression regulators		
YCR040W	MATALPHA1	Transcriptional co-activator involved in regulation of mating-type-specific gene expression; targets the transcription factor Mcm1p to the promoters of alpha-specific genes; one of two genes encoded by the alpha mating type cassette
YCL055W	KAR4	Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
Module genes		
YFL025C	BST1	Protein that negatively regulates COPII vesicle formation; functionally complements mammalian PGAP1, which is a GPI inositol-deacylase involved in GPI maturation; negative regulator of COPII vesicle formation
YCR097W	HMRA1	Silenced copy of A1, encoding a homeobox-domain containing corepressor that interacts with Alpha2p to repress haploid-specific gene transcription in diploid cells
YGL033W	HOP2	Meiosis-specific protein that localizes to chromosomes, preventing synapsis between nonhomologous chromosomes and ensuring synapsis between homologs; complexes with Mnd1p to promote homolog pairing and meiotic double-strand break repair
YIL015W	BAR1	Aspartyl protease secreted into the periplasmic space of mating type a cells, cleaves and inactivates alpha factor allowing cells to recover from alpha-factor-induced cell cycle arrest
YJL170C	ASG7	an a-specific gene that is induced to a higher expression level by alpha factor; An a-specific gene that is induced to a higher expression level by alpha factor

YHR178W	STB5	binds Sin3p in two-hybrid assay; Zinc finger (6-Cys)
YOL025W	LAG2	affects longevity; involved in determination of longevity
YLR288C	MEC3	Involved in checkpoint control and DNA repair; forms a clamp with Rad17p and Ddc1p that is loaded onto partial duplex DNA; DNA damage checkpoint protein
YNL145W	MFA2	lipopeptide mating pheromone; mating a-factor pheromone precursor
YFL027C	GYP8	GTPase-activating protein for yeast Rab family members; Ypt1p is the preferred in vitro substrate but also acts on Sec4p, Ypt31p and Ypt32p; involved in the regulation of ER to Golgi vesicle transport
YGL032C	AGA2	Adhesion subunit of a-agglutinin of a-cells, C-terminal sequence acts as a ligand for alpha-agglutinin (Sag1p) during agglutination, modified with O-linked oligomannosyl chains, linked to anchorage subunit Aga1p via two disulfide bonds
YFL026W	STE2	alpha-factor pheromone receptor; seven-transmembrane domain protein
YCR097W-A	None	
YKL209C	STE6	ABC transporter, glycoprotein, component of a-factor secretory pathway
YDR461W	MFA1	a-factor mating pheromone precursor
(51) MODULE 58		
Expression regulators		
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 utilizing Ire1p, Trl1p and Ada5p facilitates efficient Hac1p synthesis
YGL166W	CUP2	Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated copper concentrations
YGR014W	MSB2	Protein that functions as an osmosensor in parallel to the Sho1p-mediated pathway, multicopy suppressor of a temperature-sensitive mutation in CDC24, potential Cdc28p substrate
YKL126W	YPK1	76.5 kDa Serine/threonine protein kinase with similarity to protein kinase C, is 90% identical to Ypk2p
YPL026C	SKS1	multicopy suppressor of snf3 and grr1 mutants; serine/threonine protein kinase homologous to Ran1p
YGL166W	CUP2	Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated copper concentrations
YKL126W	YPK1	76.5 kDa Serine/threonine protein kinase with similarity to protein kinase C, is 90% identical to Ypk2p
Module genes		
YGL074C	None	
YML032C-A	None	
YLR374C	None	
YBL108W	None	
YLL037W	None	

YDR455C	None	
YFR056C	None	
YDL062W	None	
YDR187C	None	
YDR538W	PAD1	Phenylacrylic acid decarboxylase, confers resistance to cinnamic acid, decarboxylates aromatic carboxylic acids to the corresponding vinyl derivatives
YDL026W	None	
YPR092W	None	
YLR140W	None	
YML117W-A	None	
YLR349W	None	
YMR159C	ATG16	Protein that interacts with the Atg12p-Atg5p conjugate during formation of the pre-autophagosomal structure; essential for autophagy
YGL239C	None	
YJR079W	None	
YGR064W	None	
YLR169W	None	
YKL162C-A	None	
YBL073W	None	
YDR290W	None	
YNL205C	None	
YJL182C	None	
YGR190C	None	
YKL037W	None	
YCL023C	None	
YMR194C-A	None	
YLR122C	None	
YLR202C	None	
YJL120W	None	
YJL169W	None	
YPR142C	None	
YMR119W-A	None	
YBR124W	None	
YDR199W	None	
YAR031W	PRM9	Pheromone-regulated protein with 3 predicted transmembrane segments and an FF sequence, a motif involved in COPII binding
YGR114C	None	
YML058C-A	None	
YGR291C	None	
YMR324C	None	
YBR100W	None	

YEL059C-A	SOM1	Protein whose overexpression suppresses the imp1 mutation, may be required for the function of the Imp1p mitochondrial inner membrane peptidase and/or the protein sorting machinery
YKL118W	None	
YGL072C	None	
YBL096C	None	
YDL232W	OST4	Subunit of the oligosaccharyltransferase complex of the ER lumen, which catalyzes aspargine-linked glycosylation of newly synthesized proteins; type I membrane protein of 36 residues that binds Stt3p and Ost3p together in a subcomplex
YDL152W	None	
YHR079C-B	None	
YBR099C	None	
YCR001W	None	
YLR428C	None	
YGR290W	None	
YDR445C	None	
YPR151C	SUE1	Mitochondrial protein required for degradation of unstable forms of cytochrome c
YCR062W	None	
YLR279W	None	
YML100W-A	None	
YNL235C	None	
YJL211C	None	
YER060W-A	FCY22	Putative purine-cytosine permease, very similar to Fcy2p but cannot substitute for its function
YLR236C	None	
YGL165C	None	
YJL015C	None	
YIL141W	None	
YNL203C	None	
YOR282W	None	
YNL226W	None	
YJL018W	None	
YDR366C	None	
YOR013W	None	
YER091C-A	None	
YLR281C	None	
YHR145C	None	
YML094W	GIM5	Prefoldin subunit 5; putative homolog of subunit 5 of bovine prefoldin, a chaperone comprised of six subunits; bovine prefoldin subunit 5 homolog (putative)
YPR039W	None	
YGR039W	None	
(52) MODULE 59		

Genotype regulators		
M15_108577_154309		PHM7(7,11) YOL085C YOL085W-A ADH1(4,8) YOL086W-A YOL087C MPD2(4,6) HAL9(15,4) MSH2(2,3) SPO21(3,6) YOL092W TRM10(5,4) RFC4(1,4) HMI1(5,1) COQ3(2,0) WRS1(1,3) YOL097W-A YOL098C YOL099C PKH2(7,6) IZH4(0,5) TPT1(2,3) ITR2(0,365) NDJ1(4,456) WSC3(6,2) YOL106W YOL107W INO4(0,1) ZEO1(1,3) SHR5(1,3) YOL111C MSB4(2,0) SKM1(9,2) YOL114C TRF4(4,4) MSN1(2,5)
Module genes		
YOL113W	SKM1	Serine/threonine protein kinase with similarity to Ste20p and Cla4p
YOL104C	NDJ1	Meiosis-specific telomere protein, required for bouquet formation, effective homolog pairing, ordered cross-over distribution (interference), sister chromatid cohesion at meiotic telomeres, and segregation of small chromosomes
(53) MODULE 61		
Genotype regulators		
M15_108577_154309		PHM7(7,11) YOL085C YOL085W-A ADH1(4,8) YOL086W-A YOL087C MPD2(4,6) HAL9(15,4) MSH2(2,3) SPO21(3,6) YOL092W TRM10(5,4) RFC4(1,4) HMI1(5,1) COQ3(2,0) WRS1(1,3) YOL097W-A YOL098C YOL099C PKH2(7,6) IZH4(0,5) TPT1(2,3) ITR2(0,365) NDJ1(4,456) WSC3(6,2) YOL106W YOL107W INO4(0,1) ZEO1(1,3) SHR5(1,3) YOL111C MSB4(2,0) SKM1(9,2) YOL114C TRF4(4,4) MSN1(2,5)
Module genes		
YOL091W	SPO21	Component of the meiotic outer plaque of the spindle pole body, involved in modifying the meiotic outer plaque that is required prior to prospore membrane formation
YLL028W	TPO1	Proton-motive-force-dependent multidrug transporter of the major facilitator superfamily; able to transport eight different compounds, including polyamines, quinidine, cycloheximide, and nystatin; involved in excess spermidine detoxification
(54) MODULE 62		
Expression regulators		
YBR125C	PTC4	Phosphatase type Two C; Type 2C protein phosphatase
YBR140C	IRA1	GTPase-activating protein that negatively regulates RAS by converting it from the GTP- to the GDP-bound inactive form, required for reducing cAMP levels under nutrient limiting conditions, mediates membrane association of adenylate cyclase
Module genes		
YOR304C-A	None	
YER044C-A	MEI4	Functions in early recombination; mRNA is meiosis-specific and has 88 bp intron at 5' end spliced independently of MER1.
YOR041C	SRF5	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 85% of ORF overlaps the uncharacterized gene CUE5; deletion in cyr1 mutant results in loss of stress resistance
YBR301W	DAN3	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p,

		and Tir4p; expressed under anaerobic conditions, completely repressed during aerobic growth
YLL003W	SFI1	None
YML010W-A	None	
(55) MODULE 63		
Expression regulators		
YBR274W	CHK1	checkpoint kinase 1; homolog of the S. pombe and mammalian Chk1 checkpoint kinases; Protein kinase Chk1
YPL086C	ELP3	Histone acetyltransferase subunit of the Elongator complex, which is a component of the RNA polymerase II holoenzyme; activity is directed specifically towards histones H3 and H4; disruption confers resistance to K. lactis zymotoxin
YGR288W	MAL13	MAL-activator protein, part of complex locus MAL1; nonfunctional in genomic reference strain S288C
YGR123C	PPT1	Protein serine/threonine phosphatase with similarity to human phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth
YGL037C	PNC1	NAD(+) salvage pathway gene; pyrazinamidase and nicotinamidase
YHR122W	None	
YGL121C	GPG1	Proposed gamma subunit of the heterotrimeric G protein that interacts with the receptor Grp1p; involved in regulation of pseudohyphal growth; requires Gpb1p or Gpb2p to interact with Gpa2p
Module genes		
YBR162W-A	YSY6	Protein that participates in secretory pathway
YBR060C	ORC2	Subunit of the origin recognition complex, which directs DNA replication by binding to replication origins and is also involved in transcriptional silencing; may be phosphorylated by Cdc28p
YBR075W	None	
YBR163W	DEM1	Protein of unknown function, shows similarity to RNA-processing protein Pta1p
YBR112C	CYC8	General transcriptional co-repressor, acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters
YBR281C	None	
YBL024W	NCL1	Nuclear protein 1, similar to NOP2 and human proliferation associated nucleolar protein p120; Probable proliferating-cell nucleolar antigen (human p120)
YBL082C	RHK1	Dolichol-P-Man dependent alpha(1-3) mannosyltransferase, involved in the synthesis of dolichol-linked oligosaccharide donor for N-linked glycosylation of proteins
YBL032W	HEK2	RNA binding protein with similarity to hnRNP-K that localizes to the cytoplasm and to subtelomeric DNA; required for the proper localization of ASH1 mRNA; involved in the regulation of telomere position effect and telomere length
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 gene silencing, and formation of functional kinetochores

YOR116C	RPO31	RNA polymerase III large subunit
YBR004C	FMP44	The authentic, non-tagged protein was localized to the mitochondria
YBR245C	ISW1	Member of the imitation-switch (ISWI) class of ATP-dependent chromatin remodeling complexes; ATPase that forms a complex with Ioc2p and Ioc4p to regulate transcription elongation, and a complex with Ioc3p to repress transcription initiation
YBR261C	None	
YBR069C	TAT1	Amino acid transport protein for valine, leucine, isoleucine, and tyrosine
YBL020W	RFT1	Flippase, essential integral membrane protein that is required for translocation of Man5GlcNac2-PP-Dol from the cytoplasmic side to the lumenal side of the ER membrane; mutation is suppressed by expression human p53 protein
YBL004W	UTP20	Possible snoRNA-binding protein, based on computational analysis of large-scale protein-protein interaction data
YBL085W	BOI1	Protein implicated in polar growth, functionally redundant with Boi2p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain
YBL077W	None	
YBR065C	ECM2	Pre-mRNA splicing factor, facilitates the cooperative formation of U2/U6 helix II in association with stem II in the spliceosome, function may be regulated by Slu7p
YPR080W	TEF1	functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; translational elongation factor EF-1 alpha
YBL034C	STU1	Component of the mitotic spindle that binds to interpolar microtubules and plays an essential role in their ability to provide an outward force on the spindle poles
YBL018C	POP8	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA precursors to generate mature 5' ends
YBL081W	None	
YBR061C	TRM7	2'-O-ribose methyltransferase, methylates the 2'-O-ribose of nucleotides at positions 32 and 34 of the tRNA anticodon loop
YBR125C	PTC4	Phosphatase type Two C; Type 2C protein phosphatase
YBR029C	CDS1	CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidylyltransferase, CDP-diglyceride synthetase
YBR252W	DUT1	dUTPase, catalyzes the hydrolysis of dUTP to dUMP and PPi and thereby prevents the incorporation of uracil into DNA during replication
YBR244W	GPX2	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress
YBR084W	MIS1	mitochondrial C1-tetrahydroflate synthase
YBL014C	RRN6	involved in the transcription of 35S rRNA genes by RNA polymerase I; member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn7p and TATA-binding protein
YBR017C	KAP104	Transportin, cytosolic karyopherin beta 2 involved in delivery of

		heterogeneous nuclear ribonucleoproteins to the nucleoplasm, binds rg-nuclear localization signals on Nab2p and Hrp1p, plays a role in cell-cycle progression
YBR121C	GRS1	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation
YBR266C	None	
YBL091C	MAP2	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map1p
YBL067C	UBP13	Putative ubiquitin-specific protease
YBL083C	None	
YBL041W	PRE7	20S proteasome beta-type subunit
YBL009W	None	
YBR101C	FES1	Hsp70 (Ssa1p) nucleotide exchange factor, cytosolic homolog of Sls1p, which is the nucleotide exchange factor for BiP (Kar2p) in the endoplasmic reticulum
YBR166C	TYR1	Step of tyrosine biosynthesis pathway; Prephenate dehydrogenase (NADP+)
YBR162C	TOS1	Target of SBF
YBR154C	RPB5	RNA polymerase subunit, found in RNA polymerase complexes I, II, and III
YBR200W	BEM1	Protein containing SH3-domains, involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p
YNL273W	TOF1	Protein that interacts with topoisomerase I
YBR089W	None	
YBL035C	POL12	Subunit of the DNA polymerase alpha-primase complex, required for the initiation of DNA replication during mitotic DNA synthesis and premeiotic DNA synthesis
YBL051C	PIN4	Protein involved in G2/M phase progression and response to DNA damage, interacts with Rad53p; contains an RNA recognition motif, a nuclear localization signal, and several SQ/TQ cluster domains; hyperphosphorylated in response to DNA damage
YBR084C-A	RPL19A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl19Bp and has similarity to rat L19 ribosomal protein; rpl19a and rpl19b single null mutations result in slow growth, while the double null mutation is lethal
YGL014W	PUF4	member of the PUF protein family; YGL014W
YBL062W	None	
YBR034C	HMT1	Nuclear SAM-dependent mono- and asymmetric arginine dimethylating methyltransferase that modifies hnRNPs, including Npl3p and Hrp1p, thus facilitating nuclear export of these proteins; required for viability of npl3 mutants
YBR153W	RIB7	Diaminohydroxyphoshoribosylaminopyrimidine deaminase; catalyzes the second step of the riboflavin biosynthesis pathway
YBR233W	PBP2	RNA binding protein with similarity to mammalian heterogeneous nuclear RNP K protein, involved in the

		regulation of telomere position effect and telomere length
YBR073W	RDH54	genetic interaction with DMC1; Putative helicase similar to RAD54
YBR283C	SSH1	Sec61p homolog involved in co-translational pathway of protein transport
YBR195C	MSI1	Subunit of chromatin assembly factor I (CAF-I), regulates the RAS/cAMP pathway via sequestration of Npr1p kinase; localizes to the nucleus and cytoplasm; homologous to human retinoblastoma binding proteins RbAp48 and RbAp46
YBL076C	ILS1	Cytoplasmic isoleucine-tRNA synthetase, target of the G1-specific inhibitor reveromycin A
YBR079C	RPG1	Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes
YBL079W	NUP170	Abundant subunit of the nuclear pore complex (NPC), required for proper localization of specific nucleoporins within the NPC, involved in nuclear envelope permeability and in chromosome segregation, has similarity to Nup157p
YBR243C	ALG7	UDP-N-acetyl-glucosamine-1-P transferase, transfers Glc-Nac-P from UDP-GlcNac to Dol-P in the ER in the first step of the dolichol pathway of protein asparagine-linked glycosylation; inhibited by tunicamycin
YBR219C	None	
YBR194W	SOY1	Synthetic with Old Yellow Enzyme
YBR098W	MMS4	endonuclease
YBL052C	SAS3	Protein involved in silencing at HMR
YBL036C	None	
YBR063C	None	
YBR021W	FUR4	Uracil permease, localized to the plasma membrane; expression is tightly regulated by uracil levels and environmental cues
YBR143C	SUP45	Translation release factor involved in translation termination; mutant form acts as a recessive omnipotent suppressor
YBR078W	ECM33	GPI-anchored protein of unknown function, has a possible role in apical bud growth; GPI-anchoring on the plasma membrane crucial to function; similar to Sps2p and Pst1p
YBR094W	None	
YBR242W	None	
YBR074W	None	
YBL027W	RPL19B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl19Bp and has similarity to rat L19 ribosomal protein; rpl19a and rpl19b single null mutations result in slow growth, while the double null mutation is lethal
YBR023C	CHS3	Chitin synthase III, catalyzes the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for synthesis of the majority of cell wall chitin, the chitin ring during bud emergence, and spore wall chitosan
YBR142W	MAK5	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits

YBL031W	SHE1	Cytoskeletal protein of unknown function; overexpression causes growth arrest
YBR172C	SMY2	partial suppressor of myo2-66; Kinesin-related protein suppressing myosin defects (MYO2)
YBR106W	PHO88	Probable membrane protein, involved in phosphate transport; pho88 pho86 double null mutant exhibits enhanced synthesis of repressible acid phosphatase at high inorganic phosphate concentrations
YBR187W	None	
YBL061C	SKT5	Activator of Chs3p (chitin synthase III), recruits Chs3p to the bud neck via interaction with Bni4p; has similarity to Shc1p, which activates Chs3p during sporulation
YBL068W	PRS4	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes
YBR271W	None	
YBR159W	None	
YBR175W	SWD3	Subunit of the COMPASS complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres
YBR087W	RFC5	Subunit of heteropentameric Replication factor C (RF-C), which is a DNA binding protein and ATPase that acts as a clamp loader of the proliferating cell nuclear antigen (PCNA) processivity factor for DNA polymerases delta and epsilon
YBR263W	SHM1	Serine hydroxymethyltransferase, mitochondrial
YPL242C	IQG1	Essential protein required for determination of budding pattern, promotes localization of axial markers Bud4p and Cdc12p and functionally interacts with Sec3p, localizes to the contractile ring during anaphase, member of the IQGAP family
(56) MODULE 64		
Expression regulators		
YDL064W	UBC9	SUMO-conjugating enzyme involved in the Smt3p conjugation pathway; nuclear protein required for S- and M-phase cyclin degradation and mitotic control; involved in proteolysis mediated by the anaphase-promoting complex cyclosome (APCC)
YGR123C	PPT1	Protein serine/threonine phosphatase with similarity to human phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth
YNL030W	HHF2	One of two identical histone H4 proteins (see also HHF1); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity
YGR123C	PPT1	Protein serine/threonine phosphatase with similarity to human phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth
YPL002C	SNF8	appears to be functionally related to SNF7; involved in glucose derepression
YGR123C	PPT1	Protein serine/threonine phosphatase with similarity to human

		phosphatase PP5; present in both the nucleus and cytoplasm; expressed during logarithmic growth
YGR188C	BUB1	checkpoint gene involved in permitting entry into mitosis depending upon the assembly state of microtubules; Serine/threonine protein kinase required for cell cycle arrest in response to loss of microtubule function
Module genes		
YCL050C	APA1	Diadenosine 5',5''-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p
YER056C-A	RPL34A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl34Bp and has similarity to rat L34 ribosomal protein
YOR210W	RPB10	RNA polymerase subunit, found in RNA polymerase complexes I, II, and III
YIL018W	RPL2B	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Ap and has similarity to E. coli L2 and rat L8 ribosomal proteins; expression is upregulated at low temperatures
YDL082W	RPL13A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl13Bp; not essential for viability; has similarity to rat L13 ribosomal protein
YPR043W	RPL43A	Protein component of the large (60S) ribosomal subunit, identical to Rpl43Bp and has similarity to rat L37a ribosomal protein; null mutation confers a dominant lethal phenotype
YLR029C	RPL15A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl15Bp and has similarity to rat L15 ribosomal protein; binds to 5.8 S rRNA
YNL067W	RPL9B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Ap and has similarity to E. coli L6 and rat L9 ribosomal proteins
YKR059W	TIF1	translation initiation factor eIF4A
YGR211W	ZPR1	Essential protein with two zinc fingers, present in the nucleus of growing cells but relocates to the cytoplasm in starved cells via a process mediated by Cpr1p; binds to translation elongation factor eEF-1 (Tef1p)
YGR085C	RPL11B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11
YHR021C	RPS27B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps27Ap and has similarity to rat S27 ribosomal protein
YAL035W	FUN12	GTPase, required for general translation initiation by promoting Met-tRNAiMet binding to ribosomes and ribosomal subunit joining; homolog of bacterial IF2
YPL142C	None	
YMR142C	RPL13B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl13Ap; not essential for viability; has similarity to rat L13 ribosomal protein
YLR198C	None	

YLR340W	RPP0	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302
YDR012W	RPL4B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Ap and has similarity to E. coli L4 and rat L4 ribosomal proteins
YDR447C	RPS17B	Ribosomal protein 51 (rp51) of the small (40s) subunit; nearly identical to Rps17Ap and has similarity to rat S17 ribosomal protein
YOR224C	RPB8	RNA polymerase subunit, found in RNA polymerase complexes I, II, and III
YOR312C	RPL20B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Ap and has similarity to rat L18a ribosomal protein
YDL184C	RPL41A	Ribosomal protein L47 of the large (60S) ribosomal subunit, identical to Rpl41Bp and has similarity to rat L41 ribosomal protein; comprised of only 25 amino acids; rpl41a rpl41b double null mutant is viable
YOR369C	RPS12	Protein component of the small (40S) ribosomal subunit; has similarity to rat ribosomal protein S12
YOL121C	RPS19A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps19Bp and has similarity to rat S19 ribosomal protein
YNL265C	IST1	Putative translation initiation factor, as suggested by computational analysis of large-scale protein-protein interaction data
YLR048W	RPS0B	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0 gene reduces growth rate, deletion of both genes is lethal
YPL081W	RPS9A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Ap and has similarity to E. coli S4 and rat S9 ribosomal proteins
YMR217W	GUA1	GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5'-phosphate (IMP); transcription is not subject to regulation by guanine but is negatively regulated by nutrient starvation
YHL001W	RPL14B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Ap and has similarity to rat L14 ribosomal protein
YIL052C	RPL34B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl34Ap and has similarity to rat L34 ribosomal protein
YER074W	RPS24A	Protein component of the small (40S) ribosomal subunit; identical to Rps24Bp and has similarity to rat S24 ribosomal protein
YER146W	LSM5	Component of small nuclear ribonucleoprotein complexes involved in RNA processing, splicing, and decay
YDL130W	RPP1B	Ribosomal protein P1 beta, a component of the ribosomal stalk, which is involved in the interaction between translational elongation factors and the ribosome; accumulation of P1 in the cytoplasm is regulated by phosphorylation and interaction with the P2 stalk component

YDL228C	None	
YOR277C	None	
YNL149C	None	
YGR109C	CLB6	role in DNA replication during S phase; B-type cyclin
YBR181C	RPS6B	Protein component of the small (40S) ribosomal subunit; identical to Rps6Ap and has similarity to rat S6 ribosomal protein
YAL003W	EFB1	Translation elongation factor 1 beta; stimulates nucleotide exchange to regenerate EF-1 alpha-GTP for the next elongation cycle; part of the EF-1 complex, which facilitates binding of aminoacyl-tRNA to the ribosomal A site
YLR406C	RPL31B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Ap and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p
YGL102C	None	
YLR197W	SIK1	Component of the small (ribosomal) subunit (SSU) processosome that contains U3 snoRNA; similar to microtubule binding proteins
YPL263C	KEL3	Cytoplasmic protein of unknown function
YKL181W	PRS1	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes
YPL198W	RPL7B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Ap and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2)
YML022W	APT1	Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis
YML056C	IMD4	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, member of a four-gene family in S. cerevisiae, constitutively expressed
YDR382W	RPP2B	Ribosomal protein P2 beta, a component of the ribosomal stalk, which is involved in the interaction between translational elongation factors and the ribosome; regulates the accumulation of P1 (Rpp1Ap and Rpp1Bp) in the cytoplasm
YOR169C	None	
YDL191W	RPL35A	Protein component of the large (60S) ribosomal subunit, identical to Rpl35Bp and has similarity to rat L35 ribosomal protein
YBR031W	RPL4A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins
YGR160W	None	
YLR249W	YEF3	stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes, and binds and hydrolyses ATP; EF-3 (translational elongation factor 3)

YLR185W	RPL37A	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl37Bp and to rat L37 ribosomal protein
YKL081W	TEF4	Translation elongation factor EF-1gamma
YDR025W	RPS11A	Protein component of the small (40S) ribosomal subunit; identical to Rps11Bp and has similarity to E. coli S17 and rat S11 ribosomal proteins
YHL011C	PRS3	5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes
YGL147C	RPL9A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Bp and has similarity to E. coli L6 and rat L9 ribosomal proteins
YDR091C	RLI1	Protein with strong similarity to human RNase L Inhibitor (RLI), required for vegetative growth and early sporulation; putative member of nontransporter group of ATP-binding cassette (ABC) superfamily
YMR194W	RPL36A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl36Ap and has similarity to rat L36 ribosomal protein; binds to 5.8 S rRNA
YJR124C	None	
YDR418W	RPL12B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Ap; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins
YDR450W	RPS18A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps18Bp and has similarity to E. coli S13 and rat S18 ribosomal proteins
YER042W	MXR1	peptide Methionine sulfoXide Reductase 1; peptide methionine sulfoxide reductase
YOR309C	None	
YNL301C	RPL18B	Protein component of the large (60S) ribosomal subunit, identical to Rpl18Ap and has similarity to rat L18 ribosomal protein
YIL069C	RPS24B	Protein component of the small (40S) ribosomal subunit; identical to Rps24Ap and has similarity to rat S24 ribosomal protein
YOR276W	CAF20	binds to eIF-4E, the mRNA cap-binding protein, and represses cap-dependent translation initiation by interfering with the interaction of eIF4E and eIF4G; mRNA cap-binding protein (eIF4F) 20K subunit
YPR132W	RPS23B	Ribosomal protein 28 (rp28) of the small (40S) ribosomal subunit, required for translational accuracy; nearly identical to Rps23Ap and similar to E. coli S12 and rat S23 ribosomal proteins; deletion of both RPS23A and RPS23B is lethal
YLR062C	BUD28	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 98% of ORF overlaps the verified gene RPL22A; diploid mutant displays a weak budding pattern phenotype in a systematic assay
YJL190C	RPS22A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity to E. coli S8 and rat

		S15a ribosomal proteins
YJL189W	RPL39	Protein component of the large (60S) ribosomal subunit, has similarity to rat L39 ribosomal protein; required for ribosome biogenesis; exhibits genetic interactions with SIS1 and PAB1
YBL087C	RPL23A	Protein component of the large (60S) ribosomal subunit, identical to Rpl23Bp and has similarity to E. coli L14 and rat L23 ribosomal proteins
YER102W	RPS8B	Protein component of the small (40S) ribosomal subunit; identical to Rps8Bp and has similarity to rat S8 ribosomal protein
YJR063W	RPA12	RNA polymerase I subunit A12.2; contains two zinc binding domains, and the N terminal domain is responsible for anchoring to the RNA pol I complex
YML063W	RPS1B	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Ap and has similarity to rat S3a ribosomal protein
YBR025C	None	
YOR096W	RPS7A	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps7Bp; interacts with Kti11p; deletion causes hypersensitivity to zymocin; has similarity to rat S7 and Xenopus S8 ribosomal proteins
YOR168W	GLN4	Glutamine tRNA synthetase, monomeric class I tRNA synthetase that catalyzes the specific glutaminylation of tRNA(Glu); N-terminal domain proposed to be involved in enzyme-tRNA interactions
YOR272W	YTM1	microtubule-associated protein
YJL138C	TIF2	translation initiation factor eIF4A
YBR048W	RPS11B	Protein component of the small (40S) ribosomal subunit; identical to Rps11Ap and has similarity to E. coli S17 and rat S11 ribosomal proteins
YJL177W	RPL17B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl17Ap and has similarity to E. coli L22 and rat L17 ribosomal proteins
YGR265W	None	
YER036C	ARB1	ATPase of the ATP-binding cassette (ABC) family involved in ribosome biogenesis, has similarity to Gcn20p
YJR123W	RPS5	Protein component of the small (40S) ribosomal subunit, the least basic of the non-acidic ribosomal proteins; phosphorylated in vivo; essential for viability; has similarity to E. coli S7 and rat S5 ribosomal proteins
YIL133C	RPL16A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Bp, E. coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p
YDR395W	SXM1	Nuclear protein; has similarity to Cse1p homologs including Nmd5p, Cse1p, Lph2p, and the human cellular apoptosis susceptibility protein, CAS1; also has similarity to the karyopherin Kap95p
YDL051W	LHP1	RNA binding protein required for maturation of tRNA and snRNA precursors; acts as a molecular chaperone for RNAs transcribed by polymerase III; homologous to human La (SS-B)

		autoantigen
YDL157C	None	
YPL249C-A	RPL36B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl36Bp and has similarity to rat L36 ribosomal protein; binds to 5.8 S rRNA
YKR094C	RPL40B	Fusion protein, identical to Rpl40Ap, that is cleaved to yield ubiquitin and a ribosomal protein of the large (60S) ribosomal subunit with similarity to rat L40; ubiquitin may facilitate assembly of the ribosomal protein into ribosomes
YIL148W	RPL40A	Fusion protein, identical to Rpl40Bp, that is cleaved to yield ubiquitin and a ribosomal protein of the large (60S) ribosomal subunit with similarity to rat L40; ubiquitin may facilitate assembly of the ribosomal protein into ribosomes
YLR061W	RPL22A	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl22Bp and to rat L22 ribosomal protein
YGL031C	RPL24A	Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to Rpl24Bp and has similarity to rat L24 ribosomal protein; not essential for translation but may be required for normal translation rate
YBR189W	RPS9B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins
YBL039C	URA7	CTP synthase, catalyzes the ATP-dependent transfer of amide nitrogen from glutamine to UTP to form CTP in last step of pyrimidine biosynthesis, very similar to URA8p but appears to be responsible for the majority of CTP synthesis
YMR230W	RPS10B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps10Ap and has similarity to rat ribosomal protein S10
YJR145C	RPS4A	Protein component of the small (40S) ribosomal subunit; mutation affects 20S pre-rRNA processing; identical to Rps4Bp and has similarity to rat S4 ribosomal protein
YML073C	RPL6A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA
YDR471W	RPL27B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein
YDL081C	RPP1A	Ribosomal protein P1 alpha, a component of the ribosomal stalk, which is involved in the interaction between translational elongation factors and the ribosome; accumulation of P1 in the cytoplasm is regulated by phosphorylation and interaction with the P2 stalk component
YLR017W	MEU1	Methylthioadenosine phosphorylase (MTAP), catalyzes the initial step in the methionine salvage pathway; affects polyamine biosynthesis through regulation of ornithine decarboxylase (Spe1p) activity; regulates ADH2 gene expression
YOL139C	CDC33	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p)

YHR203C	RPS4B	Protein component of the small (40S) ribosomal subunit; identical to Rps4Bp and has similarity to rat S4 ribosomal protein
YLR186W	EMG1	Protein required for the maturation of the 18S rRNA and for 40S ribosome production; associated with spindle/microtubules; nuclear localization depends on physical interaction with Nop14p; may bind snoRNAs
YMR260C	TIF11	Translation initiation factor eIF1A
YGL076C	RPL7A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2)
YDR500C	RPL37B	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl37Ap and to rat L37 ribosomal protein
YOR021C	None	
YER131W	RPS26B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps26Ap and has similarity to rat S26 ribosomal protein
YDL061C	RPS29B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps29Ap and has similarity to rat S29 and E. coli S14 ribosomal proteins
YPR102C	RPL11A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Bp; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11
YOR182C	RPS30B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps30Ap and has similarity to rat S30 ribosomal protein
YNL302C	RPS19B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps19Ap and has similarity to rat S19 ribosomal protein
YEL054C	RPL12A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Bp; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins
YOR293W	RPS10A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps10Bp and has similarity to rat ribosomal protein S10
YGR159C	NSR1	Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis
YGL030W	RPL30	Protein component of the large (60S) ribosomal subunit, has similarity to rat L30 ribosomal protein; involved in pre-rRNA processing in the nucleolus; autoregulates splicing of its transcript
YPL079W	RPL21B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl21Ap and has similarity to rat L21 ribosomal protein
YHL015W	RPS20	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. coli S10 and rat S20 ribosomal proteins

YOR234C	RPL33B	Ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to Rpl33Ap and has similarity to rat L35a; rpl33b null mutant exhibits normal growth while rpl33a rpl33b double null mutant is inviable
YDL136W	RPL35B	Protein component of the large (60S) ribosomal subunit, identical to Rpl35Ap and has similarity to rat L35 ribosomal protein
YFR032C-A	RPL29	Protein component of the large (60S) ribosomal subunit, has similarity to rat L29 ribosomal protein; not essential for translation, but required for proper joining of the large and small ribosomal subunits and for normal translation rate
YMR116C	ASC1	WD repeat protein (G-beta like protein) that interacts with the translational machinery; G-beta like protein
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
YDR002W	YRB1	Yeast Ran Binder #1; suppressor of FUS1; homolog of mouse HTF9a and human RanBP1; nuclear GTPase-activating protein for Ran
YPL197C	None	
YDR429C	TIF35	Subunit of the core complex of translation initiation factor 3(eIF3), which is essential for translation
YGL189C	RPS26A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps26Bp and has similarity to rat S26 ribosomal protein
YOR214C	None	
YNL141W	AAH1	Adenine deaminase (adenine aminohydrolase), involved in purine salvage and nitrogen catabolism
YNL255C	GIS2	Putative zinc finger protein with similarity to human CNBP, proposed to be involved in the RAS/cAMP signaling pathway
YCR031C	RPS14A	Ribosomal protein 59 (rp59) of the small (40S) ribosomal subunit, required for ribosome assembly; mutations confer resistance to cryptopleurine; nearly identical to Rps14Bp and similar to E. coli S11 and rat S14 ribosomal proteins
YFR031C-A	RPL2A	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins
YLR150W	STM1	Protein that binds quadruplex nucleic acids; multicopy suppressor of tom1 and pop2 mutations; acts with Cdc13p to maintain telomere structure
YKL006W	RPL14A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Bp and has similarity to rat L14 ribosomal protein; rpl14a csh5 double null mutant exhibits synthetic slow growth
YKL056C	None	
YGL120C	PRP43	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from the spliceosome
YBL072C	RPS8A	Protein component of the small (40S) ribosomal subunit; identical to Rps8Ap and has similarity to rat S8 ribosomal protein
YLR367W	RPS22B	Protein component of the small (40S) ribosomal subunit; nearly

		identical to Rps22Ap and has similarity to E. coli S8 and rat S15a ribosomal proteins
YPL143W	RPL33A	N-terminally acetylated ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to Rpl33Bp and has similarity to rat L35a; rpl33a null mutant exhibits slow growth while rpl33a rpl33b double null mutant is inviable
YHL033C	RPL8A	Ribosomal protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Bp and has similarity to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits
YDR417C	None	
YGL135W	RPL1B	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal
YML024W	RPS17A	Ribosomal protein 51 (rp51) of the small (40s) subunit; nearly identical to Rps17Bp and has similarity to rat S17 ribosomal protein
YJR094W-A	RPL43B	Protein component of the large (60S) ribosomal subunit, identical to Rpl43Ap and has similarity to rat L37a ribosomal protein
YGR027C	RPS25A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein
YNL178W	RPS3	Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic (AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat S3 ribosomal proteins
YLR076C	None	
YHR010W	RPL27A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Bp and has similarity to rat L27 ribosomal protein
YJL188C	BUD19	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 88% of ORF overlaps the verified gene RPL39; diploid mutant displays a weak budding pattern phenotype in a systematic assay
YPL131W	RPL5	Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat L5 ribosomal proteins; binds 5S rRNA and is required for 60S subunit assembly
YPL211W	NIP7	Nip7p is required for 60S ribosome subunit biogenesis; involved in ribosome biogenesis
YLL045C	RPL8B	Ribosomal protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Ap and has similarity to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits
YGL123W	RPS2	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins
YJR070C	LIA1	Protein that binds to the C-terminal domain of Hyp2p (eIF5A); has four to five HEAT-like repeats
YOR167C	RPS28A	Protein component of the small (40S) ribosomal subunit; nearly

		identical to Rps28Ap and has similarity to rat S28 ribosomal protein
YOR095C	RKI1	Ribose-5-phosphate ketol-isomerase
YEL055C	POL5	Protein with sequence similarity to the human MybBP1A and weak sequence similar to B-type DNA polymerases, not required for chromosomal DNA replication; required for the synthesis of rRNA
YDL229W	SSB1	Stress-Seventy Subfamily B; involved in translation, perhaps by guiding the nascent chain through the ribosome; cytoplasmic member of the HSP70 family
YPR118W	None	
YGR118W	RPS23A	Ribosomal protein 28 (rp28) of the small (40S) ribosomal subunit, required for translational accuracy; nearly identical to Rps23Bp and similar to E. coli S12 and rat S23 ribosomal proteins; deletion of both RPS23A and RPS23B is lethal
YGR214W	RPS0A	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Bp; required for maturation of 18S rRNA along with Rps0Bp; deletion of either RPS0 gene reduces growth rate, deletion of both genes is lethal
YDL133C-A	RPL41B	Ribosomal protein L47 of the large (60S) ribosomal subunit, identical to Rpl41Ap and has similarity to rat L41 ribosomal protein; comprised of only 25 amino acids; rpl41a rpl41b double null mutant is viable
YLR167W	RPS31	Fusion protein that is cleaved to yield a ribosomal protein of the small (40S) subunit and ubiquitin; ubiquitin may facilitate assembly of the ribosomal protein into ribosomes; interacts genetically with translation factor eIF2B
YHR127W	None	
YHR089C	GAR1	Protein component of the H/ACA snoRNP pseudouridylase complex, involved in the modification and cleavage of the 18S pre-rRNA
YCR087W	None	
YGL103W	RPL28	Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can mutate to cycloheximide resistance
YML026C	RPS18B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps18Ap and has similarity to E. coli S13 and rat S18 ribosomal proteins
YNL162W	RPL42A	Protein component of the large (60S) ribosomal subunit, identical to Rpl42Bp and has similarity to rat L44 ribosomal protein
YGR148C	RPL24B	Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to Rpl24Ap and has similarity to rat L24 ribosomal protein; not essential for translation but may be required for normal translation rate
YGR034W	RPL26B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA
YLR388W	RPS29A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps29Bp and has similarity to rat S29 and E. coli

		S14 ribosomal proteins
YLL044W	None	
YDR454C	GUK1	Guanylate kinase, converts GMP to GDP; required for growth and mannose outer chain elongation of cell wall N-linked glycoproteins
YOL120C	RPL18A	Protein component of the large (60S) ribosomal subunit, identical to Rpl18Bp and has similarity to rat L18 ribosomal protein; intron of RPL18A pre-mRNA forms stem-loop structures that are a target for Rnt1p cleavage leading to degradation
YOL040C	RPS15	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S19 and rat S15 ribosomal proteins
YNL096C	RPS7B	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps7Ap; interacts with Kti11p; deletion causes hypersensitivity to zymocin; has similarity to rat S7 and Xenopus S8 ribosomal proteins
YJL136C	RPS21B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps21Bp and has similarity to rat S21 ribosomal protein
YLR441C	RPS1A	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Bp and has similarity to rat S3a ribosomal protein
YMR121C	RPL15B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl15Ap and has similarity to rat L15 ribosomal protein; binds to 5.8 S rRNA
YOL127W	RPL25	Protein compoent of the large (60S) ribosomal subunit, has similarity to E. coli L23 and rat L23a ribosomal proteins; binds to 26S rRNA via a conserved C-terminal motif
YOL039W	RPP2A	Ribosomal protein P2 alpha, a component of the ribosomal stalk, which is involved in the interaction between translational elongation factors and the ribosome; regulates the accumulation of P1 (Rpp1Ap and Rpp1Bp) in the cytoplasm
YJL183W	MNN11	Subunit of a Golgi mannosyltransferase complex that also contains Anp1p, Mnn9p, Mnn10p, and Hoc1p, and mediates elongation of the polysaccharide mannan backbone; has homology to Mnn10p
YJL191W	RPS14B	Ribosomal protein 59 (rp59) of the small (40S) ribosomal subunit, required for ribosome assembly; mutations confer resistance to cryptopleurine; nearly identical to Rps14Ap and similar to E. coli S11 and rat S14 ribosomal proteins
YLR448W	RPL6B	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA
YDR064W	RPS13	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosomal proteins
YDL083C	RPS16B	Protein component of the small (40S) ribosomal subunit; identical to Rps16Ap and has similarity to E. coli S9 and rat S16 ribosomal proteins
YDL201W	TRM8	Subunit of a tRNA methyltransferase complex composed of Trm8p and Trm82p that catalyzes 7-methylguanosine modification of tRNA

YPR044C	None	
YNL244C	SUI1	translation initiation factor eIF1
YEL042W	GDA1	Guanosine diphosphatase located in the Golgi, involved in the transport of GDP-mannose into the Golgi lumen by converting GDP to GMP after mannose is transferred its substrate
YEL026W	SNU13	part of small (ribosomal) subunit (SSU) processosome (contains U3 snoRNA); RNA binding protein (putative), similar to Nhp2p; U4/U6.U5 snRNP component
YLR333C	RPS25B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Ap and has similarity to rat S25 ribosomal protein
YLR325C	RPL38	Protein component of the large (60S) ribosomal subunit, has similarity to rat L38 ribosomal protein
YOL077C	BRX1	Nucleolar protein involved in the biogenesis of large ribosomal subunits; depletion leads to defects in rRNA processing and a block in the assembly of large ribosomal subunits; possesses a sigma(70)-like RNA-binding motif
YHR141C	RPL42B	Protein component of the large (60S) ribosomal subunit, identical to Rpl42Ap and has similarity to rat L44; required for propagation of the killer toxin-encoding M1 double-stranded RNA satellite of the L-A double-stranded RNA virus
YPL220W	RPL1A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal
YPL238C	None	
YLR372W	SUR4	Elongase III synthesizes 20-26-carbon fatty acids from C18-CoA primers; involved in fatty acid biosynthesis
YLR287C-A	RPS30A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps30Bp and has similarity to rat S30 ribosomal protein
YKL180W	RPL17A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl17Bp and has similarity to E. coli L22 and rat L17 ribosomal proteins; copurifies with the components of the outer kinetochore DASH complex
YKL156W	RPS27A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps27Bp and has similarity to rat S27 ribosomal protein
YHR068W	DYS1	Deoxyhypusine synthase, catalyzes formation of deoxyhypusine, the first step in hypusine biosynthesis; triggers posttranslational hypusination of translation elongation factor eIF-5A and regulates its intracellular levels; tetrameric
YBL092W	RPL32	Protein component of the large (60S) ribosomal subunit, has similairty to rat L32 ribosomal protein; overexpression disrupts telomeric silencing
YER117W	RPL23B	Protein component of the large (60S) ribosomal subunit, identical to Rpl23Ap and has similarity to E. coli L14 and rat L23 ribosomal proteins
YDL151C	BUD30	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 96% of ORF overlaps the verified gene RPC53; diploid mutant displays

		a weak budding pattern phenotype in a systematic assay
YNL064C	YDJ1	yeast dnaJ homolog (nuclear envelope protein); heat shock protein
YBR191W	RPL21A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl21Bp and has similarity to rat L21 ribosomal protein
YLR344W	RPL26A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Bp and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA
YLR264W	RPS28B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp and has similarity to rat S28 ribosomal protein
YPL090C	RPS6A	Protein component of the small (40S) ribosomal subunit; identical to Rps6Bp and has similarity to rat S6 ribosomal protein
YMR242C	RPL20A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp and has similarity to rat L18a ribosomal protein
YLR432W	IMD3	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, member of a four-gene family in S. cerevisiae, constitutively expressed
YHR128W	FUR1	Uracil phosphoribosyltransferase, synthesizes UMP from uracil; involved in the pyrimidine salvage pathway
(57) MODULE 65		
Expression regulators		
YPR013C	None	
YOR363C	PIP2	peroxisome induction pathway 2 (PIP2); transcriptional activator of peroxisome proliferation; may form heterodimer with Oaf1 to activate oleate-inducible gene expression; activator of peroxisome proliferation
YNL305C	None	
YDR195W	REF2	RNA-binding protein involved in the cleavage step of mRNA 3'-end formation prior to polyadenylation; also involved in snoRNA maturation
Genotype regulators		
M9_415311_420076		YVH1(2,4) DAL1(2,2) DAL4(2,2) DAL2(1,4) DCG1(3,3) YIR030W-A DAL7(1,2) DAL3(2,4) MGA2(15,4) LYS1(0,1) YIR035C YIR036C YIR036W-A HYR1(0,3) GTT1(1,20)
Module genes		
YJL077C	ICS3	Protein of unknown function
YDR259C	YAP6	Basic leucine zipper (bZIP) transcription factor
YHL035C	VMR1	Protein of unknown function, member of the ATP-binding cassette (ABC) family, potential Cdc28p substrate
YDR263C	DIN7	Mitochondrial nuclease functioning in DNA repair and replication, modulates the stability of the mitochondrial genome, induced by exposure to mutagens, also induced during meiosis at a time nearly coincident with commitment to recombination
YIR019C	MUC1	GPI-anchored cell surface glycoprotein required for diploid pseudohyphal formation and haploid invasive growth, transcriptionally regulated by the MAPK pathway (via Ste12p

		and Tec1p) and the cAMP pathway (via Flo8p)
YHL042W	None	
YPL236C	None	
YHL043W	ECM34	Non-essential protein of unknown function
YDL037C	BSC1	Protein of unconfirmed function, similar to cell surface flocculin Muc1p; ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of expression
YKL202W	None	
YDL038C	None	
YKL200C	None	
YOR009W	TIR4	None
YNL142W	MEP2	Ammonia permease; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH4+)
YDL039C	PRM7	Pheromone-regulated protein, predicted to have one transmembrane segment; promoter contains Gcn4p binding elements
(58) MODULE 67		
Genotype regulators		
M4_527445_527517		YDR034C-A YDR034W-B ARO3(0,3) EHD3(0,3) KRS1(0,3) ENA5(29,341) ENA2(24,290) ENA1(13,15)
Module genes		
YDR038C	ENA5	Protein with similarity to P-type ATPase sodium pumps
YDR033W	MRH1	Protein that localizes primarily to the plasma membrane, also found at the nuclear envelope; has similarity to Hsp30p and Yro2p, which are induced during heat shock
YDR039C	ENA2	P-type ATPase sodium pump, involved in Na+ efflux to allow salt tolerance; likely not involved in Li+ efflux
YDR040C	ENA1	P-type ATPase sodium pump, involved in Na+ and Li+ efflux to allow salt tolerance
YCR073C	SSK22	functionally redundant with, and homologous to, SSK2; protein kinase
(59) MODULE 68		
Expression regulators		
YOR047C	STD1	Protein that interacts with the Snf1p protein kinase and Spt15p in two-hybrid and in in vitro binding studies
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)-Cys(6) binuclear cluster domain type
YOR047C	STD1	Protein that interacts with the Snf1p protein kinase and Spt15p in two-hybrid and in in vitro binding studies
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
YBR212W	NGR1	negative growth regulatory protein
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 seven zinc-finger domains
YMR019W	STB4	Protein that binds Sin3p in a two-hybrid assay
Module genes		
YOR099W	KTR1	Alpha-1,2-mannosyltransferase involved in O- and N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family
YOL076W	MDM20	Subunit of the NatB N-terminal acetyltransferase, which catalyzes acetylation of the amino-terminal methionine residues of all proteins beginning with Met-Asp or Met-Glu and of some proteins beginning with Met-Asn or Met-Met; involved in mitochondrial inheritance and actin assembly
YNL169C	PSD1	Phosphatidylserine decarboxylase of the mitochondrial inner membrane, converts phosphatidylserine to phosphatidylethanolamine
YJL153C	INO1	Inositol 1-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is coregulated with other phospholipid biosynthetic genes by Ino2p and Ino4p, which bind the UASINO DNA element
YHR177W	None	
YJR106W	ECM27	Non-essential protein of unknown function
YOL013C	HRD1	Ubiquitin-protein ligase required for endoplasmic reticulum-associated degradation (ERAD) of misfolded proteins; genetically linked to the unfolded protein response (UPR); regulated through association with Hrd3p; contains an H2 ring finger
YKL073W	LHS1	Molecular chaperone of the endoplasmic reticulum lumen, involved in polypeptide translocation and folding; member of the Hsp70 family; localizes to the lumen of the ER; regulated by the unfolded protein response pathway
YCL043C	PDI1	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-surface proteins, unscrambles non-native disulfide bonds
YPL021W	ECM23	Non-essential protein of unconfirmed function; affects pre-rRNA processing, may act as a negative regulator of the transcription of genes involved in pseudohyphal growth; homologous to Srd1p
YDR516C	EMI2	Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for sporulation
YLR133W	CKI1	choline kinase
YMR214W	SCJ1	dnaJ homolog
YGL126W	SCS3	Protein required for inositol prototrophy
YJR073C	OPI3	Phospholipid methyltransferase (methylene-fatty-acyl-phospholipid synthase), catalyzes the last two steps in phosphatidylcholine biosynthesis
YDR519W	FPR2	Membrane-bound peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; expression pattern suggests possible involvement in ER protein trafficking

YKL126W	YPK1	76.5 kDa Serine/threonine protein kinase with similarity to protein kinase C, is 90% identical to Ypk2p
YHR142W	CHS7	Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p export from the ER
YDR277C	MTH1	Negative regulator of the glucose-sensing signal transduction pathway, required for repression of transcription by Rgt1p; interacts with Rgt1p and the Snf3p and Rgt2p glucose sensors; phosphorylated by Yck1p, triggering Mth1p degradation
YML028W	TSA1	Thioredoxin-peroxidase (TPx), reduces H2O2 and alkyl hydroperoxides with the use of hydrogens provided by thioredoxin, thioredoxin reductase, and NADPH; provides protection against oxidation systems that generate reactive oxygen and sulfur species
YOL031C	SIL1	ER-localized protein required for protein translocation into the ER, interacts with the ATPase domain of the Kar2p chaperone suggesting some role in modulating its activity; homolog of Yarrowia lipolytica SLS1; GrpE-like protein in the ER
YBR201W	DER1	Endoplasmic reticulum membrane protein, required for the protein degradation process associated with the ER, involved in the retrograde transport of misfolded or unassembled proteins
YDL193W	None	
YGR284C	ERV29	Protein localized to COPII-coated vesicles, involved in vesicle formation and incorporation of specific secretory cargo
YJL082W	IML2	Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus
YMR184W	None	
YML130C	ERO1	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum
YNL043C	None	
YNL170W	None	
YJL034W	KAR2	ATPase involved in protein import into the ER, also acts as a chaperone to mediate protein folding in the ER and may play a role in ER export of soluble proteins; regulates the unfolded protein response via interaction with Ire1p
YKL165C	MCD4	Protein involved in glycosylphosphatidylinositol (GPI) anchor synthesis; multimembrane-spanning protein that localizes to the endoplasmic reticulum; highly conserved among eukaryotes
YER142C	MAG1	3-methyl-adenine DNA glycosylase involved in protecting DNA against alkylating agents; initiates base excision repair by removing damaged bases to create abasic sites that are subsequently repaired
YOR288C	MPD1	Member of the protein disulfide isomerase (PDI) family; overexpression suppresses the defect in maturation of carboxypeptidase Y, and defects in other essential Pdi1p functions, caused by PDI1 deletion
YLL016W	None	
YKR011C	None	
YNL144C	None	
(60) MODULE 69		
Expression regulators		

YLR452C	SST2	Protein involved in desensitization to alpha-factor pheromone; member of the RGS (regulator of G-protein signalling) family; GTPase-activating protein
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 genes
YCL055W	KAR4	Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
YDR195W	REF2	RNA-binding protein involved in the cleavage step of mRNA 3'-end formation prior to polyadenylation; also involved in snoRNA maturation
YDR283C	GCN2	Protein kinase, phosphorylates the alpha-subunit of translation initiation factor eIF2 (Sui2p) in response to starvation; activated by uncharged tRNAs and the Gcn1p-Gcn20p complex
YPR070W	MED1	Subunit 1 of the Mediator complex essential for transcriptional regulation
Module genes		
YML048W-A	None	
YPR115W	None	
YHR005C	GPA1	Alpha subunit of G protein coupled to mating factor receptors, involved in the mating pheromone signal transduction pathway; component of pheromone response pathway common to both a and alpha cells
YJL157C	FAR1	Cyclin-dependent kinase inhibitor that mediates cell cycle arrest in response to pheromone; also forms a complex with Cdc24p, Ste4p, and Ste18p that may specify the direction of polarized growth during mating; potential Cdc28p substrate
YBR083W	TEC1	transcription factor of the TEA/ATTS DNA-binding domain family, regulator of Ty1 expression
YKL189W	HYM1	Component of the RAM signaling network that is involved in regulation of Ace2p activity and cellular morphogenesis, interacts with Kic1p and Sog2p, localizes to sites of polarized growth during budding and during the mating response
YML046W	PRP39	U1 snRNP protein involved in splicing, contains multiple tetriatricopeptide repeats
YBL016W	FUS3	Mitogen-activated protein kinase (MAPK) involved in mating pheromone response; activated by phosporylation by Ste7p; controls different aspects of the mating response by phosphorylating transcriptional and cytoplasmic targets
YMR065W	KAR5	Protein required for nuclear membrane fusion during karyogamy, localizes to the membrane with a soluble portion in the endoplasmic reticulum lumen, may form a complex with Jem1p and Kar2p; expression of the gene is regulated by pheromone
YNL192W	CHS1	Chitin synthase I, requires activation from zymogenic form in order to catalyze the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for repairing the chitin septum during cytokinesis; transcription activated by mating factor

YCR089W	FIG2	Cell wall adhesin, expressed specifically during mating; may be involved in maintenance of cell wall integrity during mating
YDL127W	PCL2	G1 cyclin, associates with Pho85p cyclin-dependent kinase (Cdk) to contribute to entry into the mitotic cell cycle, essential for cell morphogenesis; localizes to sites of polarized cell growth
YIL037C	PRM2	Pheromone-regulated protein, predicted to have 4 transmembrane segments and a coiled coil domain; regulated by Ste12p
YIL117C	PRM5	Pheromone-regulated protein, predicted to have 1 transmembrane segment; induced during cell integrity signalling
YBR040W	FIG1	Integral membrane protein required for efficient mating; may participate in or regulate the low affinity Ca2+ influx system, which affects intracellular signaling and cell-cell fusion during mating
YCL027W	FUS1	Membrane protein localized to the shmoo tip, required for cell fusion; expression regulated by mating pheromone; proposed to coordinate signaling, fusion, and polarization events required for fusion; potential Cdc28p substrate
YFR026C	None	
YDL089W	None	
YDR309C	GIC2	Protein of unknown function involved in initiation of budding and cellular polarization, interacts with Cdc42p via the Cdc42/Rac-interactive binding (CRIB) domain
YDR085C	AFR1	coordinates regulation of alpha-factor receptor signalling and induction of morphogenesis during conjugation; cytoskeletal protein, similar to arrestins
YNR044W	AGA1	Anchorage subunit of a-agglutinin of a-cells, highly O-glycosylated protein with N-terminal secretion signal and C-terminal signal for addition of GPI anchor to cell wall, linked to adhesion subunit Aga2p via two disulfide bonds
YOR343C	None	
YKL104C	GFA1	Glutamine-fructose-6-phosphate amidotransferase, catalyzes the formation of glucosamine-6-P and glutamate from fructose-6-P and glutamine in the first step of chitin biosynthesis
YJR153W	PGU1	Endo-polygalacturonase
YDR125C	ECM18	Protein of unknown function, similar to Rlp24p
YNL279W	PRM1	Pheromone-regulated multispanning membrane protein involved in membrane fusion during mating; predicted to have 5 transmembrane segments and a coiled coil domain; localizes to the shmoo tip; regulated by Ste12p
YMR232W	FUS2	Cytoplasmic protein localized to the shmoo tip; required for the alignment of parental nuclei before nuclear fusion during mating
YDR282C	None	
YNL042W	BOP3	Protein of unknown function, potential Cdc28p substrate; overproduction suppresses a pam1 slv3 double null mutation
YKR042W	UTH1	Youth, involved in determining yeast longevity; involved in cell growth
YHR084W	STE12	Transcription factor that is activated by a MAP kinase signaling cascade, activates genes involved in mating or

		pseudohyphal/invasive growth pathways; cooperates with Tec1p transcription factor to regulate genes specific for invasive growth
YDR124W	None	
(61) MODULE 70		
Expression regulators		
YDR496C	PUF6	member of the PUF protein family; YDR496C
YMR019W	STB4	Protein that binds Sin3p in a two-hybrid assay
YDR264C	AKR1	Negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; Ankyrin repeat-containing protein
Genotype regulators		
M15_1152_43217		CTR9(13,2) PSF3(1,1) PEX11(0,1) SPT20(4,15) DCP1(0,4) YOL150C GRE2(6,81) FRE7(38,11) YOL153C ZPS1(3,8) YOL155C YOL155W-A HXT11(6,53) YOL157C ENB1(5,8) YOL159C YOL159C-A YOL160W YOL161C YOL162W YOL163W YOL164W YOL164W-A AAD15(7,561) YOL166C YOL166W-A
Module genes		
YAR066W	None	
YIL169C	None	
YOL155C	None	
YAR068W	None	
YHR214W	None	
YHR214W-A	None	
(62) MODULE 71		
Expression regulators		
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation; shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
YDR043C	NRG1	Transcriptional repressor that recruits the Cyc8p-Tup1p complex to promoters; mediates glucose repression and negatively regulates a variety of processes including filamentous growth and alkaline pH response
YGR288W	MAL13	MAL-activator protein, part of complex locus MAL1; nonfunctional in genomic reference strain S288C
YCL026C-A	FRM2	Protein of unknown function, involved in the integration of lipid signaling pathways with cellular homeostasis
YKR099W	BAS1	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways
YGL180W	ATG1	Protein serine/threonine kinase, required for autophagy and for the cytoplasm-to-vacuole targeting (Cvt) pathway
YAL056W	GPB2	Proposed beta subunit of the heterotrimeric G protein that interacts with the receptor Grp1p, has signaling role in response to nutrients; involved in regulation of pseudohyphal growth through cAMP levels; homolog of Gpb1p

Module genes		
YGL249W	ZIP2	Required for 'ZIPpering' up meiotic chromosomes during chromosome synapsis; involved in meiotic recombination and disjunction
YJR154W	None	
YMR126C	DLT1	Protein of unknown function, deletion causes sensitivity to thermal stress
YGR161C	RTS3	Hypothetical ORF
YGR065C	VHT1	vitamin H transporter; H+-biotin symporter
YNR058W	BIO3	7,8-diamino-pelargonic acid aminotransferase (DAPA), catalyzes the second step in the biotin biosynthesis pathway; BIO3 is in a cluster of 3 genes (BIO3, BIO4, and BIO5) that mediate biotin synthesis
YMR271C	URA10	Fifth step in pyrimidine bio5; Orotate phosphoribosyltransferase 2
YIR005W	IST3	Component of the U2 snRNP, required for the first catalytic step of splicing and for spliceosomal assembly; interacts with Rds3p and is required for Mer1p-activated splicing
YHR199C	FMP34	The authentic, non-tagged protein was localized to the mitochondria
YGL183C	MND1	needed for Meiotic Nuclear Divisions
YER184C	None	
YOR100C	CRC1	Mitochondrial inner membrane carnitine transporter, required for carnitine-dependent transport of acetyl-CoA from peroxisomes to mitochondria during fatty acid beta-oxidation
YNL125C	ESBP6	Protein with similarity to monocarboxylate permeases, appears not to be involved in transport of monocarboxylates such as lactate, pyruvate or acetate across the plasma membrane
YPR078C	None	
YNR056C	BIO5	Putative transmembrane protein involved in the biotin biosynthesis pathway; responsible for uptake of 7-keto 8-aminopelargonic acid; BIO5 is in a cluster of 3 genes (BIO3, BIO4, and BIO5) that mediate biotin synthesis
YBR105C	VID24	also involved in vacuolar protein targeting; peripheral vesicle membrane protein
YGR154C	None	
YPL264C	None	
YLL056C	None	
YIL166C	None	
YJL037W	None	
YNR057C	BIO4	Dethiobiotin synthetase, catalyzes the third step in the biotin biosynthesis pathway; BIO4 is in a cluster of 3 genes (BIO3, BIO4, and BIO5) that mediate biotin synthesis; expression appears to be repressed at low iron levels
YJR025C	BNA1	3-hydroxyanthranilic acid dioxygenase, required for biosynthesis of nicotinic acid from tryptophan via kynurenine pathway
YLL055W	None	
YER065C	ICL1	Isocitrate lyase, catalyzes the formation of succinate and

		glyoxylate from isocitrate, a key reaction of the glyoxylate cycle; expression of ICL1 is induced by growth on ethanol and repressed by growth on glucose
YDL101C	DUN1	Cell-cycle checkpoint serine-threonine kinase required for DNA damage-induced transcription of certain target genes, phosphorylation of Rad55p and Sml1p, and transient G2/M arrest after DNA damage; also regulates postreplicative DNA repair
YNL183C	NPR1	Protein kinase that stabilizes several plasma membrane amino acid transporters by antagonizing their ubiquitin-mediated degradation
YBR294W	SUL1	Probable sulfate transport protein; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates
YCL049C	None	
YDL234C	GYP7	GTPase-activating protein for yeast Rab family members including: Ypt7p (most effective), Ypt1p, Ypt31p, and Ypt32p (in vitro); involved in vesicle mediated protein trafficking
YHL036W	MUP3	Low affinity methionine permease, similar to Mup1p
YDL214C	PRR2	Protein kinase with a possible role in MAP kinase signaling in the pheromone response pathway
YJR149W	None	
YLR152C	None	
YHR112C	None	
YIR017C	MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism
YMR306C-A	None	
YER185W	None	
YDR076W	RAD55	Protein that stimulates strand exchange by stabilizing the binding of Rad51p to single-stranded DNA; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; forms heterodimer with Rad57p
YGR110W	None	
YNR050C	LYS9	Saccharopine dehydrogenase (NADP+, L-glutamate-forming); catalyzes the formation of saccharopine from alpha-aminoadipate 6-semialdehyde, which is the seventh step in lysine biosynthesis pathway
YDR186C	None	
YOR292C	None	
YGR197C	SNG1	Protein involved in nitrosoguanidine resistance
YDL215C	GDH2	NAD(+)-dependent glutamate dehydrogenase, degrades glutamate to ammonia and alpha-ketoglutarate; expression sensitive to nitrogen catabolite repression and intracellular ammonia levels
YIR042C	None	
(63) MODULE 72		
Genotype regulators		
M4_85846_106892		ARF1(0,3) YDL193W SNF3(12,2) SEC31(6,4) YDL196W ASF2(9,4) GGC1(0,4) YDL199C MGT1(3,0) TRM8(0,4)

		MRPL11(0,4) YDL203C RTN2(0,5) HEM3(0,5) YDL206W GLE1(4,5) NHP2(1,2) CWC2(1,2) UGA4(1,9) YDL211C SHR3(1,3) NOP6(0,3)
Module genes		
YDL210W	UGA4	GABA-specific transport protein
YDL205C	HEM3	Phorphobilinogen deaminase, catalyzes the conversion of 4-porphobilinogen to hydroxymethylbilane, the third step in the heme biosynthetic pathway; localizes to both the cytoplasm and nucleus; expression is regulated by Hap2p-Hap3p
YPL201C	None	
YDL227C	HO	Site-specific endonuclease required for gene conversion at the MAT locus (homothallic switching) through the generation of a ds DNA break; expression restricted to mother cells in late G1 as controlled by Swi4p-Swi6p, Swi5p and Ash1p
(64) MODULE 73		
Genotype regulators		
M7_375499_375499		YGL063C-A PUS2(2,1) MRH4(0,1) ALG2(3,1) SGF73(6,1) NPY1(1,1) MNP1(0,0) SRF3(1,0) RPB9(0,0) RCS1(8,1) YGL072C HSF1(6,2) YGL074C MPS2(2,3)
M7_402833_415585		YGL039W HEM2(0,1) YGL041C YGL041C-B YGL041W-A YGL042C DST1(0,5) RNA15(1,3) RIM8(4,11) YGL046W YGL047W RPT6(0,1) TIF4632(5,4) YGL050W MST27(8,49) YGL052W PRM8(96,548) ERV14(0,233) OLE1(1,14) SDS23(4,14) YGL057C RAD6(0,1) YGL059W
Module genes		
YGL053W	PRM8	Pheromone-regulated protein with 2 predicted transmembrane segments and an FF sequence, a motif involved in COPII binding; forms a complex with Prp9p in the ER
YOR027W	STI1	Heat shock protein also induced by canavanine and entry into stationary phase
YGL051W	MST27	Putative integral membrane protein, involved in vesicle formation; forms complex with Mst28p; member of DUP240 gene family; binds COPI and COPII vesicles
YGL057C	None	
YNL007C	SIS1	HSP40 family chaperone; sit4 suppressor, dnaJ homolog
YAR033W	MST28	Putative integral membrane protein, involved in vesicle formation; forms complex with Mst27p; member of DUP240 gene family; binds COPI and COPII vesicles
YGL052W	None	
(65) MODULE 75		
Expression regulators		
YGL037C	PNC1	NAD(+) salvage pathway gene; pyrazinamidase and nicotinamidase
YGL099W	LSG1	Putative GTPase involved in 60S ribosomal subunit biogenesis; localized to the cytoplasm
YGL037C	PNC1	NAD(+) salvage pathway gene; pyrazinamidase and nicotinamidase
YER054C	GIP2	Putative regulatory subunit of the protein phosphatase Glc7p, proposed to be involved in glycogen metabolism; contains a

		conserved motif (GVNK motif) that is also found in Gac1p, Pig1p, and Pig2p
YBR140C	IRA1	GTPase-activating protein that negatively regulates RAS by converting it from the GTP- to the GDP-bound inactive form, required for reducing cAMP levels under nutrient limiting conditions, mediates membrane association of adenylate cyclase
YCR040W	MATALPHA1	Transcriptional co-activator involved in regulation of mating-type-specific gene expression; targets the transcription factor Mcm1p to the promoters of alpha-specific genes; one of two genes encoded by the alpha mating type cassette
YHR122W	None	
Module genes		
YGL146C	None	
YDR154C	None	
YJR019C	TES1	Thioesterase; peroxisomal acyl-CoA thioesterase
YER041W	YEN1	Protein of unknown function, has similarity to endonuclease Rth1p; potentially phosphorylated by Cdc28p
YDR513W	TTR1	Glutaredoxin (thioltransferase) (glutathione reductase)
YBR052C	None	
YBR139W	None	
YGL038C	OCH1	Mannosyltransferase of the cis-Golgi apparatus, initiates the polymannose outer chain elongation of N-linked oligosaccharides of glycoproteins
YIR037W	HYR1	Thiol peroxidase that functions as a hydroperoxide receptor to sense intracellular hydroperoxide levels and transduce a redox signal to the Yap1p transcription factor
YDR077W	SED1	Isolated as a suppressor of an erd2 deletion mutant (ERD2 is the HDEL receptor that sorts ER proteins), SED1 encodes a cell wall protein.
YDR535C	None	
YDL023C	SRF4	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 80% of ORF overlaps the verified gene GPD1; deletion in cyr1 mutant results in loss of stress resistance
YKR089C	STC1	Protein of unknown function found in lipid particles; potential Cdc28p substrate
YJL137C	GLG2	Self-glucosylating initiator of glycogen synthesis, also glucosylates n-dodecyl-beta-D-maltoside; similar to mammalian glycogenin
YKL162C	None	
YGL081W	None	
YBR203W	COS111	Protein required for wild-type resistance to the antifungal drug ciclopirox olamine; not related to the COS family of subtelomerically-encoded proteins
YMR110C	None	
YPL221W	BOP1	Protein of unknown function, overproduction suppresses a pam1 slv3 double null mutation
YLL039C	UBI4	Ubiquitin, becomes conjugated to proteins, marking them for selective degradation via the ubiquitin-26S proteasome system;

		essential for the cellular stress response
YDR343C	HXT6	High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt7p, expressed at high basal levels relative to other HXTs, repression of expression by high glucose requires SNF3
YDL022W	GPD1	glycerol-3-phosphate dehydrogenase
YLR257W	None	
YJR059W	PTK2	Putative serine/threonine protein kinase that enhances spermine uptake; putative serine)/threonine kinase involved in spermine metabolism
YBR053C	None	
YHR030C	SLT2	Suppressor of lyt2; serine/threonine MAP kinase
YAL060W	BDH1	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during fermentation and allows using 2,3-butanediol as a carbon source during aerobic growth
YHR037W	PUT2	delta-1-pyrroline-5-carboxylate dehydrogenase
YIL065C	FIS1	Mitochondrial outer membrane protein involved in membrane fission, required for loalization of Dnm1p and Mdv1p during mitochondrial division
YIL111W	COX5B	Subunit Vb of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; predominantly expressed during anaerobic growth while its isoform Va (Cox5Ap) is expressed during aerobic growth
YOR176W	HEM15	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic pathway; Yfh1p mediates the use of iron by Hem15p
YBR056W	None	
YML004C	GLO1	Monomeric glyoxalase I, catalyzes the detoxification of methylglyoxal (a by-product of glycolysis) via condensation with glutathione to produce S-D-lactoylglutathione; expression regulated by methylglyoxal levels and osmotic stress
YLL026W	HSP104	Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI+] propagation
YJR085C	None	
YFR053C	HXK1	Hexokinase isoenzyme 1, cytosolic protein that catalyzes phosphorylation of glucose during glucose metabolism, expression is highest during growth on non-glucose carbon sources and is repressed by Hxk2p
YER067W	None	
YCR030C	SYP1	Protein with a potential role in actin cytoskeletal organization; overexpression suppresses a pfy1 (profilin) null mutation
YLR327C	None	
YGR149W	None	
YDR230W	None	
YIL033C	BCY1	Regulatory subunit of the cyclic AMP-dependent protein kinase

		(PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation
YOR136W	IDH2	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle
YBR097W	VPS15	Myristoylated Serine/threonine protein kinase involved in vacuolar protein sorting
YCR075C	ERS1	Protein with similarity to human cystinosin, which is a H(+)-driven transporter involved in L-cystine export from lysosomes and implicated in the disease cystinosis; contains seven transmembrane domains
YKL066W	None	
YIL124W	AYR1	NADPH-dependent 1-acyl dihydroxyacetone phosphate reductase found in lipid particles and ER; involved in phosphatidic acid biosynthesis and required for spore germination; capable of metabolizing mammalian steroid hormones
YOL063C	HUS1	Protein of unknown function
YGR255C	COQ6	Putative flavin-dependent monooxygenase, involved in ubiquinone (Coenzyme Q) biosynthesis; located on the matrix side of the mitochondrial inner membrane
YBR149W	ARA1	Large subunit of NADP+ dependent arabinose dehydrogenase, involved in carbohydrate metabolism; small subunit is unidentified
YBR137W	None	
YLR284C	ECI1	Peroxisomal delta3,delta2-enoyl-CoA isomerase, hexameric protein that converts 3-hexenoyl-CoA to trans-2-hexenoyl-CoA, essential for the beta-oxidation of unsaturated fatty acids, oleate-induced
YHR092C	HXT4	High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high levels of glucose
YMR315W	None	
YMR155W	None	
YJL005W	CYR1	Required for START A of cell cycle, and glucose and nitrogen repression of sporulation; adenylate cyclase
YGR223C	HSV2	Phosphatidylinositol 3,5-bisphosphate-binding protein, predicted to fold as a seven-bladed beta-propeller; displays punctate cytoplasmic localization
YGL104C	VPS73	None
YBL064C	PRX1	Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity, has a role in reduction of hydroperoxides; induced during respiratory growth and under conditions of oxidative stress
YFR057W	None	
YCR011C	ADP1	Shows homology to ATP-dependent permeases; Active transport ATPase
YOR386W	PHR1	photolyase
YKL036C	None	

YPL203W	TPK2	Involved in nutrient control of cell growth and division; cAMP-dependent protein kinase catalytic subunit
YKL067W	YNK1	Nucleoside diphosphate kinase, catalyzes the phosphorylation of nucleoside diphosphates into the corresponding triphosphates for nucleic acid biosynthesis
YJR020W	None	
YOR374W	ALD4	Mitochondrial aldehyde dehydrogenase that utilizes NADP+ or NAD+ equally as coenzymes; expression is glucose repressed
YJL214W	HXT8	Protein of unknown function with similarity to hexose transporter family members, expression is induced by low levels of glucose and repressed by high levels of glucose
YNR001C	CIT1	citrate synthase. Nuclear encoded mitochondrial protein.
YHR097C	None	
YDR272W	GLO2	Cytoplasmic glyoxalase II, catalyzes the hydrolysis of S-D-lactoylglutathione into glutathione and D-lactate
YDL106C	PHO2	Homeobox transcription factor; regulatory targets include genes involved in phosphate metabolism; binds cooperatively with Pho4p to the PHO5 promoter; phosphorylation of Pho2p facilitates interaction with Pho4p
YER177W	BMH1	14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes including exocytosis and vesicle transport, Ras/MAPK signaling during pseudohyphal development, rapamycin-sentitive signaling, and others
YGR244C	LSC2	Beta subunit of succinyl-CoA ligase, which is a mitochondrial enzyme of the TCA cycle that catalyzes the nucleotide-dependent conversion of succinyl-CoA to succinate
YJL068C	None	
YJL164C	TPK1	putative catalytic subunit of cAMP-dependent protein kinase
YPL003W	ULA1	Protein that acts together with Uba3p to activate Rub1p before its conjugation to proteins (neddlyation), which may play a role in protein degradation
YKL035W	UGP1	UDP-glucose pyrophosphorylase or UTP-glucose-1-phosphate uridylyltransferase, EC:2.7.7.9
YCR091W	KIN82	Putative serine/threonine protein kinase, most similar to cyclic nucleotide-dependent protein kinase subfamily and the protein kinase C subfamily
YML110C	COQ5	2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase, involved in ubiquinone (Coenzyme Q) biosynthesis; located in mitochondria
YDL110C	None	
YOR135C	None	
YBL015W	ACH1	Acetyl-coA hydrolase, primarily localized to mitochondria; required for acetate utilization and for diploid pseudohyphal growth
YMR152W	YIM1	Mitochondrial inner membrane protease, similar to E. coli leader peptidase
YMR136W	GAT2	Protein containing GATA family zinc finger motifs; similar to Gln3p and Dal80p; expression repressed by leucine
YCL040W	GLK1	Glucokinase, catalyzes the phosphorylation of glucose at C6 in

		the first irreversible step of glucose metabolism; one of three glucose phosphorylating enzymes; expression regulated by non-fermentable carbon sources
YCR004C	YCP4	Protein of unknown function, has sequence and structural similarity to flavodoxins; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
YDR342C	HXT7	High-affinity glucose transporter of the major facilitator superfamily, nearly identical to Hxt6p, expressed at high basal levels relative to other HXTs, expression repressed by high glucose levels
YFR015C	GSY1	Glycogen synthase with similarity to Gsy2p, the more highly expressed yeast homolog; expression induced by glucose limitation, nitrogen starvation, enviromental stress, and entry into stationary phase
YOR142W	LSC1	Alpha subunit of succinyl-CoA ligase, which is a mitochondrial enzyme of the TCA cycle that catalyzes the nucleotide-dependent conversion of succinyl-CoA to succinate
(66) MODULE 76		
Expression regulators		
YKL101W	HSL1	Nim1p-related protein kinase that regulates the morphogenesis and septin checkpoints; associates with the assembled septin filament; required along with Hsl7p for bud neck recruitment, phosphorylation, and degradation of Swe1p
YKR099W	BAS1	Myb-related transcription factor involved in regulating basal and induced expression of genes of the purine and histidine biosynthesis pathways
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; expression is cell cycle-regulated; potential Cdc28p substrate
YIL119C	RPI1	Putative transcriptional regulator; overexpression suppresses the heat shock sensitivity of wild-type RAS2 overexpression and also suppresses the cell lysis defect of an mpk1 mutation
YMR001C	CDC5	Polo-like kinase with similarity to Xenopus Plx1 and S. pombe Plo1p; found at bud neck, nucleus and SPBs; has multiple functions in mitosis and cytokinesis through phosphorylation of substrates; may be a Cdc28p substrate
YPL256C	CLN2	role in cell cycle START; G(sub)1 cyclin
Genotype regulators		
M12_659357_674651		YLR257W GSY2(1,6) HSP60(0,6) LCB5(10,6) VPS63(3,0) YPT6(0,13) RBF7 RED1(13,14) YLR264C-A RPS28B(0,5) NEJ1(7,0) PDR8(8,6) BOP2(4,6) SEC22(0,3) YLR269C DCS1(0,4) YLR271W
Module genes		
YDR024W	FYV1	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; mutation decreases survival upon exposure to K1 killer toxin
YLR205C	HMX1	ER localized, heme-binding peroxidase involved in the degradation of heme; does not exhibit heme oxygenase activity despite similarity to heme oxygenases; expression regulated by AFT1

YLR056W	ERG3	C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow on non-fermentable carbon sources
YLR101C	None	
YMR061W	RNA14	Cleavage and polyadenylation factor I (CF I) component involved in cleavage and polyadenylation of mRNA 3' ends; bridges interaction between Rna15p and Hrp1p in the CF I complex
YMR009W	None	
YLR100W	ERG27	3-keto sterol reductase, catalyzes the last of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; mutants are sterol auxotrophs
YGR060W	ERG25	C-4 methyl sterol oxidase, catalyzes the first of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; mutants accumulate the sterol intermediate 4,4-dimethylzymosterol
YML008C	ERG6	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24
YNL017C	None	
YER044C	ERG28	Endoplasmic reticulum membrane protein, may facilitate protein-protein interactions between the Erg26p dehydrogenase and the Erg27p 3-ketoreductase and/or tether these enzymes to the ER
YMR015C	ERG5	C-22 sterol desaturase, a cytochrome P450 enzyme that catalyzes the formation of the C-22(23) double bond in the sterol side chain in ergosterol biosynthesis; may be a target of azole antifungal drugs
YHR039C	MSC7	Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; msc7 mutants are defective in directing meiotic recombination events to homologous chromatids
YMR134W	None	
YHR190W	ERG9	Farnesyl-diphosphate farnesyl transferase (squalene synthase), joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway
YGR049W	SCM4	Protein that suppresses ts allele of CDC4 when overexpressed
YMR202W	ERG2	C-8 sterol isomerase, catalyzes the isomerization of the delta-8 double bond to the delta-7 position at an intermediate step in ergosterol biosynthesis
YNR019W	ARE2	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity in the presence of oxygen
YNR043W	MVD1	involved in the polyisoprene biosynthesis pathway; mevalonate pyrophosphate decarboxylase
YHR007C	ERG11	Lanosterol 14-alpha-demethylase, catalyzes the C-14 demethylation of lanosterol to form 4,4''-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family

YIR024C	None	
YER145C	FTR1	High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron
YJR048W	CYC1	Cytochrome c, isoform 1; electron carrier of the mitochondrial intermembrane space that transfers electrons from ubiquinone-cytochrome c oxidoreductase to cytochrome c oxidase during cellular respiration
YGR235C	None	
YGR266W	None	
YGL055W	OLE1	Fatty acid desaturase, required for monounsaturated fatty acid synthesis and for normal distribution of mitochondria
YEL033W	None	
YGR234W	YHB1	may play a role in the oxidative stress response; Flavohemoglobin
YML126C	ERG13	3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) synthase, catalyzes the formation of HMG-CoA from acetyl-CoA and acetoacetyl-CoA; involved in the second step in mevalonate biosynthesis
YPL117C	IDI1	Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase), catalyzes an essential activation step in the isoprenoid biosynthetic pathway; required for viability
YNL111C	CYB5	cytochrome b5
YJL167W	ERG20	Farnesyl pyrophosphate synthetase, has both dimethylallyltranstransferase and geranyltranstransferase activities; catalyzes the formation of C15 farnesyl pyrophosphate units for isoprenoid and sterol biosynthesis
YMR208W	ERG12	Mevalonate kinase, acts in the biosynthesis of isoprenoids and sterols, including ergosterol, from mevalonate
YML075C	HMG1	One of two isozymes of HMG-CoA reductase that catalyzes the conversion of HMG-CoA to mevalonate, which is a rate-limiting step in sterol biosynthesis; localizes to the nuclear envelope; overproduction induces the formation of karmellae
YEL034W	HYP2	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions
YPL028W	ERG10	Acetyl-CoA C-acetyltransferase (acetoacetyl-CoA thiolase), cytosolic enzyme that transfers an acetyl group from one acetyl-CoA molecule to another, forming acetoacetyl-CoA; involved in the first step in mevalonate biosynthesis
YLL012W	YEH1	Hypothetical ORF
YJR047C	ANB1	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Hyp2p; undergoes an essential hypusination modification; expressed under anaerobic conditions
YDL086W	None	
YLR153C	ACS2	one of 2 acetyl-coA synthetases in yeast; acetyl-coenzyme A synthetase
YGL001C	ERG26	C-3 sterol dehydrogenase, catalyzes the second of three steps

		required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis
YHR072W	ERG7	Lanosterol synthase, an essential enzyme that catalyzes the cyclization of squalene 2,3-epoxide, a step in ergosterol biosynthesis
(67) MODULE 77		
Genotype regulators		
M10_461201_464261		SUI2(0,2) YJR008W TDH2(0,8) SPC1(0,1) MET3(0,24) YJR011C YJR012C GPI14(2,4) RBF22 YJR015W ILV3(1,3) ESS1(1,0) YJR018W TES1(0,1) YJR020W REC107(108,2) LSM8(0,2) YJR023C YJR024C BNA1(1,78) YJR026W
Module genes		
YNR011C	PRP2	RNA-dependent ATPase in the DEAH-box family, required for activation of the spliceosome before the first transesterification step in RNA splicing
YJR015W	None	
(68) MODULE 78		
Expression regulators		
YMR036C	MIH1	S. pombe cdc25+ homolog; homolog of S. pombe cdc25
Genotype regulators		
M5_109310_117705		EDC3(0,0) YEL016C PMP2(0,0) GTT3(1,0) YEL018C-A EAF5(0,0) MMS21(1,0) YEL020C YEL020C-B TIM9(0,3) URA3(222,250) GEA2(5,1) YEL023C RIP1(1,5) YEL025C SNU13(0,1) CUP5(0,0)
Module genes		
YLR420W	URA4	Third step in pyrimidine biosynthesis pathway; dihydrooratase
YMR241W	YHM2	Yeast suppressor gene of HM mutant (abf2); DNA-binding protein, mtDNA stabilizing protein, mitochondrial inner membrane protein with low homology to RIM2
YER088C	DOT6	Protein of unknown function, involved in telomeric gene silencing and filamentation
YOL126C	MDH2	Cytoplasmic malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in gluconeogenesis and glyoxylate cycle
YJL130C	URA2	Multifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase) that catalyzes the two first reactions of the pyrimidine pathway; carbamoyl-phophate synthetase, aspartate transcarbamylase, and glutamine amidotransferase
YOL143C	RIB4	Lumazine synthase (6,7-dimethyl-8-ribityllumazine synthase, also known as DMRL synthase); catalyzes synthesis of immediate precursor to riboflavin
YNL018C	None	
YNL065W	AQR1	Plasma membrane transporter of the major facilitator superfamily that confers resistance to short-chain monocarboxylic acids and quinidine
YKL216W	URA1	The enzyme catalyzes the conversion of dihydroorotic acid to orotic acid; dihydroorotate dehydrogenase
(69) MODULE 79		

Expression regulators		
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 seven zinc-finger domains
YPL075W	GCR1	Transcriptional activator of genes involved in glycolysis, functions and interacts with Gcr2p
YGL014W	PUF4	member of the PUF protein family; YGL014W
Genotype regulators		
M10_336317_353027		YJL043W GYP6(4,4) YJL045W YJL046W RTT101(1,0) YJL047C-A UBX6(0,8) YJL049W MTR4(5,11) YJL051W YJL052C-A TDH1(1,1) PEP8(2,1) TIM54(1,3) YJL055W ZAP1(10,2) YJL057C BIT61(4,2)
Module genes		
YAR023C	None	
YGL258W	None	
YDR284C	DPP1	Diacylglycerol pyrophosphate (DGPP) phosphatase, zinc-regulated vacuolar membrane-associated lipid phosphatase, dephosphorylates DGPP to phosphatidate (PA) and Pi, then PA to diacylglycerol; involved in lipid signaling and cell metabolism
YNL254C	None	
YOR387C	None	
YOL154W	ZPS1	Putative GPI-anchored protein; transcription is induced under low-zinc conditions, as mediated by the Zap1p transcription factor, and at alkaline pH
YKL175W	ZRT3	Vacuolar membrane zinc transporter, transports zinc from storage in the vacuole to the cytoplasm when needed; transcription is induced under conditions of zinc deficiency
YIL045W	PIG2	Interacts with Gsy2p; Protein with 30% identity to protein corresponding to YER054
YGL256W	ADH4	Alcohol dehydrogenase type IV, dimeric enzyme demonstrated to be zinc-dependent despite sequence similarity to iron-activated alcohol dehydrogenases; transcription is induced in response to zinc deficiency; alcohol dehydrogenase isoenzyme IV
YPL104W	MSD1	Mitochondrial aspartyl-tRNA synthetase, required for acylation of aspartyl-tRNA; yeast and bacterial aspartyl-, asparaginyl-, and lysyl-tRNA synthetases contain regions with high sequence similarity, suggesting a common ancestral gene
(70) MODULE 80		
Genotype regulators		
M12_131338_131338		SPO75(2,1) MMM1(104,0) YLL006W-A YLL007C DRS1(1,0) COX17(0,0) PSR1(5,8) SOF1(0,6) YEH1(4,5) PUF3(226,5) YLL014W
Module genes		
YLL007C	None	
YLL013C	PUF3	member of the PUF protein family, which is named for the founding members, PUmilio and Fbf

(71) MODULE 81		
Expression regulators		
YDR213W	UPC2	involved in sterol uptake; zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
YDL230W	PTP1	phosphotyrosine-specific protein phosphatase
YGL229C	SAP4	Protein required for function of the Sit4p protein phosphatase, member of a family of similar proteins that form complexes with Sit4p, including Sap155p, Sap185p, and Sap190p
Module genes		
YOR393W	ERR1	Protein of unknown function, has similarity to enolases
YNR073C	None	
YCR007C	None	
YBL095W	None	
YJR150C	DAN1	Cell wall mannoprotein with similarity to Tir1p, Tir2p, Tir3p, and Tir4p; expressed under anaerobic conditions, completely repressed during aerobic growth
YOR010C	TIR2	Cold shock-induced protein of the Srp1p/Tip1p family of serine-alanine-rich proteins
YMR153C-A	None	
(72) MODULE 83		
Expression regulators		
YDR264C	AKR1	Negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; Ankyrin repeat-containing protein
YJR122W	CAF17	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins
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 inactivates Mig3p, allowing induction of damage response genes
YIR017C	MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism
YBR150C	TBS1	Probable Zn-finger protein
YCL055W	KAR4	Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
YHR099W	TRA1	Histone acetyltransferase component, putative ortholog of human TRRAP which is an essential cofactor of c-Myc
Module genes		
YOR187W	TUF1	Translation elongation factor Tu, mitochondrial
YNL185C	MRPL19	Mitochondrial ribosomal protein of the large subunit
YDR114C	None	
YBR268W	MRPL37	Mitochondrial ribosomal protein of the large subunit
YOR020C	HSP10	Mitochondrial matrix co-chaperonin that inhibits the ATPase activity of Hsp60p, a mitochondrial chaperonin; involved in

		protein folding and sorting in the mitochondria; 10 kD heat shock protein with similarity to E. coli groES
YPR166C	MRP2	Mitochondrial ribosomal protein of the small subunit
YCR046C	IMG1	Mitochondrial ribosomal protein of the small subunit, required for respiration and for maintenance of the mitochondrial genome
YJL104W	PAM16	Constituent of the mitochondrial import motor associated with the presequence translocase, along with Ssc1p, Tim44p, Mge1p, and Pam18p; has similarity to J-domain containing proteins
YLR259C	HSP60	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL
YGR181W	TIM13	Translocase of the inner membrane; mitochondrial intermembrane space protein mediating import and insertion of polytopic inner membrane proteins; Subunit of mitochondrial protein import machinery
YIL098C	FMC1	Mitochondrial matrix protein, required for assembly or stability at high temperature of the F1 sector of mitochondrial F1F0 ATP synthase
YPR099C	None	
YLR139C	SLS1	Mitochondrial membrane protein required for assembly of respiratory-chain enzyme complexes III and IV; coordinates expression of mitochondrially-encoded genes; may facilitate delivery of mRNA to membrane-bound translation machinery
YDR296W	MHR1	Protein involved in mitochondrial homologous DNA recombination and in transcription regulation; binds to activation domains of acidic activators; presence in RNA pol II holoenzyme may help recruit an Ssn3p-active form of the holoenzyme to target promoters
YJL131C	None	
YGR082W	TOM20	Translocase of Outer Mitochondrial membrane; 20 kDa mitochondrial outer membrane protein import receptor
YER174C	GRX4	Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx3p and Grx5p; protects cells from oxidative damage
YOR286W	FMP31	The authentic, non-tagged protein was localized to the mitochondria
YLL009C	COX17	Copper metallochaperone that shuttles copper from the cytosol to the mitochondrial intermembrane space for delivery to cytochrome c oxidase
YEL020W-A	TIM9	Mitochondrial intermembrane space protein mediating import and insertion of polytopic inner membrane proteins
YPR133W-A	TOM5	Translocase of the Outer Mitochondrial membrane; Membrane protein involved in protein translocation to the mitochondria
YOR334W	MRS2	Mitochondrial inner membrane Mg(2+) channel, required for maintenance of intramitochondrial Mg(2+) concentrations at the correct level to support splicing of group II introns
YPL183W-A	None	
YHR005C-A	MRS11	Essential protein of the mitochondrial intermembrane space,

		forms a complex with Tim9p (TIM10 complex) that mediates insertion of hydrophobic proteins at the inner membrane, has homology to Mrs5p, which is also involved in this process
(73) MODULE 84		
Expression regulators		
YFR009W	GCN20	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA
YOR337W	TEA1	Mutants are defective in Ty1 Enhancer-mediated Activation; Ty1 enhancer activator
YJR122W	CAF17	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins
YDR283C	GCN2	Protein kinase, phosphorylates the alpha-subunit of translation initiation factor eIF2 (Sui2p) in response to starvation; activated by uncharged tRNAs and the Gcn1p-Gcn20p complex
YDR225W	HTA1	One of two nearly identical (see also HTA2) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p
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 principal activation function of the complex
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 principal activation function of the complex
Module genes		
YPL097W	MSY1	Tyrosyl-tRNA synthetase
YMR193W	MRPL24	Mitochondrial ribosomal protein of the large subunit
YDR337W	MRPS28	Mitochondrial ribosomal protein of the small subunit
YNL083W	SAL1	Probable transporter, member of the Ca2+-binding subfamily of the mitochondrial carrier family, with two EF-hand motifs; Pet9p and Sal1p have an overlapping function critical for viability; polymorphic in different S. cerevisiae strains
YCR003W	MRPL32	Mitochondrial ribosomal protein of the large subunit
YBR251W	MRPS5	Mitochondrial ribosomal protein of the small subunit
YLR382C	NAM2	mitochondrial leucyl tRNA synthetase
YHR116W	COX23	Protein that functions in mitochondrial copper homeostasis and is essential for functional cytochrome oxidase expression; homologous to COX17, localized to the mitochondrial intermembrane space
YPL173W	MRPL40	Mitochondrial ribosomal protein of the large subunit
YDR237W	MRPL7	Mitochondrial ribosomal protein of the large subunit
YDR375C	BCS1	Protein of the mitochondrial inner membrane that functions as an ATP-dependent chaperone, required for the assembly of the cytochrome bc(1) complex from the Rip1p and Qcr10p proteins;

		member of the CDC48/PAS1/SEC18 ATPase family
YDR494W	RSM28	Mitochondrial ribosomal protein of the small subunit
YER182W	FMP10	The authentic, non-tagged protein was localized to the mitochondria
YBR120C	CBP6	Translational activator of COB mRNA
YNL177C	MRPL22	Mitochondrial ribosomal protein of the large subunit
YBR185C	MBA1	Protein involved in assembly of mitochondrial respiratory complexes; may act as a receptor for proteins destined for export from the mitochondrial matrix to the inner membrane
YJL096W	MRPL49	Mitochondrial ribosomal protein of the large subunit
YKL138C	MRPL31	Mitochondrial ribosomal protein of the large subunit
YER058W	PET117	Protein required for assembly of cytochrome c oxidase
YDL202W	MRPL11	Mitochondrial ribosomal protein of the large subunit
YKR085C	MRPL20	Mitochondrial ribosomal protein of the large subunit
YLR204W	QRI5	Mitochondrial protein of unknown function
YPL029W	SUV3	ATP-dependent RNA helicase, component of the mitochondrial degradosome along with the RNase Msu1p; the degradosome associates with the ribosome and mediates turnover of aberrant or unprocessed RNAs
YIR021W	MRS1	Protein required for the splicing of two mitochondrial group I introns (BI3 in COB and AI5beta in COX1); forms a splicing complex, containing four subunits of Mrs1p and two subunits of the BI3-encoded maturase, that binds to the BI3 RNA
YDR175C	RSM24	Mitochondrial ribosomal protein of the small subunit
YMR286W	MRPL33	Mitochondrial ribosomal protein of the large subunit
YDR462W	MRPL28	Mitochondrial ribosomal protein of the large subunit
YNL137C	NAM9	Mitochondrial ribosomal protein of the small subunit; can mutate to suppress nonsense mutations in mitochondrial genes
YNL081C	SWS2	Putative mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S13 ribosomal protein
YLR312W-A	MRPL15	Mitochondrial ribosomal protein of the large subunit
YBR192W	RIM2	Protein of the mitochondrial carrier (MCF) family that is required for respiration; Probable carrier protein, mitochondrial
YDR041W	RSM10	Mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S10 ribosomal protein; essential for viability, unlike most other mitoribosomal proteins
YIL093C	RSM25	Mitochondrial ribosomal protein of the small subunit
YBR037C	SCO1	inner mitochondrial membrane protein
YGR028W	MSP1	40 kDa putative membrane-spanning ATPase
YLR253W	None	
YKL087C	CYT2	links heme covalently to apocytochrome c1; cytochrome c1 heme lyase
YKL167C	MRP49	Mitochondrial ribosomal protein of the large subunit, not essential for mitochondrial translation
YHR109W	CTM1	Cytochrome c lysine methyltransferase, trimethylates residue 72 of apo-cytochrome c (Cyc1p) in the cytosol; not required for normal respiratory growth
YGL143C	MRF1	Mitochondrial polypeptide chain release factor, involved in stop

		codon recognition and hydrolysis of the peptidyl-tRNA bond during mitochondrial translation; lack of MRF1 causes mitochondrial genome instability
YMR158W	MRPS8	Mitochondrial ribosomal protein of the small subunit
YFR007W	None	
YER087W	None	
YJL112W	MDV1	WD repeat protein that regulates steps in the Dnm1p-dependent process of mitochondrial fission
YHR147C	MRPL6	Mitochondrial ribosomal protein of the large subunit
YHR091C	MSR1	Nuclear-encoded mitochondrial protein; Arginyl-tRNA synthetase
YGL107C	RMD9	Mitochondrial protein required for sporulation
YMR188C	MRPS17	Mitochondrial ribosomal protein of the small subunit
YDR322W	MRPL35	Mitochondrial ribosomal protein of the large subunit
YNL005C	MRP7	Mitochondrial ribosomal protein of the large subunit
YDL107W	MSS2	cox1 pre-mRNA splicing factor
YPR100W	MRPL51	Mitochondrial ribosomal protein of the large subunit
YGR062C	COX18	Mitochondrial inner membrane protein, required for export of the Cox2p C terminus from the mitochondrial matrix to the intermembrane space during its assembly into cytochrome c oxidase; similar to Oxa2p of N.crassa
YBR262C	FMP51	The authentic, non-tagged protein was localized to the mitochondria
YLR239C	LIP2	Lipoyl ligase, involved in the modification of mitochondrial enzymes by the attachment of lipoic acid groups
YGR165W	MRPS35	Mitochondrial ribosomal protein of the small subunit
YPL118W	MRP51	Mitochondrial ribosomal protein of the large subunit; MRP51 exhibits genetic interactions with mutations in the COX2 and COX3 mRNA 5'-untranslated leader sequences
YML129C	COX14	Mitochondrial membrane protein, required for assembly of cytochrome c oxidase
YOR354C	MSC6	Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to mitochondria; msc6 mutants are defective in directing meiotic recombination events to homologous chromatids
YOL033W	MSE1	Mitochondrial glutamyl-tRNA synthetase, encoded by a nuclear gene
YPL172C	COX10	Heme A:farnesyltransferase, catalyzes the first step in the conversion of protoheme to the heme A prosthetic group required for cytochrome c oxidase activity; human ortholog is associated with mitochondrial disorders
YNR020C	None	
YKL170W	MRPL38	Mitochondrial ribosomal protein of the large subunit; appears as two protein spots (YmL34 and YmL38) on two-dimensional SDS gels
YGL236C	MTO1	Mitochondrial protein required for respiration in paromomycin-resistant 15S rRNA mutants; forms a heterodimer complex with Mss1p that plays a role in optimizing mitochondrial protein synthesis

YBL090W	MRP21	Mitochondrial ribosomal protein of the large subunit; MRP21 exhibits genetic interactions with mutations in the COX2 and COX3 mRNA 5'-untranslated leader sequences
YMR267W	PPA2	Mitochondrial inorganic pyrophosphatase, required for mitochondrial function and possibly involved in energy generation from inorganic pyrophosphate
YDR347W	MRP1	Mitochondrial ribosomal protein of the small subunit; MRP1 exhibits genetic interactions with PET122, encoding a COX3-specific translational activator, and with PET123, encoding a small subunit mitochondrial ribosomal protein
YPR125W	None	
YKL053C-A	MDM35	Mitochondrial Distribution and Morphology; Similar to human sequence predicted by GENSCAN
YHR038W	RRF1	Ribosomal Recycling Factor 1; originally characterized as FIL1, a Factor for Isocitrate Lyase expression; mitochondrial ribosome recycling factor
YBL038W	MRPL16	Mitochondrial ribosomal protein of the large subunit
YML009C	MRPL39	Mitochondrial ribosomal protein of the large subunit
YJR113C	RSM7	Mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S7 ribosomal protein
YDR511W	ACN9	Protein of the mitochondrial intermembrane space, required for acetate utilization and gluconeogenesis; has orthologs in higher eukaryotes
YNL122C	None	
YEL050C	RML2	Mitochondrial ribosomal protein of the large subunit, has similarity to E. coli L2 ribosomal protein; fat21 mutant allele causes inability to utilize oleate and may interfere with activity of the Adr1p transcription factor
YBR122C	MRPL36	Mitochondrial ribosomal protein of the large subunit; overproduction suppresses mutations in the COX2 leader peptide-encoding region
YNL073W	MSK1	Mitochondrial lysine-tRNA synthetase, required for import of both aminoacylated and deacylated forms of tRNA(Lys) into mitochondria
YDR116C	MRPL1	Mitochondrial ribosomal protein of the large subunit
YKL195W	MIA40	Essential protein of the mitochondrial intermembrane space, involved in import and assembly of intermembrane space proteins
YGL235W	None	
YKR006C	MRPL13	Mitochondrial ribosomal protein of the large subunit, not essential for mitochondrial translation
YIL070C	MAM33	Acidic protein of the mitochondrial matrix involved in oxidative phosphorylation; related to the human complement receptor gC1q-R
YJL063C	MRPL8	Mitochondrial ribosomal protein of the large subunit
YGR021W	None	
YMR257C	PET111	Specific translational activator for the COX2 mRNA, located in the mitochondrial inner membrane
YPL215W	CBP3	Protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex); involved in

		cytochrome-c reductase assembly
YLR439W	MRPL4	Mitochondrial ribosomal protein of the large subunit
YNL315C	ATP11	Molecular chaperone, required for the assembly of alpha and beta subunits into the F1 sector of mitochondrial F1F0 ATP synthase
YBR282W	MRPL27	Mitochondrial ribosomal protein of the large subunit
YMR157C	FMP39	The authentic, non-tagged protein was localized to the mitochondria
YHR059W	FYV4	Protein of unknown function, required for survival upon exposure to K1 killer toxin
YGL069C	SRF3	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; 92% of ORF overlaps the uncharacterized ORF YGL068W; deletion in cyr1 mutant results in loss of stress resistance
YER078C	None	
YJL046W	None	
YKL169C	None	
YGL129C	RSM23	Mitochondrial ribosomal protein of the small subunit, has similarity to mammalian apoptosis mediator proteins; null mutation prevents induction of apoptosis by overproduction of metacaspase Mca1p
YNR040W	None	
YOR266W	PNT1	Involved in targeting of proteins to the mitochondrial inner membrane; Pentamidine resistance protein; involved in pentamidine resistance protein
YNL284C	MRPL10	Mitochondrial ribosomal protein of the large subunit; appears as two protein spots (YmL10 and YmL18) on two-dimensional SDS gels
YNL306W	MRPS18	Mitochondrial ribosomal protein of the small subunit; essential for viability, unlike most other mitoribosomal proteins
YJL180C	ATP12	Molecular chaperone, required for the assembly of alpha and beta subunits into the F1 sector of mitochondrial F1F0 ATP synthase
YGR076C	MRPL25	Mitochondrial ribosomal protein of the large subunit
YGR084C	MRP13	Mitochondrial ribosomal protein of the small subunit
YBR146W	MRPS9	Mitochondrial ribosomal protein of the small subunit
YDR316W	OMS1	None
YGL068W	MNP1	Putative mitochondrial-nucleoid specific ribosomal protein; Protein required for cell viability
YHL004W	MRP4	Mitochondrial ribosomal protein of the small subunit
YML087C	None	
YOR158W	PET123	Mitochondrial ribosomal protein of the small subunit; PET123 exhibits genetic interactions with PET122, which encodes a COX3 mRNA-specific translational activator
YLR008C	PAM18	Constituent of the mitochondrial import motor associated with the presequence translocase, along with Ssc1p, Tim44p, Mge1p, and Pam16p; stimulates the ATPase activity of Ssc1p to drive mitochondrial import; contains a J domain
YNL184C	None	

YCR024C	None	
YOL071W	EMI5	Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1, also required for sporulation
YMR098C	None	
YER050C	RSM18	Mitochondrial ribosomal protein of the small subunit, has similarity to E. coli S18 ribosomal protein
YDR194C	MSS116	Mitochondrial RNA helicase of the DEAD box family, necessary for splicing of several mitochondrial introns
YNL252C	MRPL17	Mitochondrial ribosomal protein of the large subunit
YGR220C	MRPL9	Mitochondrial ribosomal protein of the large subunit
YLR069C	MEF1	mitochondrial elongation factor G-like protein
YHR011W	DIA4	Probable mitochondrial seryl-tRNA synthetase, mutant displays increased invasive and pseudohyphal growth
YMR166C	None	
YHR198C	FMP22	The authentic, non-tagged protein was localized to the mitochondria
YDR430C	CYM1	Cytosolic metalloprotease; computational analysis of large-scale protein-protein interaction data suggests a possible role in pyruvate metabolism
YJR101W	RSM26	Mitochondrial ribosomal protein of the small subunit
YOR150W	MRPL23	Mitochondrial ribosomal protein of the large subunit
YOL023W	IFM1	Mitochondrial translation initiation factor 2
YGR169C	PUS6	RNA:Psi-synthase
YMR024W	MRPL3	Mitochondrial ribosomal protein of the large subunit
YKL194C	MST1	mitochondrial threonine-tRNA synthetase
(74) MODULE 85		
Expression regulators		
YBR158W	AMN1	Involved in daughter cell separation and Chromosome STability; Chromosome STability
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
Genotype regulators		
M5_553222_568734		ECM32(5,17) BMH1(0,3) PDA1(0,1) DMC1(44,9) ISC10(6,4) SLO1(0,9) YER181C FMP10(2,4) FAU1(1,31) YER184C YER185W YER186C YER186W-A YER187W YER188C-A YER188W YER189W YER190C-A YER190C-B YRF1-2(809,5)
Module genes		
YLL065W	None	
YDR543C	None	
YKL225W	None	
YNL337W	None	
YNR077C	None	
YER188W	None	
YJR162C	None	

YFL063W	None	
(75) MODULE 86		
Expression regulators		
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation; shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
YGL037C	PNC1	NAD(+) salvage pathway gene; pyrazinamidase and nicotinamidase
YPL204W	HRR25	Similar to YCK1 and YCK2, two other casein kinase I isoforms; found primarily in nucleus; may be involved in DNA-damage repair; casein kinase I isoform
YJL089W	SIP4	Possibly involved in Snf1p regulated transcriptional activation; shows homology to DNA binding domain of Gal4p, has a leucine zipper motif and acidic region; lexA-Sip4p activates transcription
YDR259C	YAP6	Basic leucine zipper (bZIP) transcription factor
Genotype regulators		
M3_79091_92391		YCL012C YCL012W YCL013W BUD3(10,152) DCC1(2,9) NFS1(40,7) LEU2(246,526) YCL019W YCL020W YCL021W YCL021W-A YCL022C YCL023C KCC4(6,2) AGP1(6,1) YCL026C FRM2(1,3) YCL026C-B FUS1(0,1) RNQ1(0,0) BIK1(0,0) YCLX06C YCLX07W YCLX08C YCLX09W YCLX10C
Module genes		
YGL138C	None	
YPL181W	CTI6	Protein that relieves transcriptional repression by binding to the Cyc8p-Tup1p corepressor and recruiting the SAGA complex to the repressed promoter; contains a PHD finger domain
YKL120W	OAC1	Mitochondrial inner membrane transporter, transports oxaloacetate, sulfate, and thiosulfate; member of the mitochondrial carrier family
YCR005C	CIT2	non-mitochondrial citrate synthase
YJR016C	ILV3	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids
YGR146C	None	
YGL062W	PYC1	converts pyruvate to oxaloacetate; pyruvate carboxylase
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 and Ure2p
YOR226C	ISU2	Conserved protein of the mitochondrial matrix, required for synthesis of mitochondrial and cytosolic iron-sulfur proteins, performs a scaffolding function in mitochondria during Fe/S cluster assembly; isu1 isu2 double mutant is inviable
YLR348C	DIC1	Mitochondrial dicarboxylate carrier, integral membrane protein, catalyzes a dicarboxylate-phosphate exchange across the inner mitochondrial membrane, transports cytoplasmic dicarboxylates into the mitochondrial matrix

YGL010W	None	
YOR375C	GDH1	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh3p; expression regulated by nitrogen and carbon sources
YKL030W	None	
YOR225W	None	
YOR271C	None	
YKR071C	DRE2	Protein of unknown function; mutation displays synthetic lethal interaction with the pol3-13 allele of CDC2
YAL062W	GDH3	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh1p; expression regulated by nitrogen and carbon sources
YCL017C	NFS1	Required for the post-transcriptional thio-modification of both mitochondrial and cytoplasmic tRNAs, also functions in mitochondrial iron-sulfur cluster biogenesis; NifS-like protein
YGL009C	LEU1	Isopropylmalate isomerase, catalyzes the second step in the leucine biosynthesis pathway
YER073W	ALD5	Mitochondrial aldehyde dehydrogenase that is activated by K+ and utilizes NADP+ as the preferred coenzyme
YBR068C	BAP2	High-affinity leucine permease, functions as a branched-chain amino acid permease involved in the uptake of leucine, isoleucine and valine; contains 12 predicted transmembrane domains
YLR149C	None	
YKL029C	MAE1	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids
YMR108W	ILV2	Acetolactate synthase, localizes in the mitochondria; expression of the gene is under general amino acid control
YPL269W	KAR9	Karyogamy protein required for correct positioning of the mitotic spindle and for orienting cytoplasmic microtubules, localizes at the shmoo tip in mating cells and at the tip of the growing bud in small-budded cells through anaphase
YHR208W	BAT1	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase
(76) MODULE 87		
Expression regulators		
YMR179W	SPT21	Protein required for normal transcription at several loci including HTA2-HTB2 and HHF2-HHT2, but not required at the other histone loci; functionally related to Spt10p
YMR019W	STB4	Protein that binds Sin3p in a two-hybrid assay
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 DNA; mediates aerobic transcriptional repression of COX5b

YHL028W	WSC4	cell wall integrity and stress response component 4; Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC3
YDR224C	HTB1	One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation
YCL055W	KAR4	Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
YBL052C	SAS3	Protein involved in silencing at HMR
Module genes		
YDR112W	None	
YIL130W	None	
YDL070W	BDF2	Protein involved in transcription initiation at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf1p
YBR049C	REB1	RNA polymerase I enhancer binding protein; DNA binding protein which binds to genes transcribed by both RNA polymerase I and RNA polymerase II; required for termination of RNA polymerase I transcription
YOL149W	DCP1	Decapping enzyme, essential phosphoprotein component of mRNA decapping complex, plays key role in mRNA decay by cleaving off the 5' cap to leave the end susceptible to exonucleolytic degradation; regulated by DEAD box protein Dhh1p
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; expression is induced in G1 by bound SBF
YKL101W	HSL1	Nim1p-related protein kinase that regulates the morphogenesis and septin checkpoints; associates with the assembled septin filament; required along with Hsl7p for bud neck recruitment, phosphorylation, and degradation of Swe1p
YDR111C	ALT2	putative alanine transaminase (glutamyc pyruvic transaminase)
YPL256C	CLN2	role in cell cycle START; G(sub)1 cyclin
YJL187C	SWE1	Protein kinase that regulates the G2/M transition by inhibition of Cdc28p kinase activity; localizes to the nucleus and to the daughter side of the mother-bud neck; homolog of S. pombe Wee1p; potential Cdc28p substrate
YML053C	None	
YDL003W	MCD1	Essential protein required for sister chromatid cohesion in mitosis and meiosis; subunit of the cohesin complex; expression is cell cycle regulated and peaks in S phase
YPL255W	BBP1	Protein required for the spindle pole body (SPB) duplication, localized at the central plaque periphery; forms a complex with a nuclear envelope protein Mps2p and SPB components Spc29p

		and Kar1p; required for mitotic functions of Cdc5p
YMR075W	RCO1	Hypothetical ORF
YPL032C	SVL3	Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck
YPL153C	RAD53	Protein kinase, required for cell-cycle arrest in response to DNA damage; activated by trans autophosphorylation when interacting with hyperphosphorylated Rad9p
YJR053W	BFA1	Component of the GTPase-activating Bfa1p-Bub2p complex involved in multiple cell cycle checkpoint pathways that control exit from mitosis
YMR001C	CDC5	Polo-like kinase with similarity to Xenopus Plx1 and S. pombe Plo1p; found at bud neck, nucleus and SPBs; has multiple functions in mitosis and cytokinesis through phosphorylation of substrates; may be a Cdc28p substrate
YMR032W	HOF1	Bud neck-localized, SH3 domain-containing protein required for cytokinesis; regulates actomyosin ring dynamics and septin localization; interacts with the formins, Bni1p and Bnr1p, and with Cyk3p, Vrp1p, and Bni5p
(77) MODULE 89		
Genotype regulators		
M12_450041_508029		YLR149C-A STM1(0,0) PCD1(0,2) YLR152C ACS2(2,0) RNH203(0,3) YLR154C-G YLR154C-H TAR1(0,0) YLR154W-B YLR154W-C YLR154W-E YLR154W-F ASP3-1(193,529) YLR156C-A YLR156W ASP3-2(193,524) YLR157C-C YLR157W-A YLR157W-C ASP3-3(193,529) YLR159C-A YLR159W ASP3-4(193,529) YLR161W YLR162W YLR162W-A YLR162W- MAS1(3,5) YLR163W-A YLR164W PUS5(3,1) SEC10(7,11) RPS31(0,11) YLR168C YLR169W APS1(1,2) YLR171W DPH5(0,5) YLR173W IDP2(0,3) CBF5(1,2) RFX1(13,11) YLR177W TFS1(1,3) YLR179C SAM1(0,10) VTA1(4,4)
Module genes		
YLR179C	None	
YLR151C	PCD1	Peroxisomal nudix pyrophosphatase with specificity for coenzyme A and CoA derivatives, may function to remove potentially toxic oxidized CoA disulfide from peroxisomes to maintain the capacity for beta-oxidation of fatty acids
YIL066C	RNR3	Ribonucleotide-diphosphate reductase (RNR), large subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits
YJL026W	RNR2	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits
(78) MODULE 90		
Expression regulators		
YOR090C	PTC5	Phosphatase type Two C; Type 2C Protein Phosphatase

YHR056C	RSC30	RSC complex component
Module genes		
YER098W	UBP9	Ubiquitin-specific protease that cleaves ubiquitin-protein fusions
YPL083C	SEN54	Subunit of the tRNA splicing endonuclease, which is composed of Sen2p, Sen15p, Sen34p, and Sen54p
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
YPR121W	THI22	Protein with similarity to hydroxymethylpyrimidine phosphate kinases; member of a gene family with THI20 and THI21; not required for thiamine biosynthesis
YNL105W	None	
YBR178W	None	
YJL150W	None	
YGL088W	None	
(79) MODULE 93		
Expression regulators		
YAL017W	PSK1	One of two (see also PSK2) PAS domain containing S/T protein kinases; coordinately regulates protein synthesis and carbohydrate metabolism and storage in response to a unknown metabolite that reflects nutritional status
Genotype regulators		
M12_1042072_1054302		HMG2(4,5) LEU3(6,0) SST2(2,0) RIF2(6,6) FMP27(8,6) YLR455W YLR456W NBP1(2,5) YLR458W GAB1(1,5) YLR460C PAU4(1,435)
Module genes		
YGL157W	None	
YLR438W	CAR2	ornithine aminotransferase
YCR105W	ADH7	NADP(H)-dependent alcohol dehydrogenase; ORF
YGL263W	COS12	Protein of unknown function, member of a family of conserved, often subtelomerically-encoded proteins
YCR106W	RDS1	Regulator of drug sensitivity; transcriptional regulator
YOL165C	AAD15	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role
YCR107W	AAD3	Putative aryl-alcohol dehydrogenase with similarity to P. chrysosporium aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role
(80) MODULE 94		
Expression regulators		
YNL239W	LAP3	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p
YPL002C	SNF8	appears to be functionally related to SNF7; involved in glucose derepression
Genotype regulators		
M14_486861_486861		RPL16B(8,0) TOM7(0,3) LAT1(1,0) RNH201(0,0) MSK1(1,0) MLF3(4,0) IMP4(0,1) MKS1(1,0) APJ1(1,1) NIS1(1,0)

		TPM1(0,0) YNL080C
Module genes		
YDR089W	None	
YCR048W	ARE1	Acyl-CoA:sterol acyltransferase, isozyme of Are2p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity in the absence of oxygen
YGL209W	MIG2	Involved in repression, along with Mig1p, of SUC2 (invertase) expression by high levels of glucose; binds to Mig1p-binding sites in SUC2 promoter; Protein containing zinc fingers very similar to zinc fingers in Mig1p
YJL052W	TDH1	Glyceraldehyde-3-phosphate dehydrogenase 1
YPR157W	None	
YJR009C	TDH2	glyceraldehyde 3-phosphate dehydrogenase
YOR383C	FIT3	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall
YKL060C	FBA1	Fructose 1,6-bisphosphate adolase, required for glycolysis and gluconeogenesis
YEL047C	None	
YFR009W	GCN20	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA
YBR196C	PGI1	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation
YNL046W	None	
YOR230W	WTM1	WD repeat containing transcriptional modulator 1; Transcriptional modulator
(81) MODULE 95		
Module genes		
YDR345C	HXT3	Low affinity glucose transporter of the major facilitator superfamily, expression is induced in low or high glucose conditions
(82) MODULE 97		
Genotype regulators		
M8_80014_95469		RPL14B(43,144) YHL002C-A HSE1(1,3) LAG1(1,4) MRP4(0,2) YHL005C SHU1(2,2) YHL006W-A STE20(7,2) YHL008C YAP3(10,400) YHL010C PRS3(0,3) YHL012W YHL013C YLF2(0,0) RPS20(0,0) YHL015W-A DUR3(0,3) YHL017W
Module genes		
YHL010C	None	
YCL055W	KAR4	Transcription factor required for induction of KAR3 and CIK1 during mating, also required during meiosis; exists in two forms, a slower-migrating form more abundant during vegetative growth and a faster-migrating form induced by pheromone
YJL113W	None	

YLR452C	SST2	Protein involved in desensitization to alpha-factor pheromone; member of the RGS (regulator of G-protein signalling) family; GTPase-activating protein
YHL009C	YAP3	bZIP transcription factor
YHL022C	SPO11	Meiosis-specific protein that initiates meiotic recombination by catalyzing the formation of double-strand breaks in DNA via a transesterifcation reaction; required for homologous chromosome pairing and synaptonemal complex formation
(83) MODULE 99		
Expression regulators		
YFR009W	GCN20	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn1p; proposed to stimulate Gcn2p activation by an uncharged tRNA
YOL113W	SKM1	Serine/threonine protein kinase with similarity to Ste20p and Cla4p
YJL005W	CYR1	Required for START A of cell cycle, and glucose and nitrogen repression of sporulation; adenylate cyclase
YPL016W	SWI1	Global transcription activator that acts in complex with Snf2p, Snf5p, Snf6p, and Swi3p to assist gene-specific activators; involved in the regulation of expression of many genes, including ADH1, ADH2, GAL1, HO, INO1 and SUC2; Zinc-finger transcription factor
Module genes		
YBR044C	TCM62	mitochondrial protein; (putative) chaperone
YIL022W	TIM44	48.8 kDa protein involved in mitochondrial protein import
YJR122W	CAF17	Mitochondrial protein that interacts with Ccr4p in the two-hybrid system; 3'-untranslated region contains a putative mRNA localization element common to genes encoding mitochondrial proteins
YOL166C	None	
YOR201C	PET56	Ribose methyltransferase that modifies a functionally critical, conserved nucleotide in mitochondrial 21S rRNA
YPL140C	MKK2	Member of MAP kinase pathway involving PKC1, BCK1, and SLT2. Shows functional redundancy with MKK1; protein kinase
YHR099W	TRA1	Histone acetyltransferase component, putative ortholog of human TRRAP which is an essential cofactor of c-Myc
YGL215W	CLG1	cyclin-like protein that interacts with Pho85p in affinity chromatography; cyclin-like protein that interacts with Pho85
YMR316C-A	None	
YBR227C	MCX1	Mitochondrial ATP-binding protein, possibly a mitochondrial chaperone with non-proteolytic function; similar to bacterial ClpX proteins
YMR316W	DIA1	Protein of unknown function, involved in invasive and pseudohyphal growth; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
YFL016C	MDJ1	Protein involved in folding of mitochondrially synthesized proteins in the mitochondrial matrix; localizes to the mitochondrial inner membrane; member of the DnaJ family of molecular chaperones
YLR193C	None	

YHR217C	None	
YDR393W	SHE9	Mitochondrial inner membrane protein required for normal mitochondrial morphology, may be involved in fission of the inner membrane; forms a homo-oligomeric complex
YPR047W	MSF1	Mitochondrial phenylalanyl-tRNA synthetase alpha subunit, active as a monomer, unlike the cytoplasmic subunit which is active as a dimer complexed to a beta subunit dimer; similar to the alpha subunit of E. coli phenylalanyl-tRNA synthetase
(84) MODULE 100		
Expression regulators		
YJL098W	SAP185	Protein that forms a complex with the Sit4p protein phosphatase and is required for its function; member of a family of similar proteins including Sap4p, Sap155p, and Sap190p
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; member of the Swi4p/Mbp1p family; potential Cdc28p substrate
Module genes		
YPL262W	FUM1	Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting sequence and protein conformation
YGL158W	RCK1	Serine/threonine protein kinase
YGR279C	SCW4	Cell wall protein with similarity to glucanases; scw4 scw10 double mutants exhibit defects in mating
YPL275W	None	
YDR247W	VHS1	Gene whose overexpression suppresses the synthetic lethality of the hal3 sit4 double mutation
YDR529C	QCR7	ubiquinol-cytochrome c oxidoreductase subunit 7 (14 kDa)
YPL276W	None	
YPR156C	TPO3	Polyamine transport protein
YOR388C	FDH1	NAD(+)-dependent formate dehydrogenase, may protect cells from exogenous formate
YKL123W	None	
YAR053W	None	
YMR304C-A	None	
YPR193C	HPA2	Tetrameric histone acetyltransferase with similarity to Gcn5p, Hat1p, Elp3p, and Hpa3p; acetylates histones H3 and H4 in vitro and exhibits autoacetylation activity
(85) MODULE 101		
Genotype regulators		
M5_109310_117705		EDC3(0,0) YEL016C PMP2(0,0) GTT3(1,0) YEL018C-A EAF5(0,0) MMS21(1,0) YEL020C YEL020C-B TIM9(0,3) URA3(222,250) GEA2(5,1) YEL023C RIP1(1,5) YEL025C SNU13(0,1) CUP5(0,0)
Module genes		
YIL171W	None	
YEL021W	URA3	orotidine-5'-phosphate decarboxylase

YMR011W	HXT2	High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high levels of glucose
YEL038W	UTR4	Protein of unknown function, found in both the cytoplasm and nucleus
(86) MODULE 102		
Genotype regulators		
M13_905780_922268		YMR310C GLC8(0,3) ELP6(1,3) TGL3(1,5) PRE5(0,5) YMR315W YMR315W-A YMR316C-A YMR316C-B DIA1(1,4) YMR317W ADH6(0,8) FET4(1,8) YMR320W YMR321C SNO4(1,20) ERR3 YMR324C YMR325W YMR326C
Module genes		
YMR319C	FET4	Low-affinity Fe(II) transporter of the plasma membrane
(87) MODULE 108		
Expression regulators		
YGL166W	CUP2	Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated copper concentrations
YIR017C	MET28	Transcriptional activator in the Cbf1p-Met4p-Met28p complex, participates in the regulation of sulfur metabolism
Module genes		
YJL065C	DLS1	Subunit of ISW2/yCHRAC chromatin accessibility complex along with Itc1p, Isw2p, and Dpb4p; involved in inheritance of telomeric silencing
YJR071W	None	
YDL009C	None	
YBR278W	DPB3	Third-largest subunit of DNA polymerase II (DNA polymerase epsilon), required to maintain fidelity of chromosomal replication and also for inheritance of telomeric silencing; mRNA abundance peaks at the G1/S boundary of the cell cycle
YGR242W	None	
YCR063W	BUD31	Protein involved in bud-site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern
(88) MODULE 109		
Expression regulators		
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; member of the Swi4p/Mbp1p family; potential Cdc28p substrate
YPR070W	MED1	Subunit 1 of the Mediator complex essential for transcriptional regulation
Module genes		
YIR020W-B	None	
YOR032C	HMS1	C2H2 zinc-finger protein with similarity to myc-family transcription factors; overexpression confers hyperfilamentous growth and suppresses the pseudohyphal filamentation defect of a diploid mep1 mep2 homozygous null mutant
YOR107W	RGS2	Negative regulator of glucose-induced cAMP signaling; directly

		activates the GTPase activity of the heterotrimeric G protein alpha subunit Gpa2p
YGR108W	CLB1	Involved in mitotic induction; G(sub)2-specific B-type cyclin
YBR072W	HSP26	Small heat shock protein with chaperone activity that is regulated by a heat induced transition from an inactive oligomeric (24-mer) complex to an active dimer; induced by heat, upon entry into stationary phase, and during sporulation
YER103W	SSA4	member of 70 kDa heat shock protein family
YHL028W	WSC4	cell wall integrity and stress response component 4; Putative integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC3
YIL059C	None	
YKL051W	SFK1	Suppressor of PI Four Kinase
YER038C	KRE29	Essential protein of unknown function; heterozygous mutant shows haploinsufficiency in K1 killer toxin resistance
YIL119C	RPI1	Putative transcriptional regulator; overexpression suppresses the heat shock sensitivity of wild-type RAS2 overexpression and also suppresses the cell lysis defect of an mpk1 mutation
YNL202W	SPS19	late sporulation specific gene which may function during spore wall formation; peroxisomal 2,4-dienoyl-CoA reductase
(89) MODULE 111		
Expression regulators		
YDL064W	UBC9	SUMO-conjugating enzyme involved in the Smt3p conjugation pathway; nuclear protein required for S- and M-phase cyclin degradation and mitotic control; involved in proteolysis mediated by the anaphase-promoting complex cyclosome (APCC)
Genotype regulators		
M10_646911_646911		NNF1(0,0) YJR112W-A RSM7(0,0) SRF2(1,0) YJR115W YJR116W STE24(2,2) ILM1(1,0) YJR119C YJR120W ATP2(1,0) CAF17(0,2) RPS5(0,1) YJR124C ENT3(0,0)
Module genes		
YJR095W	SFC1	Mitochondrial succinate-fumarate transporter, transports succinate into and fumarate out of the mitochondrion; required for ethanol and acetate utilization
YJR131W	MNS1	specific alpha-mannosidase
YFL061W	DDI2	Hypothetical ORF
YNL333W	SNZ2	Snooze: stationary phase-induced gene family; member of the stationary phase-induced gene family
YFL060C	SNO3	Protein of unknown function, nearly identical to Sno2p; expression is induced before the diauxic shift and also in the absence of thiamin
YFL059W	SNZ3	Snooze: stationary phase-induced gene family; member of the stationary phase-induced gene family
(90) MODULE 117		
Genotype regulators		
M14_314883_330368		YNL158W ASI2(0,0) YGP1(3,1) CBK1(3,1) RPL42A(1,2) YNL162W-A RIA1(1,3) IBD2(0,0) YNL165W BNI5(133,2) SKO1(1,0) FMP41(0,1) PSD1(0,0) YNL170W YNL171C

		APC1(4,1) MDG1(1,1) YNL174W NOP13(1,3) YNL176C
Module genes		
YNL179C	SRF6	Dubious open reading frame, unlikely to encode a protein; not conserved in closely related Saccharomyces species; deletion in cyr1 mutant results in loss of stress resistance
(91) MODULE 119		
Genotype regulators		
M11_354466_354466		PTM1(17,1) NFU1(0,1) VPS24(1,0) SPC42(1,2) PHD1(1,1) YKL044W PRI2(1,6) DCW1(0,6) YKL047W ELM1(0,0) CSE4(0,0)
Module genes		
YKL043W	PHD1	protein similar to StuA of Aspergillus nidulans; putative transcription factor
(92) MODULE 121		
Genotype regulators		
M10_22213_34098		NUC1(1,2) CBP1(6,3) PEX2(1,6) YJL211C OPT1(3,6) YJL213W HXT8(93,12) YJL215C YJL216C YJL217W YJL218W HXT9(12,50) YJL220W FSP2(4,32) VTH2(323,435)
Module genes		
YJL221C	FSP2	Protein of unknown function, expression is induced during nitrogen limitation
YJL218W	None	
(93) MODULE 122		
Genotype regulators		
M16_70847_70853		GYP5(1,2) RPL36B(5,6) ICY2(1,12) YPL250W-A YPL251W YAH1(1,2) VIK1(4,3) HFI1(1,3) BBP1(0,4) CLN2(1,3) YPL257W
Module genes		
YPL252C	YAH1	Iron-sulfur protein of the mitochondrial matrix, homologous to human adrenodoxin; involved in heme a biosynthesis
(94) MODULE 124		
Genotype regulators		
M6_134096_161065		DEG1(3,5) SPB4(2,5) YFL002W-A MSH4(5,187) VTC2(2,4) SEC4(1,3) YFL006W BLM3(10,3) LOC1(0,49) NIC96(2,3) YPI1(0,3) RPN11(0,3) SAD1(5,3) YFR006W YFR007W FAR7(2,1) GCN20(1,13) YFR009W-A UBP6(0,2) YFR010W-A YFR011C YFR012W YFR012W-A
Module genes		
YFL010C	WWM1	WW domain containing protein interacting with Metacaspase (MCA1)
YFL011W-A	None	
(95) MODULE 125		
Genotype regulators		
M15_968429_968429		UBC11(0,0) RPA43(1,3) RPA190(2,3) YOR342C YOR343C TYE7(0,0)
Module genes		
YOR345C	None	

YOR346W	REV1	Deoxycytidyl transferase, forms a complex with the subunits of DNA polymerase zeta, Rev3p and Rev7p; involved in repair of abasic sites in damaged DNA
(96) MODULE 126		
Genotype regulators		
M12_131338_131338		SPO75(2,1) MMM1(104,0) YLL006W-A YLL007C DRS1(1,0) COX17(0,0) PSR1(5,8) SOF1(0,6) YEH1(4,5) PUF3(226,5) YLL014W
Module genes		
YGR144W	THI4	Protein required for thiamine biosynthesis and for mitochondrial genome stability
(97) MODULE 128		
Genotype regulators		
M4_1344550_1344670		PPZ2(1,0) YDR437W YDR438W LRS4(0,0) DOT1(2,10) APT2(1,6) YDR442W SSN2(4,1) YDR444W YDR445C ECM11(0,156)
Module genes		
YDR451C	YHP1	acts as a repressor at early cell cycle boxes (ECBs) to restrict their activity to the M/G1 phase of the cell cycle.
YDR441C	APT2	Apparent pseudogene, not transcribed or translated under normal conditions; encodes a protein with similarity to adenine phosphoribosyltransferase, but artificially expressed protein exhibits no enzymatic activity
(98) MODULE 130		
Genotype regulators		
M8_161987_176994		MYO1(16,4) MAS2(0,2) THR1(1,2) PPA1(0,1) RPN1(3,8) DAP2(3,22) YHR028W-A YHR029C SLT2(0,4) RRM3(3,12) YHR032C-A YHR032W YHR032W-A YHR033W PIH1(4,6) YHR035W YHR036W PUT2(2,1) RRF1(2,10) MSC7(0,7)
Module genes		
YHR022C	None	
(99) MODULE 131		
Genotype regulators		
M15_290670_301077		YOL008W MDM12(1,3) RCL1(0,2) PLB3(0,1) HTZ1(0,1) HRD1(1,2) YOL013W-A YOL013W-B YOL014W YOL015W CMK2(1,1) ESC8(5,2) TLG2(0,2) YOL019W YOL019W-A TAT2(0,2) DIS3(2,2) YOL022C
Module genes		
YOL019W	None	
(100) MODULE 132		
Genotype regulators		
M2_216978_246135		ECM15(0,22) HTB2(0,13) HTA2(0,13) UTP20(35,140) PDR3(3,1) YBL005W-A YBL005W-B LDB7(2,1) YBL006W-A SLA1(9,2) HIR1(3,0) YBL008W-A YBL009W NTH2(7,4) RER2(1,2) COQ1(1,2) GPI18 RCR1(2,2) UGA2(0,5) DSF2(9,8) FLR1(5,15) HHF1(0,331)
Module genes		
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 PDREs (PDR responsive elements)
(101) MODULE 133		
Genotype regulators		
M5_240105_244117		GLN3(4,0) YEN1(4,1) MXR1(0,2) SAH1(0,1) ERG28(0,3) MEI4(95,2) ACA1(9,27) SPO73(1,14) YER046W-A SAP1(7,5) CAJ1(0,8) YER048W-A YER049W
Module genes		
YER047C	SAP1	Putative ATPase of the AAA family, interacts with the Sin1p transcriptional repressor in the two-hybrid system
(102) MODULE 134		
Genotype regulators		
M16_368086_368296		RPS6A(2,377) GLR1(3,4) SSU1(6,10) NOG1(0,3) SEC62(0,3) YPL095C ERI1(1,0) PNG1(0,0) MSY1(0,0) YPL098C FMP14(0,0) ATG21(1,0) ELP4(0,2) YPL102C FMP30(0,2)
Module genes		
YPL091W	GLR1	Cytosolic and mitochondrial glutathione oxidoreductase, converts oxidized glutathione to reduced glutathione
(103) MODULE 135		
Genotype regulators		
M14_571885_595885		PBI2(0,6) PUB1(1,20) YNL017C YNL018C YNL019C ARK1(3,10) HDA1(2,3) YNL022C FAP1(10,9) YNL024C YNL024C-A SSN8(1,8) SAM50(3,2) CRZ1(3,1) YNL028W KTR5(5,1) HHF2(0,7) HHT2(0,7) SIW14(1,13) YNL033W YNL034W YNL035C
Module genes		
YNL019C	None	
(104) MODULE 136		
Genotype regulators		
M2_380926_388862		TIP1(6,9) BAP2(3,7) TAT1(3,3) YBR070C YBR071W YBR072C-A HSP26(2,26) RDH54(5,2) YBR074W YBR075W YBR076C-A ECM8(195,23) EGO3 ECM33(64,7) RPG1(551,164)
Module genes		
YBR066C	NRG2	Transcriptional repressor that mediates glucose repression and negatively regulates filamentous growth; has similarity to Nrg1p
(105) MODULE 137		
Genotype regulators		
M10_535311_548177		CYC1(0,8) UTR1(2,1) ISY1(0,1) OSM1(0,1) RAD7(0,2) BFA1(1,3) YJR054W HIT1(2,350) YJR056C CDC8(1,119) APS2(0,5) PTK2(89,5) CBF1(2,7) YJR061W NTA1(2,5) RPA12(0,5) CCT5(0,0)
Module genes		
YJR060W	CBF1	Helix-loop-helix protein that binds the motif CACRTG (R=A or G), which is present at several sites including MET gene promoters and centromere DNA element I (CDEI); required for nucleosome positioning at this motif; targets Isw1p to DNA

(106) MODULE 138		
Genotype regulators		
M5_44605_48845		VMA8(0,5) AFG1(139,5) MAK10(1,5) YEL053W-A RPL12A(0,7) POL5(9,7) HAT2(2,16) YEL057C PCM1(4,5) SOM1(0,5) YEL059W PRB1(4,2) CIN8(4,4) NPR2(2,6)
Module genes		
YEL057C	None	
(107) MODULE 139		
Genotype regulators		
M16_704388_711614		YPR074W-A OPY2(1,1) YPR076W YPR077C YPR078C MRL1(0,2) TEF1(0,318) GRS2(0,0) DIB1(1,0) MDM36(0,0) YPR084W YPR085C SUA7(1,2) VPS69(5,0) SRP54(196,0) YPR089W YPR090W YPR091C YPR092W ASR1(1,14) RDS3(0,14)
Module genes		
YPR085C	None	
(108) MODULE 140		
Genotype regulators		
M15_481586_481586		RTS2(2,1) BUD21(1,1) ATX2(0,1) DIA2(11,1) STC2(0,3) YOR082C WHI5(0,4) YOR084W OST3(0,2) TCB1(547,473) YVC1(2,7) YOR088W VPS21(0,5)
Module genes		
YOR081C	STC2	Protein of unknown function, localizes to lipid particles; potential Cdc28p substrate
(109) MODULE 141		
Genotype regulators		
M15_290670_301077		YOL008W MDM12(1,3) RCL1(0,2) PLB3(0,1) HTZ1(0,1) HRD1(1,2) YOL013W-A YOL013W-B YOL014W YOL015W CMK2(1,1) ESC8(5,2) TLG2(0,2) YOL019W YOL019W-A TAT2(0,2) DIS3(2,2) YOL022C
Module genes		
YOL014W	None	
(110) MODULE 142		
Genotype regulators		
M7_3714_23129		YGL250W HFM1(22,0) RTG2(1,1) HXK2(0,11) FZF1(2,3) ZRT1(27,1) ADH4(6,1) MNT2(11,1) YGL258W YGL258W-A YPS5(0,2) YGL260W YGL261C YGL262W COS12(141,872)
Module genes		
YGL262W	None	
(111) MODULE 143		
Genotype regulators		
M2_424450_427683		RPL19A(1,370) YBR085C-A AAC3(1,15) IST2(7,8) RFC5(0,8) POL30(0,0) NHP6B(1,2) YBR089W YBR090C YBR090C-A MRS5(0,6) PHO3(2,5) PHO5(1,10) YBR094W RXT2(3,1) YBR096W
Module genes		
YBR103W	SIF2	Sir4p-Interacting Factor; 535 amino acid protein containing 4

		WD-40 repeats and a nuclear localization signal
(112) MODULE 144		
Genotype regulators		
M4_1213416_1213416		CDC40(0,0) ESF1(0,407) YDR366C YDR367W YPR1(0,0) XRS2(2,0) YDR370C YDR371C-A CTS2(3,0) VPS74(0,1) FRQ1(0,1)
Module genes		
YDR367W	None	
(113) MODULE 145		
Expression regulators		
YOR090C	PTC5	Phosphatase type Two C; Type 2C Protein Phosphatase
Module genes		
YLR282C	None	
(114) MODULE 146		
Genotype regulators		
M14_371953_394161		DCP2(10,13) NCS2(2,2) YNL120C TOM70(1,2) YNL122C YNL123W NAF1(5,3) ESBP6(7,3) SPC98(1,0) FAR11(1,1) TEP1(1,0) NRK1(1,0) CPT1(18,1) YNL130C-A TOM22(0,0) KRE33(3,3) FYV6(1,3) YNL134C FPR1(0,2) EAF7(3,1) NAM9(1,1) SRV2(3,3) RCP10(2,0) RLR1(9,0)
Module genes		
YNL134C	None	
(115) MODULE 147		
Genotype regulators		
M7_98231_117900		MDS3(20,6) YIP4(0,3) YGL199C EMP24(0,3) MCM6(4,9) ARO8(1,144) KEX1(260,309) YGL204C POX1(7,6) CHC1(6,6) SPT16(2,10) SIP2(3,0) MIG2(1,10) YPT32(0,1) YGL210W-A NCS6(1,1) VAM7(3,0) SKI8(1,0) YGL214W CLG1(14,3)
Module genes		
YGL201C	MCM6	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex
(116) MODULE 148		
Genotype regulators		
M2_477206_486640		RAD16(2,9) LYS2(372,217) YBR116C TKL2(0,22) TEF2(0,20) MUD1(8,5) CBP6(0,4) GRS1(3,3) YBR121C-A MRPL36(0,5) TFC1(3,4) YBR124W PTC4(0,9) TPS1(0,1) YBR126W-A YBR126W-B VMA2(0,0) ATG14(0,0) OPY1(0,2) SHE3(1,0)
Module genes		
YBR115C	LYS2	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p
(117) MODULE 149		
Genotype regulators		

M14_571885_595885		PBI2(0,6) PUB1(1,20) YNL017C YNL018C YNL019C ARK1(3,10) HDA1(2,3) YNL022C FAP1(10,9) YNL024C YNL024C-A SSN8(1,8) SAM50(3,2) CRZ1(3,1) YNL028W KTR5(5,1) HHF2(0,7) HHT2(0,7) SIW14(1,13) YNL033W YNL034W YNL035C
Module genes		
YNL040W	None	
(118) MODULE 150		
Genotype regulators		
M10_461201_464261		SUI2(0,2) YJR008W TDH2(0,8) SPC1(0,1) MET3(0,24) YJR011C YJR012C GPI14(2,4) RBF22 YJR015W ILV3(1,3) ESS1(1,0) YJR018W TES1(0,1) YJR020W REC107(108,2) LSM8(0,2) YJR023C YJR024C BNA1(1,78) YJR026W
Module genes		
YJR010C-A	SPC1	Subunit of the signal peptidase complex (SPC), which cleaves the signal sequence from proteins targeted to the endoplasmic reticulum (ER), homolog of the SPC12 subunit of mammalian signal peptidase complex
(119) MODULE 151		
Genotype regulators		
M7_592983_592983		RME1(1,0) YGR045C YGR046W TFC4(1,1) UFD1(0,1) SCM4(0,3) YGR050C YGR051C FMP48(0,9) YGR053C YGR054W MUP1(0,6)
Module genes		
YGR050C	None	
(120) MODULE 152		
Genotype regulators		
M12_131338_131338		SPO75(2,1) MMM1(104,0) YLL006W-A YLL007C DRS1(1,0) COX17(0,0) PSR1(5,8) SOF1(0,6) YEH1(4,5) PUF3(226,5) YLL014W
Module genes		
YLL010C	PSR1	Plasma membrane associated protein phosphatase involved in the general stress response; required along with binding partner Whi2p for full activation of STRE-mediated gene expression, possibly through dephosphorylation of Msn2p
(121) MODULE 153		
Genotype regulators		
M2_133737_151686		HEK2(3,6) RIB1(0,6) STU1(4,1) POL12(5,2) YBL036C APL3(4,2) MRPL16(2,21) URA7(0,21) YBL039C-A YBL039W-A ERD2(7,5) PRE7(23,9) FUI1(5,9) ECM13(0,2) YBL044W COR1(2,5) YBL046W EDE1(5,2) YBL048W MOH1(0,4) SEC17(10,4) PIN4(6,4)
Module genes		
YBL044W	None	
(122) MODULE 154		
Genotype regulators		
M2_745748_754059		FMP51(0,0) SHM1(0,0) YPT10(0,0) TSC10(1,0) SLM6 REI1(3,0) MRPL37(1,0) FMP21(0,3) YBR270C YBR271W

		HSM3(4,2) UBX7(5,1) CHK1(1,1) RIF1(27,6) PPS1(4,0) YBR277C DPB3(1,0) PAF1(0,0) YBR280C
Module genes		
YBR274W	CHK1	checkpoint kinase 1; homolog of the S. pombe and mammalian Chk1 checkpoint kinases; Protein kinase Chk1
(123) MODULE 155		
Genotype regulators		
M5_546664_549142		RAD24(3,1) GRX4(3,2) TMT1(2,1) YER175W-A ECM32(5,17) BMH1(0,3) PDA1(0,1) DMC1(44,9) ISC10(6,4) SLO1(0,9) YER181C FMP10(2,4) FAU1(1,31) YER184C
Module genes		
YER187W	None	
(124) MODULE 156		
Genotype regulators		
M14_314883_330368		YNL158W ASI2(0,0) YGP1(3,1) CBK1(3,1) RPL42A(1,2) YNL162W-A RIA1(1,3) IBD2(0,0) YNL165W BNI5(133,2) SKO1(1,0) FMP41(0,1) PSD1(0,0) YNL170W YNL171C APC1(4,1) MDG1(1,1) YNL174W NOP13(1,3) YNL176C
Module genes		
YNL180C	RHO5	Non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, likely involved in protein kinase C (Pkc1p)-dependent signal transduction pathway that controls cell integrity
(125) MODULE 157		
Genotype regulators		
M16_932310_932538		AQY1(17,26) HPA2(1,8) OPT2(25,180) YPR195C YPR196W YPR197C SGE1(0,0) ARR1(0,0) ARR2(0,0) ARR3(4,0)
Module genes		
YPR201W	ARR3	Arsenite transporter of the plasma membrane, required for resistance to arsenic compounds; transcription is activated by Arr1p in the presence of arsenite
(126) MODULE 158		
Genotype regulators		
M15_338018_348934		ALG6(3,0) YSP3(2,0) YOR004W DNL4(2,0) YOR006C SGT2(0,7) SLG1(0,0) YOR008C-A YOR008W-B TIR4(5,2) TIR2(0,1) AUS1(5,8) YOR011W-A YOR012W YOR013W RTS1(2,11)
Module genes		
YOR019W	None	
(127) MODULE 159		
Genotype regulators		
M15_248746_248746		YOL036W YOL037C YOL038C-A PRE6(0,2) RPP2A(0,3) RPS15(0,3) NOP12(4,1) NGL1(1,1) NTG2(4,1) PEX15(230,1) PSK2(3,4) YOL046C YOL047C YOL048C GSH2(0,3)
Module genes		
YOL043C	NTG2	DNA N-glycosylase and apurinic/apyrimidinic (AP) lyase involved in base excision repair, localizes to the nucleus
(128) MODULE 160		

Genotype regulators		
M15_409775_439041		PEP12(0,1) CYC2(2,1) HIR2(2,1) CKB2(0,1) GLO4(0,1) SRF5(2,0) CUE5(3,3) WHI2(5,7) YOR044W TOM6(0,5) DBP5(1,12) STD1(4,17) RAT1(3,31) RSB1(1,12) YOR050C YOR051C YOR052C YOR053W VHS3(12,4) YOR055W NOB1(0,3) SGT1(4,3) ASE1(5,11) YOR059C YOR060C CKA2(0,6) YOR062C RPL3(0,7) YNG1(1,1) CYT1(0,1)
Module genes		
YOR049C	RSB1	Suppressor of sphingoid long chain base (LCB) sensitivity of an LCB-lyase mutation; putative integral membrane transporter or flippase that may transport LCBs from the cytoplasmic side toward the extracytoplasmic side of the membrane
(129) MODULE 161		
Genotype regulators		
M4_432483_478080		RMD1(0,1) NHP10(0,1) MCD1(5,22) ATP16(0,2) MED2(8,2) PTC1(0,4) RPT2(0,382) APC11(1,8) YDL009C YDL010W YDL011C YDL012C HEX3(0,1) NOP1(0,3) TSC13(1,3) YDL016C CDC7(2,0) ERP3(39,0) NTH1(0,4) YRB1(0,4) RCR2(0,5) YDR003W-A RAD57(1,3) MAF1(2,2) SOK1(0,4) TRP1(1,4) YDR008C GAL3(1,4) YDR010C SNQ2(277,9) RPL4B(0,2) PSF1(0,0) RAD61(51,0) YDR015C DAD1(0,0) KCS1(2,2) YDR018C GCV1(0,5) YDR020C FAL1(2,0)
Module genes		
YDL012C	None	
(130) MODULE 162		
Genotype regulators		
M11_354466_354466		PTM1(17,1) NFU1(0,1) VPS24(1,0) SPC42(1,2) PHD1(1,1) YKL044W PRI2(1,6) DCW1(0,6) YKL047W ELM1(0,0) CSE4(0,0)
Module genes		
YKL044W	None	
(131) MODULE 163		
Genotype regulators		
M13_149075_159533		YML053C CYB2(0,2) YML054C-A SPC2(0,3) IMD4(59,289) YML057C-A CMP2(1,7) SML1(0,1) HUG1(0,0) NTE1 OGG1(0,1) PIF1(2,1) MFT1(0,1) RPS1B(0,8) TEM1(0,8) ORC1(2,9) SMA2(2,9) ERV41(12,2)
Module genes		
YML066C	SMA2	Spore Membrane Assembly
(132) MODULE 164		
Genotype regulators		
M8_193175_209245		RRF1(2,10) MSC7(0,7) VMA10(1,3) YHR039C-B BCD1(0,5) SRB2(6,3) NCP1(4,3) DOG2(11,284) DOG1(11,0) YHR045W INM1(1,6) AAP1'(0,0) YHR048W YHR049C-A FSH1(0,0) SMF2(49,1) YHR050W-A COX6(0,0) CIC1(5,2) YHR052W-A CUP1-1(0,7) YHR054C YHR054W-A CUP1-2(0,7) RSC30(4,1) YHR056W-A CPR2(0,3)
Module genes		

YHR043C	DOG2	2-deoxyglucose-6-phosphate phosphatase, member of a family of low molecular weight phosphatases, similar to Dog1p, induced by oxidative and osmotic stress, confers 2-deoxyglucose resistance when overexpressed
(133) MODULE 165		
Genotype regulators		
M15_854265_880786		FSH3(1,9) PLP2(4,1) YOR282W YOR283W HUA2(6,1) YOR285W FMP31(1,4) YOR287C MPD1(1,0) YOR289W SNF2(6,29) YOR291W YOR292C YOR293C-A RPS10A(17,1) RRS1(0,0) UAF30(0,0) YOR296W TIM18(1,1) MBF1(0,0) YOR298W BUD7(0,1) YOR300W RAX1(2,1) YOR302W CPA1(2,0) YOR304C-A ISW2(4,0) YOR305W MCH5(8,9)
Module genes		
YOR285W	None	
(134) MODULE 166		
Genotype regulators		
M4_1310380_1318073		YDR417C RPL12B(0,346) RAD30(0,2) HKR1(861,636) ARO80(1,0) SIP1(3,1) CAD1(3,0) DYN2(16,0) SNX41(1,0) YDR426C RPN9(0,2) YDR428C TIF35(0,0) CYM1(0,0)
Module genes		
YDR423C	CAD1	Transcriptional activator involved in resistance to 1,10-phenanthroline; member of yeast Jun-family of transcription factors related to mammalian c-jun; basic leucine zipper transcription factor
(135) MODULE 167		
Genotype regulators		
M12_824230_824230		YLR342W-A GAS2(11,6) RPL26A(6,480) YLR345W YLR346C KAP95(1,2) YLR347W-A DIC1(0,10) YLR349W ORM2(1,10) NIT3(1,21) YLR352W
Module genes		
YLR343W	GAS2	Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p
(136) MODULE 168		
Genotype regulators		
M13_245457_255564		YML003W GLO1(3,12) TRM12(4,5) GIS4(3,4) YML007C-A YAP1(3,7) ERG6(1,1) MRPL39(0,5) YML009C-A YML009W-B SPT5(7,4) YML010W-A YML010C-B YML010W-B YML011C YML012C-A ERV25(1,0) SEL1(4,0) YML013C-A TRM9(91,0) TAF11(1,0) PPZ1(1,9) PSP2(6,10)
Module genes		
YMR006C	PLB2	Phospholipase B 2; lysophospholipase/phospholipase B
(137) MODULE 169		
Genotype regulators		
M7_98231_117900		MDS3(20,6) YIP4(0,3) YGL199C EMP24(0,3) MCM6(4,9) ARO8(1,144) KEX1(260,309) YGL204C POX1(7,6) CHC1(6,6) SPT16(2,10) SIP2(3,0) MIG2(1,10) YPT32(0,1) YGL210W-A NCS6(1,1) VAM7(3,0) SKI8(1,0) YGL214W CLG1(14,3)
Module genes		

YGL204C	None	
(138) MODULE 170		
Genotype regulators		
M10_374040_387893		PET130(2,2) APS3(7,5) RRN7(0,1) YJL026C-A RNR2(1,2) YJL027C YJL028W VPS53(2,8) MAD2(0,2) BET4(2,2) YJL032W HCA4(4,1) KAR2(0,2) TAD2(4,2) SNX4(1,18) YJL037W YJL038C NUP192(3,22) NSP1(48,118)
Module genes		
YJL035C	TAD2	tRNA-specific adenosine-34 deaminase subunit Tad2p
(139) MODULE 171		
Genotype regulators		
M5_6335_17399		HPA3(1,9) YEL067C YEL068C HXT13(4,11) DSF1(0,31) DLD3(1,7) RMD6(1,14) YEL073C YEL074W YEL075C YEL075W-A YEL076C YEL076C-A YEL076W-C YEL077C YEL077W-A
Module genes		
YEL073C	None	
(140) MODULE 172		
Genotype regulators		
M4_161196_165032		YDL157C YDL158C YDL159C-B STE7(1,1) YDL159W-A DHH1(0,1) YDL160C-A ENT1(0,3) YDL162C YDL163W CDC9(1,3) CDC36(0,6) FAP7(0,6) NRP1(128,0) SFA1(2,12) UGX2(6,13) UGA3(3,6) GLT1(5,6)
Module genes		
YDL168W	SFA1	Long-chain alcohol dehydrogenase (glutathione-dependent formaldehyde dehydrogenase)
(141) MODULE 173		
Genotype regulators		
M13_649250_649253		SGS1(4,3) SPG5(5,3) GYL1(1,10) YMR193C-A MRPL24(1,2) YMR194C-A YMR194C-B RPL36A(5,2) ICY1(0,1) YMR196W VTI1(0,2)
Module genes		
YMR193C-A	None	
(142) MODULE 174		
Genotype regulators		
M4_45364_54225		CDC13(11,3) YDL221W FMP45(0,3) HBT1(485,1) WHI4(370,467) SHS1(276,0) GCS1(130,0) HO(573,520) YDL228C SSB1(0,0) PTP1(2,2) BRE4(2,2) OST4(0,0) YDL233W
Module genes		
YDL231C	BRE4	Zinc finger protein containing five transmembrane domains; null mutant exhibits strongly fragmented vacuoles and sensitivity to brefeldin A, a drug which is known to affect intracellular transport
(143) MODULE 175		
Genotype regulators		
M11_522777_522777		GAP1(1,43) YKR040C YKR041W UTH1(7,0) YKR043C

		UIP5(4,0) YKR045C PET10(0,10) YKR047W NAP1(2,0) FMP46(0,9) TRK2(109,7) YKR051W MRS4(1,5)
Module genes		
YKR039W	GAP1	General amino acid permease; localization to the plasma membrane is regulated by nitrogen source
(144) MODULE 176		
Genotype regulators		
M4_1499294_1507292		YDR524C-A YDR524C-B YDR524W-A API2(1,0) SNA2(0,3) YDR526C RBA50(7,3) HLR1(63,10) QCR7(0,2) APA2(0,4) YDR531W YDR532C HSP31(1,13) FIT1(32,68) YDR535C STL1(2,7) YDR537C PAD1(2,11) YDR539W
Module genes		
YDR539W	None	
(145) MODULE 177		
Genotype regulators		
M12_247886_257512		YLR046C YLR047C RPS0B(30,9) YLR049C YLR050C YLR051C IES3(2,2) YLR053C OSW2(8,3) SPT8(8,3) ERG3(2,12) YLR057W SHM2(0,4) REX2(3,2) FRS1(2,2) RPL22A(4,7) BUD28(0,0) YLR063W YLR064W YLR065C SPC3(0,2)
Module genes		
YLR049C	None	
(146) MODULE 178		
Genotype regulators		
M16_70847_70853		GYP5(1,2) RPL36B(5,6) ICY2(1,12) YPL250W-A YPL251W YAH1(1,2) VIK1(4,3) HFI1(1,3) BBP1(0,4) CLN2(1,3) YPL257W
Module genes		
YPL251W	None	
(147) MODULE 179		
Genotype regulators		
M9_415311_420076		YVH1(2,4) DAL1(2,2) DAL4(2,2) DAL2(1,4) DCG1(3,3) YIR030W-A DAL7(1,2) DAL3(2,4) MGA2(15,4) LYS1(0,1) YIR035C YIR036C YIR036W-A HYR1(0,3) GTT1(1,20)
Module genes		
YIR039C	YPS6	Putative GPI-anchored aspartic protease
(148) MODULE 180		
Genotype regulators		
M13_227254_243624		YML007C-A ERG6(1,1) MRPL39(0,5) YML009C-A YML009W-B SPT5(7,4) YML010W-A YML010C-B YML010W-B YML011C YML012C-A ERV25(1,0) SEL1(4,0) YML013C-A TRM9(91,0) TAF11(1,0) PPZ1(1,9) PSP2(6,10) YML018C OST6(2,0) YML020W UNG1(1,5) APT1(1,0) YML023C RPS17A(1,13) YML6(10,13) RPS18B(16,5) YOX1(0,5) TSA1(0,0) USA1(0,1)
Module genes		
YML016C	PPZ1	Serine/threonine protein phosphatase Z, isoform of Ppz2p; involved in regulation of potassium transport, which affects

		osmotic stability, cell cycle progression, and halotolerance
(149) MODULE 181		
Genotype regulators		
M9_190794_205191		THS1(2,4) AIR1(3,4) YIL080W YIL082W YIL082W-A YIL083C SDS3(1,4) KTR7(3,2) YIL086C YIL087C AVT7(3,3) YIL089W YIL090W YIL091C YIL092W RSM25(0,5) LYS12(0,2) PRK1(1,9) YIL096C FYV10(1,1)
Module genes		
YIL089W	None	
(150) MODULE 182		
Genotype regulators		
M16_182953_207356		YPL176C CUP9(0,2) CBC2(1,339) PPQ1(1,0) TCO89(2,1) CTI6(0,7) YPL182C YPL183C YPL183W-A YPL184C YPL185W UIP4(1,1) MF(ALPHA)1(21,1) POS5(1,1) YPL189C-A GUP2(1,4) NAB3(1,1) YPL191C PRM3(2,3) RSA1(0,0) DDC1(2,0) APL5(0,1) OXR1(0,1) YPL197C RPL7B(35,181)
Module genes		
YPL189W	GUP2	Multimembrane-spanning protein and putative glycerol transporter that is essential for proton symport of glycerol; Gup1p homolog
(151) MODULE 183		
Genotype regulators		
M1_1_37068		ACS1(2,7) PEX22(3,3) YAL056C-A GPB2(10,6) CNE1(9,5) YAL058C-A YAL059C-A ECM1(4,2) BDH1(6,5) YAL061W GDH3(0,50) FLO9(880,506) YAL063C-A YAL064C-A YAL064W YAL064W-B YAL065C YAL066W SEO1(370,503) YAL067W-A YAL068C YAL068W-A YAL069W
Module genes		
YAL064C-A	None	
(152) MODULE 184		
Genotype regulators		
M10_509429_513451		HUL4(6,3) YJR037W YJR038C YJR039W GEF1(5,5) URB2(8,4) NUP85(5,4) POL32(5,9) VPS55(0,3) SSC1(1,3) TAH11(2,3)
Module genes		
YJR035W	RAD26	Protein involved in transcription-coupled repair nucleotide exicision repair of UV-induced DNA lesions; homolog of human CSB protein
(153) MODULE 186		
Genotype regulators		
M7_985414_995892		YAP1802(4,1) YGR242W FMP43(0,1) LSC2(2,3) SDA1(0,0) BRF1(9,6) CPD1(2,6) SOL4(2,4) MGA1(3,20) YGR250C YGR251W GCN5(0,7) PUP2(0,17) ENO1(0,4) COQ6(0,15) GND2(2,15)
Module genes		
YGR247W	CPD1	Cyclic nucleotide phosphodiesterase, hydrolyzes ADP-ribose 1",

		2"-cyclic phosphate to ADP-ribose 1"-phosphate; no detectable phenotype is conferred by null mutation or by overexpression
(154) MODULE 187		
Genotype regulators		
M7_167587_192140		YGL160W YIP5(1,2) SUT1(2,13) RAD54(2,42) YRB30(1,2) YGL165C CUP2(2,4) PMR1(4,4) HUR1(2,36) SUA5(4,8) SPO74(4,8) ROK1(3,2) NUP49(5,0) KEM1(8,2) BUD13(2,3) SAE2(1,3) YGL176C YGL177W MPT5(2,4) TOS3(1,10) ATG1(0,2) GTS1(4,1)
Module genes		
YGL169W	SUA5	Protein required for respiratory growth; null mutation suppresses the Cyc1p translation defect caused by the presence of an aberrant ATG codon upstream of the correct start
(155) MODULE 188		
Genotype regulators		
M14_648788_648788		ATG3(0,0) LRO1(0,0) YNR009W CSE2(3,0) PRP2(38,2) URK1(2,1) PHO91(1,2) YNR014W SMM1(0,0) ACC1(1,2)
Module genes		
YNR013C	PHO91	Low-affinity phosphate transporter; deletion of pho84, pho87, pho89, pho90, and pho91 causes synthetic lethality; transcription independent of Pi and Pho4p activity; overexpression results in vigorous growth
(156) MODULE 189		
Genotype regulators		
M9_334195_341216		YIL002W-A CFD1(0,2) BET1(3,2) EPS1(0,0) YIL006W NAS2(0,0) URM1(0,6) EST3(90,13) FAA3(3,6) DOT5(4,3) TIR3(37,8) YIL012W PDR11(2,10) YIL014C-A MNT3(2,124) YIL015C-A
Module genes		
YIL014W	MNT3	Alpha-1,3-mannosyltransferase, adds the fourth and fifth alpha-1,3-linked mannose residues to O-linked glycans during protein O-glycosylation
(157) MODULE 190		
Genotype regulators		
M8_161987_176994		MYO1(16,4) MAS2(0,2) THR1(1,2) PPA1(0,1) RPN1(3,8) DAP2(3,22) YHR028W-A YHR029C SLT2(0,4) RRM3(3,12) YHR032C-A YHR032W YHR032W-A YHR033W PIH1(4,6) YHR035W YHR036W PUT2(2,1) RRF1(2,10) MSC7(0,7)
Module genes		
YHR028C	DAP2	Dipeptidyl aminopeptidase, synthesized as a glycosylated precursor; localizes to the vacuolar membrane; similar to Ste13p
(158) MODULE 191		
Genotype regulators		
M3_100213_105042		RER1(0,0) YCL001W-A YCL001W-B YCL002C PGS1(1,1) YCL005W VMA9(4,0) YCL006C YCL007C STP22(0,0) ILV6(1,0) SGF29(1,0) GBP2(1,0) YCL012C YCL012W YCL013W BUD3(10,152) DCC1(2,9) NFS1(40,7) LEU2(246,526) YCLX10C YCLX11W YCLX12W
Module genes		

YCL018W	LEU2	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway
(159) MODULE 192		
Genotype regulators		
M12_238298_246579		YLR040C YLR041W YLR042C TRX1(0,0) PDC1(0,11) STU2(5,4) YLR046C YLR047C RPS0B(30,9) YLR049C YLR050C YLR051C IES3(2,2) YLR053C OSW2(8,3) SPT8(8,3) ERG3(2,12)
Module genes		
YLR050C	None	
(160) MODULE 193		
Genotype regulators		
M14_402312_412269		YAF9(3,1) YNL108C YNL109W NOP15(0,2) CYB5(0,1) DBP2(1,2) RPC19(0,14) YNL114C YNL115C DMA2(5,1) MLS1(2,13) DCP2(10,13) NCS2(2,2) YNL120C TOM70(1,2) YNL122C YNL123W NAF1(5,3)
Module genes		
YNL136W	EAF7	Subunit of the NuA4 histone acetyltransferase complex
(161) MODULE 194		
Genotype regulatorsGenotype regulators		
M11_79182_98336		PRS1(0,1) FAS1(2,2) YKL183C-A LOT5(1,2) SPE1(2,1) ASH1(1,8) MTR2(0,11) YKL187C PXA2(3,7) HYM1(1,36) CNB1(18,1) DPH2(4,7) ACP1(1,7) SDS22(0,0) MST1(2,19) MIA40(3,0) YKT6(0,0) PEX1(1,20) PTK1(23,2)
Module genes		
YKL187C	None	
(162) MODULE 195		
Genotype regulators		
M4_263770_273846		ARR4(0,1) DUN1(149,2) CDC2(426,139) QRI1(2,3) QRI7(4,3) QRI2(1,2) PHO2(2,2) MSS2(4,4) KIN28(0,2) YDL109C YDL110C RRP42(1,4) TRM3(12,5) ATG20(3,5) YDL114W YDL114W-A IWR1(0,6)
Module genes		
YDL105W	QRI2	Nuclear protein of unknown function
(163) MODULE 196		
Genotype regulators		
M16_387239_420441		CWC27(7,5) VPS28(2,2) YPL066W YPL067C YPL068C BTS1(1,3) MUK1(0,0) YPL071C UBP16(2,2) YPL073C YTA6(0,0) GCR1(5,0) GPI2(0,0) YPL077C ATP4(1,2) RPL21B(4,0) YPL080C RPS9A(3,13) MOT1(1,4) SEN54(2,1) BRO1(3,3) SEC16(11,3) ELP3(0,3) YDC1(0,3) YPL088W RLM1(41,4) RPS6A(2,377)
Module genes		
YPL088W	None	
(164) MODULE 197		

Genotype regulators		
M16_511400_523450		RRP12(5,1) MRPS16(0,1) YPL014W HST2(1,2) SWI1(12,30) YPL017C CTF19(3,5) VTC3(271,210) ULP1(2,6) ECM23(4,18) RAD1(9,2) MET12(4,2) NCE4(0,13) YPL025C SKS1(14,5)
Module genes		
YPL016W	SWI1	Global transcription activator that acts in complex with Snf2p, Snf5p, Snf6p, and Swi3p to assist gene-specific activators; involved in the regulation of expression of many genes, including ADH1, ADH2, GAL1, HO, INO1 and SUC2; Zinc-finger transcription factor
(165) MODULE 198		
Genotype regulators		
M13_371857_379981		YMR046C YMR046W-A NUP116(9,3) CSM3(3,3) ERB1(3,1) YMR050C YMR052C-A FAR3(2,38) STB2(4,0) STV1(1,0) BUB2(1,4) AAC1(1,15) YMR057C FET3(4,15)
Module genes		
YMR048W	CSM3	Protein required for accurate chromosome segregation during meiosis