

Supplemental Table S3. Gene Expression Responses to 6NDA in S.cerevisiae Strain BY4742				
ORF	Gene Symbol	Description	Fold-change in BY4742	Fold-change in S288C
YHR139C	SPS100	Protein required for spore wall maturation; expressed during sporulation; may be a component of the spore wall; expression also induced in cells	74.9	22.5
YBR054W	YRO2	Putative protein of unknown function; the authentic, non-tagged protein is detected in a phosphorylated state in highly purified mitochondria in high-	41.6	7.7
YPL223C	GRE1	Hydrophilin of unknown function; stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway	38.1	4.1
YDR380W	ARO10	Phenylpyruvate decarboxylase, catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in	33.6	9.7
YKL163W	PIR3	O-glycosylated covalently-bound cell wall protein required for cell wall stability; expression is cell cycle regulated, peaking in M/G1 and also	29.7	16.1
YJL116C	NCA3	Protein that functions with Nca2p to regulate mitochondrial expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase; member of	29.6	23.2
YOL052C-A	DDR2	Multistress response protein, expression is activated by a variety of xenobiotic agents and environmental or physiological stresses	27.1	13.8
YBR072W	HSP26	Small heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation;	27.1	6.0
YHR096C	HXT5	Hexose transporter with moderate affinity for glucose, induced in the presence of non-fermentable carbon sources, induced by a decrease in	26.5	17.0
YHR087W	RTC3	Protein of unknown function involved in RNA metabolism; has structural similarity to SBDS, the human protein mutated in Shwachman-Diamond	22.7	21.5
YOR273C	TPO4	Polyamine transport protein, recognizes spermine, putrescine, and spermidine; localizes to the plasma membrane; member of the major	22.1	7.3
YGR213C	RTA1	Protein involved in 7-aminocholesterol resistance; has seven potential membrane-spanning regions; expression is induced under both low-	20.8	84.1
YGR043C	NQM1	Transaldolase of unknown function; transcription is repressed by Mot1p and induced by alpha-factor and during diauxic shift	20.6	73.0
YMR169C	ALD3	Cytoplasmic aldehyde dehydrogenase, involved in beta-alanine synthesis; uses NAD+ as the preferred coenzyme; very similar to Ald2p;	20.3	9.1
YNL160W	YGP1	Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associated growth arrest and upon entry into stationary phase; may be	20.2	18.9
YDR034W-B			20.1	31.7
YOR134W	BAG7	Rho GTPase activating protein (RhoGAP), stimulates the intrinsic GTPase activity of Rho1p, which plays a role in actin cytoskeleton	18.9	156.5
YER185W	PUG1	Plasma membrane protein with roles in the uptake of protoporphyrin IX and the efflux of heme; expression is induced under both low-heme and	17.7	11.5
YAL061W	BDH2	Putative medium-chain alcohol dehydrogenase with similarity to BDH1; transcription induced by constitutively active PDR1 and PDR3	17.1	13.2
YBL049W	MOH1	Protein of unknown function, has homology to kinase Snf7p; not required for growth on nonfermentable carbon sources; essential for survival in	16.9	8.2
YLR054C	OSW2	Protein of unknown function proposed to be involved in the assembly of the spore wall	16.0	44.4
YGR052W	FMP48	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies;	15.8	3.8
YDL223C	HBT1	Substrate of the Hub1p ubiquitin-like protein that localizes to the shmoo tip (mating projection); mutants are defective for mating projection	15.6	3.8
YGL121C	GPG1	Proposed gamma subunit of the heterotrimeric G protein that interacts with the receptor Gpr1p; involved in regulation of pseudohyphal growth;	15.1	17.8
YLR346C			14.3	7.4
YMR175W	SIP18	Phospholipid-binding protein; expression is induced by osmotic stress	13.9	3.5
YDR070C	FMP16	Putative protein of unknown function; proposed to be involved in responding to conditions of stress; the authentic, non-tagged protein is	13.2	3.4
YNL194C			13.2	12.4
YNL093W	YPT53	Rab family GTPase, similar to Ypt51p and Ypt52p and to mammalian rab5; required for vacuolar protein sorting and endocytosis	12.8	17.9
YGR256W	GND2	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway;	12.7	13.6
YDL222C	FMP45	Integral membrane protein localized to mitochondria (untagged protein); required for sporulation and maintaining sphingolipid content; has	12.3	3.8

YIL101C	XBP1	Transcriptional repressor that binds to promoter sequences of the cyclin genes, CYS3, and SMF2; expression is induced by stress or starvation	12.2	22.5
YNR034W-A			12.1	
YER037W	PHM8	Protein of unknown function, expression is induced by low phosphate levels and by inactivation of Pho85p	11.6	13.8
YOL084W	PHM7	Protein of unknown function, expression is regulated by phosphate levels; green fluorescent protein (GFP)-fusion protein localizes to the cell	10.6	6.1
YGR236C	SPG1	Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources; the authentic,	10.2	21.2
YNR064C			10.2	10.1
YLR031W			10.0	6.6
YJR078W	BNA2	Putative tryptophan 2,3-dioxygenase or indoleamine 2,3-dioxygenase, required for de novo biosynthesis of NAD from tryptophan via	9.8	10.7
YBR085C-A			9.8	8.7
YBR117C	TKL2	Transketolase, similar to Tkl1p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and	9.7	6.6
YMR174C	PAI3	Cytoplasmic proteinase A (Pep4p) inhibitor, dependent on Pbs2p and Hog1p protein kinases for osmotic induction; intrinsically unstructured, N-	9.4	7.4
YDR453C	TSA2	Stress inducible cytoplasmic thioredoxin peroxidase; cooperates with Tsa1p in the removal of reactive oxygen, nitrogen and sulfur species	9.4	7.3
YOR049C	RSB1	Suppressor of sphingoid long chain base (LCB) sensitivity of an LCB-lyase mutation; putative integral membrane transporter or flippase that	9.0	12.0
YMR107W	SPG4	Protein required for survival at high temperature during stationary phase; not required for growth on nonfermentable carbon sources	8.5	8.1
YLR030W			8.4	4.4
YER150W	SPI1	GPI-anchored cell wall protein involved in weak acid resistance; basal expression requires Msn2p/Msn4p; expression is induced under	8.3	6.0
YOL151W	GRE2	3-methylbutanal reductase and NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic,	8.2	7.7
YML128C	MSC1	Protein of unknown function; mutant is defective in directing meiotic recombination events to homologous chromatids; the authentic, non-	8.1	3.8
YML054C	CYB2	Cytochrome b2 (L-lactate cytochrome-c oxidoreductase), component of the mitochondrial intermembrane space, required for lactate utilization;	7.9	2.6
YGR088W	CTT1	Cytosolic catalase T, has a role in protection from oxidative damage by hydrogen peroxide	7.9	7.2
YKL107W			7.9	5.0
YPR160W	GPH1	Non-essential glycogen phosphorylase required for the mobilization of glycogen, activity is regulated by cyclic AMP-mediated phosphorylation,	7.8	
YJR008W			7.8	2.6
YLR142W	PUT1	Proline oxidase, nuclear-encoded mitochondrial protein involved in utilization of proline as sole nitrogen source; PUT1 transcription is	7.7	
YFL014W	HSP12	Plasma membrane localized protein that protects membranes from desiccation; induced by heat shock, oxidative stress, osmostress,	7.5	42.1
YJR095W	SFC1	Mitochondrial succinate-fumarate transporter, transports succinate into and fumarate out of the mitochondrion; required for ethanol and acetate	7.2	
YGR131W	FHN1	Protein of unknown function; induced by ketoconazole; promoter region contains sterol regulatory element motif, which has been identified as a	7.2	6.7
YHR160C	PEX18	Peroxin required for targeting of peroxisomal matrix proteins containing PTS2; interacts with Pex7p; partially redundant with Pex21p	7.2	8.8
YDR223W	CRF1	Transcriptional corepressor involved in repression of ribosomal protein (RP) gene transcription via the TOR signaling pathway which promotes	7.1	5.9
YCL064C	CHA1	Catabolic L-serine (L-threonine) deaminase, catalyzes the degradation of both L-serine and L-threonine; required to use serine or threonine as the	7.1	
YDL244W	THI13	Protein involved in synthesis of the thiamine precursor hydroxymethylpyrimidine (HMP); member of a subtelomeric gene family	7.1	7.9
YLR149C			7.0	9.3
YNR002C	ATO2	Putative transmembrane protein involved in export of ammonia, a starvation signal that promotes cell death in aging colonies;	6.9	4.7

YDL085W	NDE2	Mitochondrial external NADH dehydrogenase, catalyzes the oxidation of cytosolic NADH; Nde1p and Nde2p are involved in providing the	6.9	2.7
YJL144W			6.9	18.6
YDR124W			6.8	
YGR059W	SPR3	Sporulation-specific homolog of the yeast CDC3/10/11/12 family of bud neck microfilament genes; septin protein involved in sporulation;	6.8	5.1
YMR090W			6.7	2.4
YGL156W	AMS1	Vacuolar alpha mannosidase, involved in free oligosaccharide (fOS) degradation; delivered to the vacuole in a novel pathway separate from	6.6	18.8
YOR120W	GCY1	Putative NADP(+) coupled glycerol dehydrogenase, proposed to be involved in an alternative pathway for glycerol catabolism; member of the	6.6	3.1
YJL048C	UBX6	UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48p, transcription is repressed when cells are grown in media	6.6	3.7
YMR085W			6.4	6.6
YKR049C	FMP46	Putative redox protein containing a thioredoxin fold; the authentic, non-tagged protein is detected in highly purified mitochondria in high-	6.4	6.3
YDL048C	STP4	Protein containing a Kruppel-type zinc-finger domain; has similarity to Stp1p, Stp2p, and Stp3p	6.4	
YOL047C			6.2	12.6
YMR322C	SNO4	Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp31p, Hsp33p, and Sno4p; member of the DJ-	6.2	6.4
YNL274C	GOR1	Glyoxylate reductase; null mutation results in increased biomass after diauxic shift; the authentic, non-tagged protein is detected in highly	6.1	
YJL108C	PRM10	Pheromone-regulated protein, proposed to be involved in mating; predicted to have 5 transmembrane segments; induced by treatment with	6.0	10.5
YMR196W			6.0	4.1
YDR222W			5.8	2.7
YIL160C	POT1	3-ketoacyl-CoA thiolase with broad chain length specificity, cleaves 3-ketoacyl-CoA into acyl-CoA and acetyl-CoA during beta-oxidation of fatty	5.8	3.6
YMR250W	GAD1	Glutamate decarboxylase, converts glutamate into gamma-aminobutyric acid (GABA) during glutamate catabolism; involved in response to	5.8	4.5
YPR015C			5.8	
YOR338W			5.8	6.0
YKR046C	PET10	Protein of unknown function that co-purifies with lipid particles; expression pattern suggests a role in respiratory growth; computational	5.7	3.9
YEL057C			5.6	6.9
YEL035C	UTR5	Protein of unknown function; transcription may be regulated by Gcr1p; essential for growth under standard (aerobic) conditions but not under	5.6	
YHR097C			5.5	5.0
YOR173W	DCS2	Non-essential, stress induced regulatory protein containing a HIT (histidine triad) motif; modulates m7G-oligoribonucleotide metabolism;	5.5	6.0
YLR121C	YPS3	Aspartic protease, member of the yapsin family of proteases involved in cell wall growth and maintenance; attached to the plasma membrane via	5.5	18.2
YHR138C			5.4	9.4
YHR124W	NDT80	Meiosis-specific transcription factor required for exit from pachytene and for full meiotic recombination; activates middle sporulation genes;	5.3	4.5
YLR461W	PAU4	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; expression induced by	5.2	6.4
YPL186C	UIP4	Protein that interacts with Ulp1p, a Ubl (ubiquitin-like protein)-specific protease for Smt3p protein conjugates; detected in a phosphorylated	5.2	2.8
YCR007C			5.2	9.1
YLR312C			5.2	

YHR033W			5.2	
YPL230W	USV1	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved in growth on non-	5.1	2.9
YJL153C	INO1	Inositol 1-phosphate synthase, involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is	5.0	4.6
YGR174W-A			5.0	
YGR144W	THI4	Thiazole synthase, catalyzes formation of a thiazole intermediate during thiamine biosynthesis; required for mitochondrial genome stability in	4.9	4.8
YNL202W	SPS19	Peroxisomal 2,4-dienoyl-CoA reductase, auxiliary enzyme of fatty acid beta-oxidation; homodimeric enzyme required for growth and sporulation	4.9	4.4
YER078W-A			4.9	
YPL017C	IRC15	Microtubule associated protein; regulates microtubule dynamics; required for accurate meiotic chromosome segregation; null mutant	4.8	2.1
YDR218C	SPR28	Sporulation-specific homolog of the yeast CDC3/10/11/12 family of bud neck microfilament genes; meiotic septin expressed at high levels during	4.8	2.4
YOR237W	HES1	Protein implicated in the regulation of ergosterol biosynthesis; one of a seven member gene family with a common essential function and non-	4.8	7.6
YGR110W	CLD1	Mitochondrial cardiolipin-specific phospholipase; functions upstream of Taz1p to generate monolysocardiolipin; transcription increases upon	4.8	3.8
YOL101C	IZH4	Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family, expression induced by fatty acids and altered zinc	4.7	22.7
YGR087C	PDC6	Minor isoform of pyruvate decarboxylase, decarboxylates pyruvate to acetaldehyde, involved in amino acid catabolism; transcription is glucose-	4.7	2.9
YJL016W			4.6	2.1
YFL030W	AGX1	Alanine:glyoxylate aminotransferase (AGT), catalyzes the synthesis of glycine from glyoxylate, which is one of three pathways for glycine	4.6	3.4
YKL026C	GPX1	Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and	4.6	2.9
YCR021C	HSP30	Hydrophobic plasma membrane localized, stress-responsive protein that negatively regulates the H(+)-ATPase Pma1p; induced by heat shock,	4.6	
YGR149W			4.6	3.6
YML100W	TSL1	Large subunit of trehalose 6-phosphate synthase (Tps1p)/phosphatase (Tps2p) complex, which converts uridine-5'-diphosphoglucose and	4.5	5.9
YDL024C	DIA3	Protein of unknown function, involved in invasive and pseudohyphal growth	4.5	2.7
YOR178C	GAC1	Regulatory subunit for Glc7p type-1 protein phosphatase (PP1), tethers Glc7p to Gsy2p glycogen synthase, binds Hsf1p heat shock transcription	4.5	
YBL064C	PRX1	Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity, has a role in reduction of hydroperoxides; reactivation requires	4.4	3.4
YMR096W	SNZ1	Protein involved in vitamin B6 biosynthesis; member of a stationary phase-induced gene family; coregulated with SNO1; interacts with Sno1p	4.4	2.9
YDL204W	RTN2	Protein of unknown function; has similarity to mammalian reticulon proteins; member of the RTNLA (reticulon-like A) subfamily	4.4	3.2
YER184C			4.3	5.4
YMR206W			4.3	
YGR201C			4.3	
YGL183C	MND1	Protein required for recombination and meiotic nuclear division; forms a complex with Hop2p, which is involved in chromosome pairing and repair	4.3	4.6
YJL219W	HXT9	Putative hexose transporter that is nearly identical to Hxt11p, has similarity to major facilitator superfamily (MFS) transporters, expression	4.3	
YOR289W			4.3	5.5
YMR105C	PGM2	Phosphoglucomutase, catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose	4.3	
YGR248W	SOL4	6-phosphogluconolactonase with similarity to Sol3p	4.2	
YOR152C			4.2	4.8

YKR097W	PCK1	Phosphoenolpyruvate carboxykinase, key enzyme in gluconeogenesis, catalyzes early reaction in carbohydrate biosynthesis, glucose represses	4.2	2.4
YHR137W	ARO9	Aromatic aminotransferase II, catalyzes the first step of tryptophan, phenylalanine, and tyrosine catabolism	4.2	
YMR095C	SNO1	Protein of unconfirmed function, involved in pyridoxine metabolism; expression is induced during stationary phase; forms a putative	4.2	2.2
YPL033C	SRL4	Protein of unknown function; involved in regulation of dNTP production; null mutant suppresses the lethality of lcd1 and rad53 mutations;	4.2	
YIL099W	SGA1	Intracellular sporulation-specific glucoamylase involved in glycogen degradation; induced during starvation of a/a diploids late in sporulation,	4.2	4.0
YMR084W			4.1	7.3
YBR056W-A			4.1	
YNL092W			4.1	4.6
YOL162W			4.1	
YNL195C			4.0	2.1
YBL078C	ATG8	Component of autophagosomes and Cvt vesicles; undergoes conjugation to phosphatidylethanolamine (PE); Atg8p-PE is anchored to	4.0	5.1
YDL110C	TMA17	Protein of unknown function that associates with ribosomes; heterozygous deletion demonstrated increases in chromosome instability	4.0	4.0
YMR040W	YET2	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; homolog of human BAP31 protein	4.0	4.9
YFR023W	PES4	Poly(A) binding protein, suppressor of DNA polymerase epsilon mutation, similar to Mip6p	4.0	
YHR140W			4.0	2.9
YLR099C	ICT1	Lysophosphatidic acid acyltransferase, responsible for enhanced phospholipid synthesis during organic solvent stress; null displays	4.0	9.4
YGL053W	PRM8	Pheromone-regulated protein with 2 predicted transmembrane segments and an FF sequence, a motif involved in COPII binding; forms a complex	4.0	3.8
YMR034C			4.0	7.2
YHL021C	AIM17	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; null	3.9	4.1
YDL169C	UGX2	Protein of unknown function, transcript accumulates in response to any combination of stress conditions	3.9	3.0
YJL045W			3.9	2.5
YBR169C	SSE2	Member of the heat shock protein 70 (HSP70) family; may be involved in protein folding; localized to the cytoplasm; highly homologous to the heat	3.9	3.3
YDR391C			3.9	3.5
YNL134C			3.9	2.2
YHR209W	CRG1	Putative S-adenosylmethionine-dependent methyltransferase; mediates cantharidin resistance	3.8	18.0
YLR327C	TMA10	Protein of unknown function that associates with ribosomes; putative homolog of the F1F0-ATPase synthase regulator Stf2p	3.8	11.4
YER158C			3.8	
YBR006W	UGA2	Succinate semialdehyde dehydrogenase involved in the utilization of gamma-aminobutyrate (GABA) as a nitrogen source; part of the 4-	3.8	2.2
YJL161W	FMP33	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	3.8	5.3
YJL038C	LOH1	Protein of unknown function with proposed roles in maintenance of genome integrity and also in spore wall assembly; induced during	3.8	
YHL048C-A			3.7	
YFR022W	ROG3	Protein that binds the ubiquitin ligase Rsp5p via its 2 PY motifs; has similarity to Rod1p; mutation suppresses the temperature sensitivity of	3.6	4.4
YDR402C	DIT2	N-formyltyrosine oxidase, sporulation-specific microsomal enzyme involved in the production of N,N-bisformyl dityrosine required for spore	3.6	3.5

YJR096W			3.6	3.8
YPR159C-A			3.6	
YOL131W			3.6	3.1
YBR033W	EDS1	Putative zinc cluster protein; YBR033W is not an essential gene	3.6	5.8
YLR080W	EMP46	Integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles, which function in ER to Golgi transport	3.6	3.9
YJL103C	GSM1	Putative zinc cluster protein of unknown function; proposed to be involved in the regulation of energy metabolism, based on patterns of	3.6	2.7
YMR271C	URA10	Minor orotate phosphoribosyltransferase (OPRTase) isozyme that catalyzes the fifth enzymatic step in the de novo biosynthesis of	3.6	2.0
YGR008C	STF2	Protein involved in regulation of the mitochondrial F1F0-ATP synthase; Stf1p and Stf2p may act as stabilizing factors that enhance inhibitory	3.6	3.2
YLR194C			3.5	10.1
YEL073C			3.5	
YHL022C	SPO11	Meiosis-specific protein that initiates meiotic recombination by catalyzing the formation of double-strand breaks in DNA via a transesterification	3.5	
YMR173W	DDR48	DNA damage-responsive protein, expression is increased in response to heat-shock stress or treatments that produce DNA lesions; contains	3.5	2.9
YNL015W	PBI2	Cytosolic inhibitor of vacuolar proteinase B (PRB1), required for efficient vacuole inheritance; with thioredoxin forms protein complex LMA1, which	3.5	2.7
YOR385W			3.5	5.0
YDL181W	INH1	Protein that inhibits ATP hydrolysis by the F1F0-ATP synthase; inhibitory function is enhanced by stabilizing proteins Stf1p and Stf2p; has	3.5	
YMR081C	ISF1	Serine-rich, hydrophilic protein with similarity to Mbr1p; overexpression suppresses growth defects of hap2, hap3, and hap4 mutants; expression	3.5	
YMR008C	PLB1	Phospholipase B (lysophospholipase) involved in lipid metabolism, required for deacylation of phosphatidylcholine and	3.4	7.3
YDR055W	PST1	Cell wall protein that contains a putative GPI-attachment site; secreted by regenerating protoplasts; up-regulated by activation of the cell	3.4	6.0
YOR062C			3.4	2.3
YOR036W	PEP12	Target membrane receptor (t-SNARE) for vesicular intermediates traveling between the Golgi apparatus and the vacuole; controls entry of	3.4	4.2
YOL163W			3.4	
YDR074W	TPS2	Phosphatase subunit of the trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage	3.4	3.7
YML131W			3.4	2.2
YNL014W	HEF3	Translational elongation factor EF-3; paralog of YEF3 and member of the ABC superfamily; stimulates EF-1 alpha-dependent binding of aminoacyl-	3.4	2.6
YIL136W	OM45	Protein of unknown function, major constituent of the mitochondrial outer membrane; located on the outer (cytosolic) face of the outer membrane	3.4	2.9
YJL163C			3.3	3.0
YPL088W			3.3	10.8
YOL002C	IZH2	Plasma membrane protein involved in zinc homeostasis and osmotin-induced apoptosis; transcription regulated by Zap1p, zinc and fatty acid	3.3	3.2
YER106W	MAM1	Monopolin, kinetochore associated protein involved in chromosome attachment to meiotic spindle	3.3	4.6
YKL093W	MBR1	Protein involved in mitochondrial functions and stress response; overexpression suppresses growth defects of hap2, hap3, and hap4	3.3	
YKL151C			3.3	5.0
YPL222W	FMP40	Putative protein of unknown function; proposed to be involved in responding to environmental stresses; the authentic, non-tagged protein	3.3	2.6
YCR083W	TRX3	Mitochondrial thioredoxin, highly conserved oxidoreductase required to maintain the redox homeostasis of the cell, forms the mitochondrial	3.3	2.5

YGL015C			3.3	3.0
YPR184W	GDB1	Glycogen debranching enzyme containing glucanotransferase and alpha-1,6-amyloglucosidase activities, required for glycogen degradation;	3.3	
YOR065W	CYT1	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed	3.3	
YLR297W			3.3	
YFR017C			3.2	
YLR307W	CDA1	Chitin deacetylase, together with Cda2p involved in the biosynthesis ascospore wall component, chitosan; required for proper rigidity of the	3.2	4.3
YMR316W	DIA1	Protein of unknown function, involved in invasive and pseudohyphal growth; green fluorescent protein (GFP)-fusion protein localizes to the	3.2	8.1
YJR115W			3.2	
YMR136W	GAT2	Protein containing GATA family zinc finger motifs; similar to Gln3p and Dal80p; expression repressed by leucine	3.2	
YKL150W	MCR1	Mitochondrial NADH-cytochrome b5 reductase, involved in ergosterol biosynthesis	3.2	2.2
YLR152C			3.2	
YLR178C	TFS1	Protein that interacts with and inhibits carboxypeptidase Y and Ira2p; phosphatidylethanolamine-binding protein (PEBP) family member;	3.2	4.1
YDR273W	DON1	Meiosis-specific component of the spindle pole body, part of the leading edge protein (LEP) coat, forms a ring-like structure at the leading edge of	3.2	
YOR220W	RCN2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and is induced in response to the DNA-	3.1	4.7
YLR417W	VPS36	Component of the ESCRT-II complex; contains the GLUE (GRAM Like Ubiquitin binding in EAP45) domain which is involved in interactions with	3.1	2.5
YDL037C	BSC1	Protein of unconfirmed function, similar to cell surface flocculin Muc1p; ORF exhibits genomic organization compatible with a translational	3.1	
YBR284W			3.1	2.9
YGR066C			3.1	3.1
YBR076W	ECM8	Non-essential protein of unknown function	3.1	2.9
YLR174W	IDP2	Cytosolic NADP-specific isocitrate dehydrogenase, catalyzes oxidation of isocitrate to alpha-ketoglutarate; levels are elevated during growth on	3.1	
YKL221W	MCH2	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic acids across the plasma	3.1	3.1
YJL082W	IML2	Protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	3.1	3.1
YER103W	SSA4	Heat shock protein that is highly induced upon stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and	3.1	2.7
YBR203W	COS111	Protein required for resistance to the antifungal drug ciclopirox olamine; not related to the subtelomerically-encoded COS family; the authentic,	3.0	4.2
YFR012W-A			3.0	2.1
YJL107C			3.0	12.8
YPL054W	LEE1	Zinc-finger protein of unknown function	3.0	
YKL050C			3.0	
YLL019C	KNS1	Nonessential putative protein kinase of unknown cellular role; member of the LAMMER family of protein kinases, which are serine/threonine	3.0	3.0
YER035W	EDC2	RNA-binding protein, activates mRNA decapping directly by binding to the mRNA substrate and enhancing the activity of the decapping proteins	3.0	2.8
YOR185C	GSP2	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport;	3.0	4.3
YCR018C	SRD1	Protein involved in the processing of pre-rRNA to mature rRNA; contains a C2/C2 zinc finger motif; srd1 mutation suppresses defects caused by	3.0	3.4
YOL083W	ATG34	Receptor protein involved in selective autophagy during starvation; specifically involved in the transport of cargo protein alpha-mannosidase	3.0	4.0

YPR030W	CSR2	Nuclear protein proposed to regulate utilization of nonfermentable carbon sources and endocytosis of plasma membrane proteins; overproduction	3.0	2.5
YKR061W	KTR2	Mannosyltransferase involved in N-linked protein glycosylation; member of the KRE2/MNT1 mannosyltransferase family	3.0	4.8
YJR019C	TES1	Peroxisomal acyl-CoA thioesterase likely to be involved in fatty acid oxidation rather than fatty acid synthesis; conserved protein also found in	3.0	3.5
YDR379C-A			2.9	4.2
YOL132W	GAS4	1,3-beta-glucanosyltransferase, involved with Gas2p in spore wall assembly; has similarity to Gas1p; localizes to the cell wall	2.9	2.2
YJL057C	IKS1	Putative serine/threonine kinase; expression is induced during mild heat stress; deletion mutants are hypersensitive to copper sulphate and	2.9	3.0
YBR280C	SAF1	F-Box protein involved in proteasome-dependent degradation of Aah1p during entry of cells into quiescence; interacts with Skp1	2.9	3.2
YIL055C			2.9	3.4
YNL144C			2.9	
YDL239C	ADY3	Protein required for spore wall formation, thought to mediate assembly of a Don1p-containing structure at the leading edge of the prospore	2.9	2.5
YPR026W	ATH1	Acid trehalase required for utilization of extracellular trehalose	2.9	2.1
YOR107W	RGS2	Negative regulator of glucose-induced cAMP signaling; directly activates the GTPase activity of the heterotrimeric G protein alpha subunit Gpa2p	2.9	
YBR214W	SDS24	One of two <i>S. cerevisiae</i> homologs (Sds23p and Sds24p) of the <i>S. pombe</i> Sds23 protein, which is implicated in APC/cyclosome regulation;	2.9	6.6
YLR168C	UPS2	Mitochondrial intermembrane space protein involved in regulation of mitochondrial cardiolipin and phosphatidylethanolamine levels; null has	2.9	
YNL115C			2.9	3.4
YGL184C	STR3	Cystathionine beta-lyase, converts cystathionine into homocysteine	2.9	
YGR138C	TPO2	Polyamine transport protein specific for spermine; localizes to the plasma membrane; transcription of TPO2 is regulated by Haa1p;	2.9	
YGR127W			2.9	2.0
YNR019W	ARE2	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity	2.8	4.6
YDR009W	GAL3	Transcriptional regulator involved in activation of the GAL genes in response to galactose; forms a complex with Gal80p to relieve Gal80p	2.8	
YBR250W	SPO23	Protein of unknown function; associates with meiosis-specific protein Spo1p	2.8	
YKR053C	YSR3	Dihydro sphingosine 1-phosphate phosphatase, membrane protein involved in sphingolipid metabolism; has similarity to Lcb3p	2.8	2.9
YGR243W	FMP43	Putative protein of unknown function; expression regulated by osmotic and alkaline stresses; the authentic, non-tagged protein is detected in	2.8	3.8
YDR001C	NTH1	Neutral trehalase, degrades trehalose; required for thermotolerance and may mediate resistance to other cellular stresses; may be	2.8	3.6
YDR247W	VHS1	Cytoplasmic serine/threonine protein kinase; identified as a high-copy suppressor of the synthetic lethality of a <i>sis2 sit4</i> double mutant,	2.8	
YHR004C	NEM1	Probable catalytic subunit of Nem1p-Spo7p phosphatase holoenzyme; regulates nuclear growth by controlling phospholipid biosynthesis,	2.8	2.3
YLR251W	SYM1	Protein required for ethanol metabolism; induced by heat shock and localized to the inner mitochondrial membrane; homologous to	2.8	3.0
YMR009W	ADI1	Acireductone dioxygenase involved in the methionine salvage pathway; ortholog of human MTCBP-1; transcribed with YMR010W and regulated	2.8	2.4
YCR010C	ADY2	Acetate transporter required for normal sporulation; phosphorylated in mitochondria	2.8	2.7
YIR027C	DAL1	Allantoinase, converts allantoin to allantoate in the first step of allantoin degradation; expression sensitive to nitrogen catabolite repression	2.8	
YJL089W	SIP4	C6 zinc cluster transcriptional activator that binds to the carbon source-responsive element (CSRE) of gluconeogenic genes; involved in the	2.8	
YDR018C			2.8	2.9
YBR230C	OM14	Integral mitochondrial outer membrane protein; abundance is decreased in cells grown in glucose relative to other carbon sources; appears to	2.8	2.0

YLL042C	ATG10	Conserved E2-like conjugating enzyme that mediates formation of the Atg12p-Atg5p conjugate, which is a critical step in autophagy	2.7	
YLR377C	FBP1	Fructose-1,6-bisphosphatase, key regulatory enzyme in the gluconeogenesis pathway, required for glucose metabolism; undergoes	2.7	
YER053C	PIC2	Mitochondrial phosphate carrier, imports inorganic phosphate into mitochondria; functionally redundant with Mir1p but less abundant than	2.7	
YOR019W			2.7	2.9
YDR171W	HSP42	Small heat shock protein (sHSP) with chaperone activity; forms barrel-shaped oligomers that suppress unfolded protein aggregation; involved	2.7	4.5
YDL130W-A	STF1	Protein involved in regulation of the mitochondrial F1F0-ATP synthase; Stf1p and Stf2p may act as stabilizing factors that enhance inhibitory	2.7	2.9
YDR059C	UBC5	Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived, abnormal, or excess proteins, including histone H3; central	2.7	2.3
YER054C	GIP2	Putative regulatory subunit of the protein phosphatase Glc7p, involved in glycogen metabolism; contains a conserved motif (GVNK motif) that is	2.7	
YBR056W			2.7	5.2
YHR048W	YHK8	Presumed antiporter of the DHA1 family of multidrug resistance transporters; contains 12 predicted transmembrane spans; expression of	2.7	
YAL037W			2.7	
YDR178W	SDH4	Membrane anchor subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer	2.7	
YCR061W			2.7	3.1
YAL008W	FUN14	Mitochondrial protein of unknown function	2.7	3.3
YIL045W	PIG2	Putative type-1 protein phosphatase targeting subunit that tethers Glc7p type-1 protein phosphatase to Gsy2p glycogen synthase	2.7	
YER130C			2.6	2.3
YPL247C			2.6	
YBR066C	NRG2	Transcriptional repressor that mediates glucose repression and negatively regulates filamentous growth; has similarity to Nrg1p	2.6	
YGL006W	PMC1	Vacuolar Ca ²⁺ ATPase involved in depleting cytosol of Ca ²⁺ ions; prevents growth inhibition by activation of calcineurin in the presence of	2.6	3.1
YEL039C	CYC7	Cytochrome c isoform 2, expressed under hypoxic conditions; electron carrier of the mitochondrial intermembrane space that transfers electrons	2.6	
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	2.6	3.3
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	2.6	
YLR270W	DCS1	Non-essential hydrolase involved in mRNA decapping, may function in a feedback mechanism to regulate deadenylation, contains	2.6	2.7
YKR009C	FOX2	Multifunctional enzyme of the peroxisomal fatty acid beta-oxidation pathway; has 3-hydroxyacyl-CoA dehydrogenase and enoyl-CoA	2.6	2.0
YAL034C	FUN19	Non-essential protein of unknown function; expression induced in response to heat stress	2.6	2.3
YLR162W-A	RRT15	Putative protein of unknown function identified by fungal homology comparisons and RT-PCR; identified in a screen for mutants with	2.6	2.8
YFR032C	RRT5	Putative protein of unknown function; non-essential gene identified in a screen for mutants with increased levels of rDNA transcription;	2.6	
YCL038C	ATG22	Vacuolar integral membrane protein required for efflux of amino acids during autophagic body breakdown in the vacuole; null mutation causes	2.6	3.2
YOR020W-A			2.6	2.1
YHR106W	TRR2	Mitochondrial thioredoxin reductase involved in protection against oxidative stress, required with Glr1p to maintain the redox state of Trx3p;	2.6	
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	2.6	5.5
YDL020C	RPN4	Transcription factor that stimulates expression of proteasome genes; Rpn4p levels are in turn regulated by the 26S proteasome in a negative	2.6	2.9
YNL128W	TEP1	Homolog of human tumor suppressor gene PTEN/MMAC1/TEP1 that has lipid phosphatase activity and is linked to the phosphatidylinositol	2.6	

YLR414C	PUN1	Putative protein of unknown function; localizes to bud and cytoplasm; co-localizes with Sur7p in punctate patches in the plasma membrane; null	2.6	3.2
YER179W	DMC1	Meiosis-specific protein required for repair of double-strand breaks and pairing between homologous chromosomes; homolog of Rad51p and the	2.6	3.7
YBL043W	ECM13	Non-essential protein of unknown function; induced by treatment with 8-methoxypsoralen and UVA irradiation	2.5	
YKL159C	RCN1	Protein involved in calcineurin regulation during calcium signaling; has similarity to H. sapiens DSCR1 which is found in the Down Syndrome	2.5	5.2
YER096W	SHC1	Sporulation-specific activator of Chs3p (chitin synthase III), required for the synthesis of the chitosan layer of ascospores; has similarity to Skt5p,	2.5	
YDR058C	TGL2	Triacylglycerol lipase that is localized to the mitochondria; has lipolytic activity towards triacylglycerols and diacylglycerols when expressed in E.	2.5	3.5
YOL108C	INO4	Transcription factor required for derepression of inositol-choline-regulated genes involved in phospholipid synthesis; forms a complex,	2.5	
YGL038C	OCH1	Mannosyltransferase of the cis-Golgi apparatus, initiates the polymannose outer chain elongation of N-linked oligosaccharides of	2.5	2.5
YBL093C	ROX3	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme	2.5	3.4
YJL185C			2.5	2.0
YNL200C			2.5	
YLL064C	PAU18	Protein of unknown function, member of the seripauperin multigene family encoded mainly in subtelomeric regions; identical to Pau6p ///	2.5	4.8
YMR114C			2.5	2.3
YER015W	FAA2	Medium chain fatty acyl-CoA synthetase, activates imported fatty acids; accepts a wide range of fatty acid chain lengths with a preference for	2.5	2.2
YDR317W	HIM1	Protein of unknown function involved in DNA repair	2.5	2.6
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	2.5	
YOR161C-C			2.5	
YOR348C	PUT4	Proline permease, required for high-affinity transport of proline; also transports the toxic proline analog azetidine-2-carboxylate (AzC); PUT4	2.5	
YPL123C	RNY1	Vacuolar RNase of the T(2) family, relocalizes to the cytosol where it cleaves tRNAs upon oxidative or stationary phase stress; promotes	2.5	2.6
YBR269C	FMP21	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	2.5	2.3
YHR001W-A	QCR10	Subunit of the ubiquinol-cytochrome c oxidoreductase complex which includes Cobp, Rip1p, Cyt1p, Cor1p, Qcr2p, Qcr6p, Qcr7p, Qcr8p,	2.5	
YMR053C	STB2	Protein that interacts with Sin3p in a two-hybrid assay and is part of a large protein complex with Sin3p and Stb1p	2.5	5.1
YNR075W	COS10	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins	2.5	6.0
YDR123C	INO2	Component of the heteromeric Ino2p/Ino4p basic helix-loop-helix transcription activator that binds inositol/choline-responsive elements	2.5	2.1
YGL051W	MST27	Putative integral membrane protein, involved in vesicle formation; forms complex with Mst28p; member of DUP240 gene family; binds COPI and	2.5	2.5
YOR328W	PDR10	ATP-binding cassette (ABC) transporter, multidrug transporter involved in the pleiotropic drug resistance network; regulated by Pdr1p and Pdr3p	2.5	
YLL039C	UBI4	Ubiquitin, becomes conjugated to proteins, marking them for selective degradation via the ubiquitin-26S proteasome system; essential for the	2.5	6.3
YNL024C			2.5	2.7
YMR323W	ERR3	Protein of unknown function, has similarity to enolases ///	2.5	3.9
YOR177C	MPC54	Component of the meiotic outer plaque, a membrane-organizing center which is assembled on the cytoplasmic face of the spindle pole body	2.5	2.3
YDL079C	MRK1	Glycogen synthase kinase 3 (GSK-3) homolog; one of four GSK-3 homologs in S. cerevisiae that function to activate Msn2p-dependent	2.5	
YOL048C	RRT8	Putative protein of unknown function; identified in a screen for mutants with increased levels of rDNA transcription; green fluorescent protein	2.5	2.7
YOL110W	SHR5	Subunit of a palmitoyltransferase, composed of Shr5p and Erf2p, that adds a palmitoyl lipid moiety to heterolipidated substrates such as Ras1p	2.5	

YGR250C			2.4	
YPL170W	DAP1	Heme-binding protein involved in regulation of cytochrome P450 protein Erg11p; damage response protein, related to mammalian membrane	2.4	3.8
YEL011W	GLC3	Glycogen branching enzyme, involved in glycogen accumulation; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a	2.4	
YOL016C	CMK2	Calmodulin-dependent protein kinase; may play a role in stress response, many CA ⁺⁺ /calmodulin dependent phosphorylation	2.4	5.9
YML118W	NGL3	Putative endonuclease, has a domain similar to a magnesium-dependent endonuclease motif in mRNA deadenylase Ccr4p; similar to Ng11p and	2.4	3.3
YLR107W	REX3	RNA exonuclease; required for maturation of the RNA component of RNase MRP; functions redundantly with Rnh70p and Rex2p in	2.4	3.2
YDL027C			2.4	2.6
YOL024W			2.4	
YGL157W	ARI1	NADPH-dependent aldehyde reductase, utilizes aromatic and alicyclic aldehyde substrates; member of the short-chain	2.4	3.8
YOL155C	HPF1	Haze-protective mannoprotein that reduces the particle size of aggregated proteins in white wines	2.4	3.2
YMR181C			2.4	3.8
YHR015W	MIP6	Putative RNA-binding protein, interacts with Mex67p, which is a component of the nuclear pore involved in nuclear mRNA export	2.4	2.1
YKL051W	SFK1	Plasma membrane protein that may act together with or upstream of Stt4p to generate normal levels of the essential phospholipid PI4P, at	2.4	2.0
YDL057W			2.4	2.7
YKR098C	UBP11	Ubiquitin-specific protease that cleaves ubiquitin from ubiquitinated proteins	2.4	3.0
YJL141C	YAK1	Serine-threonine protein kinase that is part of a glucose-sensing system involved in growth control in response to glucose availability; translocates	2.4	
YJL027C			2.4	
YKL071W			2.4	
YGL081W			2.4	
YGL166W	CUP2	Copper-binding transcription factor; activates transcription of the metallothionein genes CUP1-1 and CUP1-2 in response to elevated	2.4	3.4
YDR258C	HSP78	Oligomeric mitochondrial matrix chaperone that cooperates with Ssc1p in mitochondrial thermotolerance after heat shock; able to prevent the	2.4	3.9
YJL066C	MPM1	Mitochondrial membrane protein of unknown function, contains no hydrophobic stretches	2.4	3.1
YCL049C			2.3	2.9
YHR092C	HXT4	High-affinity glucose transporter of the major facilitator superfamily, expression is induced by low levels of glucose and repressed by high	2.3	
YDR072C	IPT1	Inositolphosphotransferase, involved in synthesis of mannanose-(inositol-P)2-ceramide (M(IP)2C), the most abundant sphingolipid; can mutate to	2.3	2.9
YOR052C			2.3	2.0
YPL130W	SPO19	Meiosis-specific prospore protein; required to produce bending force necessary for proper assembly of the prospore membrane during	2.3	
YIR039C	YPS6	Putative GPI-anchored aspartic protease, member of the yapsin family of proteases involved in cell wall growth and maintenance	2.3	7.5
YOR018W	ROD1	Membrane protein that binds the ubiquitin ligase Rsp5p via its 2 PY motifs; overexpression confers resistance to the GST substrate o-	2.3	2.2
YGL144C	ROG1	Protein with putative serine active lipase domain	2.3	2.1
YKL148C	SDH1	Flavoprotein subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer	2.3	
YBR105C	VID24	Peripheral membrane protein located at Vid (vacuole import and degradation) vesicles; regulates fructose-1,6-bisphosphatase (FBPase)	2.3	
YPR049C	ATG11	Adapter protein for pexophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; directs receptor-bound cargo to the phagophore assembly	2.3	

YBR053C			2.3	3.3
YLR173W			2.3	
YLL026W	HSP104	Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated	2.3	3.9
YPR134W	MSS18	Nuclear encoded protein needed for efficient splicing of mitochondrial COX1 α 5beta intron; mss18 mutations block cleavage of 5' exon - intron	2.3	2.3
YDR436W	PPZ2	Serine/threonine protein phosphatase Z, isoform of Ppz1p; involved in regulation of potassium transport, which affects osmotic stability, cell	2.3	2.3
YOR349W	CIN1	Tubulin folding factor D involved in beta-tubulin (Tub2p) folding; isolated as mutant with increased chromosome loss and sensitivity to benomyl	2.3	
YJL101C	GSH1	Gamma glutamylcysteine synthetase catalyzes the first step in glutathione (GSH) biosynthesis; expression induced by oxidants,	2.3	
YDR533C	HSP31	Possible chaperone and cysteine protease with similarity to E. coli Hsp31; member of the DJ-1/ThiJ/PfpI superfamily, which includes human	2.3	
YGR249W	MGA1	Protein similar to heat shock transcription factor; multicopy suppressor of pseudohyphal growth defects of ammonium permease mutants	2.3	3.2
YFL020C	PAU5	Member of the seripauperin multigene family encoded mainly in subtelomeric regions; induced during alcoholic fermentation; induced by	2.3	
YER067W	RG11	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YER067W is not	2.3	
YGL104C	VPS73	Mitochondrial protein; mutation affects vacuolar protein sorting; putative transporter; member of the sugar porter family	2.3	3.2
YHR202W			2.3	
YHR157W	REC104	Protein involved in early stages of meiotic recombination; required for meiotic crossing over; forms a complex with Rec102p and Spo11p	2.3	
YDR182W-A			2.3	
YLL060C	GTT2	Glutathione S-transferase capable of homodimerization; functional overlap with Gtt2p, Grx1p, and Grx2p	2.3	
YOL011W	PLB3	Phospholipase B (lysophospholipase) involved in phospholipid metabolism; hydrolyzes phosphatidylinositol and phosphatidylserine and	2.3	2.0
YJR025C	BNA1	3-hydroxyanthranilic acid dioxygenase, required for the de novo biosynthesis of NAD from tryptophan via kynurenine; expression	2.2	
YIR029W	DAL2	Allantoicase, converts allantoate to urea and ureidoglycolate in the second step of allantoin degradation; expression sensitive to nitrogen	2.2	
YNL036W	NCE103	Carbonic anhydrase; poorly transcribed under aerobic conditions and at an undetectable level under anaerobic conditions; involved in non-	2.2	3.0
YJR142W			2.2	2.9
YML042W	CAT2	Carnitine acetyl-CoA transferase present in both mitochondria and peroxisomes, transfers activated acetyl groups to carnitine to form	2.2	2.4
YDR125C	ECM18	Protein of unknown function, similar to Rlp24p	2.2	
YJR119C	JHD2	JmjC domain family histone demethylase specific for H3-K4 (histone H3 Lys4); removes methyl groups specifically added by Set1p	2.2	
YDL107W	MSS2	Peripherally bound inner membrane protein of the mitochondrial matrix involved in membrane insertion of C-terminus of Cox2p, interacts	2.2	
YDR492W	IZH1	Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family; transcription is regulated directly by Zap1p,	2.2	
YPL042C	SSN3	Cyclin-dependent protein kinase, component of RNA polymerase II holoenzyme; involved in phosphorylation of the RNA polymerase II C-	2.2	
YNL192W	CHS1	Chitin synthase I, requires activation from zymogenic form in order to catalyze the transfer of N-acetylglucosamine (GlcNAc) to chitin; required	2.2	4.2
YDL234C	GYP7	GTPase-activating protein for yeast Rab family members including: Ypt7p (most effective), Ypt1p, Ypt31p, and Ypt32p (in vitro); involved in	2.2	3.9
YFR053C	HXK1	Hexokinase isoenzyme 1, a cytosolic protein that catalyzes phosphorylation of glucose during glucose metabolism; expression is	2.2	
YGR126W			2.2	3.2
YCR091W	KIN82	Putative serine/threonine protein kinase implicated in the regulation of phospholipid asymmetry through the activation of phospholipid	2.2	2.0
YGL045W	RIM8	Protein involved in proteolytic activation of Rim101p in response to alkaline pH; interacts with ESCRT-1 subunits Stp22p and Vps28p;	2.2	2.3

YLR004C	THI73	Putative plasma membrane permease proposed to be involved in carboxylic acid uptake and repressed by thiamine; substrate of	2.2	
YLL041C	SDH2	Iron-sulfur protein subunit of succinate dehydrogenase (Sdh1p, Sdh2p, Sdh3p, Sdh4p), which couples the oxidation of succinate to the transfer	2.2	
YNL012W	SPO1	Meiosis-specific prospore protein; required for meiotic spindle pole body duplication and separation; required to produce bending force necessary	2.2	2.8
YEL020C			2.2	2.3
YDR403W	DIT1	Sporulation-specific enzyme required for spore wall maturation, involved in the production of a soluble LL-dityrosine-containing precursor of the	2.2	2.3
YBR045C	GIP1	Meiosis-specific regulatory subunit of the Glc7p protein phosphatase, regulates spore wall formation and septin organization, required for	2.2	2.6
YDR490C	PKH1	Serine/threonine protein kinase involved in sphingolipid-mediated signaling pathway that controls endocytosis; activates Ypk1p and Ykr2p,	2.2	2.1
YBR022W	POA1	Phosphatase that is highly specific for ADP-ribose 1"-phosphate, a tRNA splicing metabolite; may have a role in regulation of tRNA splicing	2.2	
YDR085C	AFR1	Protein required for pheromone-induced projection (shmoo) formation; regulates septin architecture during mating; has an RVXF motif that	2.2	4.7
YDR530C	APA2	Diadenosine 5',5"-P1,P4-tetraphosphate phosphorylase II (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl)	2.2	2.1
YAL028W	FRT2	Tail-anchored endoplasmic reticulum membrane protein, interacts with homolog Frt1p but is not a substrate of calcineurin (unlike Frt1p),	2.2	2.4
YMR165C	PAH1	Mg ²⁺ -dependent phosphatidate (PA) phosphatase, catalyzes the dephosphorylation of PA to yield diacylglycerol and	2.2	2.3
YKL183C-A			2.2	3.0
YOR274W	MOD5	Delta 2-isopentenyl pyrophosphate:tRNA isopentenyl transferase, required for biosynthesis of the modified base isopentenyladenosine in	2.2	2.3
YER144C	UBP5	Putative ubiquitin-specific protease, closest paralog of Doa4p but has no functional overlap; concentrates at the bud neck	2.2	2.7
YLR460C			2.2	
YOR176W	HEM15	Ferrochelatase, a mitochondrial inner membrane protein, catalyzes the insertion of ferrous iron into protoporphyrin IX, the eighth and final step in	2.2	2.0
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	2.2	
YLR307C-A			2.1	2.4
YOL107W			2.1	2.7
YPR191W	QCR2	Subunit 2 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport	2.1	
YLR329W	REC102	Protein involved in early stages of meiotic recombination; required for chromosome synapsis; forms a complex with Rec104p and Spo11p	2.1	
YAR027W	UIP3	Putative integral membrane protein of unknown function; interacts with Ulp1p at the nuclear periphery; member of DUP240 gene family	2.1	2.7
YGL254W	FZF1	Transcription factor involved in sulfite metabolism, sole identified regulatory target is SSU1, overexpression suppresses sulfite-sensitivity	2.1	
YDR277C	MTH1	Negative regulator of the glucose-sensing signal transduction pathway, required for repression of transcription by Rgt1p; interacts with Rgt1p	2.1	
YMR280C	CAT8	Zinc cluster transcriptional activator necessary for derepression of a variety of genes under non-fermentative growth conditions, active after	2.1	
YKL091C			2.1	2.6
YGR237C			2.1	3.0
YJL070C			2.1	
YDR275W	BSC2	Protein of unknown function, ORF exhibits genomic organization compatible with a translational readthrough-dependent mode of	2.1	2.6
YHR067W	HTD2	Mitochondrial 3-hydroxyacyl-thioester dehydratase involved in fatty acid biosynthesis, required for respiratory growth and for normal mitochondrial	2.1	
YIR033W	MGA2	ER membrane protein involved in regulation of OLE1 transcription, acts with homolog Spt23p; inactive ER form dimerizes and one subunit is	2.1	3.7
YPL148C	PPT2	Phosphopantetheine:protein transferase (PPTase), activates mitochondrial acyl carrier protein (Acp1p) by phosphopantetheinylation	2.1	

YFL041W-A			2.1	3.5
YGR035C			2.1	
YOR374W	ALD4	Mitochondrial aldehyde dehydrogenase, required for growth on ethanol and conversion of acetaldehyde to acetate; phosphorylated; activity is K+	2.1	
YGR036C	CAX4	Dolichyl pyrophosphate (Dol-P-P) phosphatase with a lumenally oriented active site in the ER, cleaves the anhydride linkage in Dol-P-P, required	2.1	2.2
YMR020W	FMS1	Polyamine oxidase, converts spermine to spermidine, which is required for the essential hypusination modification of translation factor eIF-5A;	2.1	3.6
YDR030C	RAD28	Protein involved in DNA repair, related to the human CSA protein that is involved in transcription-coupled repair nucleotide excision repair	2.1	2.5
YGR161C	RTS3	Putative component of the protein phosphatase type 2A complex	2.1	3.4
YGR183C	QCR9	Subunit 9 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport	2.1	
YMR140W	SIP5	Protein of unknown function; interacts with both the Reg1p/Glc7p phosphatase and the Snf1p kinase	2.1	2.8
YLR345W			2.1	2.4
YOL015W	IRC10	Putative protein of unknown function; null mutant displays increased levels of spontaneous Rad52p foci	2.1	2.1
YKL086W	SRX1	Sulfiredoxin, contributes to oxidative stress resistance by reducing cysteine-sulfinic acid groups in the peroxiredoxin Tsa1p, which is formed	2.1	3.3
YPR093C	ASR1	Ubiquitin ligase that modifies and regulates RNA Pol II; involved in a putative alcohol-responsive signaling pathway; accumulates in the	2.0	
YGL227W	VID30	Protein involved in proteasome-dependent catabolite degradation of fructose-1,6-bisphosphatase (FBPase); binds FBPase; shifts the balance	2.0	2.3
YJR152W	DAL5	Allantoate permease; ureidosuccinate permease; also transports dipeptides, though with lower affinity than for allantoate and	2.0	
YNL009W	IDP3	Peroxisomal NADP-dependent isocitrate dehydrogenase, catalyzes oxidation of isocitrate to alpha-ketoglutarate with the formation of	2.0	
YFR030W	MET10	Subunit alpha of assimilatory sulfite reductase, which converts sulfite into sulfide	2.0	
YMR030W	RSF1	Protein required for respiratory growth; localized to both the nucleus and mitochondrion; may interact with transcription factors to mediate the	2.0	
YER062C	HOR2	One of two redundant DL-glycerol-3-phosphatases (RHR2/GPP1 encodes the other) involved in glycerol biosynthesis; induced in response	2.0	4.6
YIL071C	PCI8	Possible shared subunit of Cop9 signalosome (CSN) and eIF3, binds eIF3b subunit Prt1p, has possible dual functions in transcriptional and	2.0	
YDR042C			2.0	
YFL062W	COS4	Protein of unknown function, member of the DUP380 subfamily of conserved, often subtelomerically-encoded proteins /// Protein of	2.0	2.0
YHL010C	ETP1	Putative protein of unknown function that is required for growth on ethanol; contains a zinc finger region and has homology to human	2.0	
YDR255C	RMD5	Conserved protein that has an E3-like ubiquitin ligase activity necessary for polyubiquitination and degradation of the gluconeogenic enzyme	2.0	2.7
YLR132C			2.0	
YHL009W-B			2.0	
YDL149W	ATG9	Transmembrane protein involved in forming Cvt and autophagic vesicles; cycles between the phagophore assembly site (PAS) and other cytosolic	2.0	
YPR121W	THI22	Protein with similarity to hydroxymethylpyrimidine phosphate kinases; member of a gene family with THI20 and THI21; not required for	2.0	
YLR120C	YPS1	Aspartic protease, member of the yapsin family of proteases involved in cell wall growth and maintenance; attached to the plasma membrane via	2.0	4.0
YFL003C	MSH4	Protein involved in meiotic recombination, required for normal levels of crossing over, colocalizes with Zip2p to discrete foci on meiotic	2.0	
YKL129C	MYO3	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes	2.0	2.4
YEL049W	PAU2	Member of the seripauperin multigene family encoded mainly in subtelomeric regions, active during alcoholic fermentation, regulated by	2.0	
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	2.0	32.9

YIL004C	BET1	Type II membrane protein required for vesicular transport between the endoplasmic reticulum and Golgi complex; v-SNARE with similarity to	-2.0	
YOL058W	ARG1	Arginosuccinate synthetase, catalyzes the formation of L-argininosuccinate from citrulline and L-aspartate in the arginine	-2.0	
YDL090C	RAM1	Beta subunit of the CAAX farnesyltransferase (FTase) that prenylates the a-factor mating pheromone and Ras proteins; required for the	-2.0	
YMR179W	SPT21	Protein with a role in transcriptional silencing; required for normal transcription at several loci including HTA2-HTB2 and HHF2-HHT2, but	-2.0	
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	-2.0	-2.0
YOR321W	PMT3	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts	-2.0	
YOR342C			-2.0	-2.3
YDR503C	LPP1	Lipid phosphate phosphatase, catalyzes Mg(2+)-independent dephosphorylation of phosphatidic acid (PA), lysophosphatidic acid, and	-2.0	
YDR144C	MKC7	GPI-anchored aspartyl protease, member of the yapsin family of proteases involved in cell wall growth and maintenance; shares functions	-2.0	
YEL038W	UTR4	Protein with sequence similarity to 2,3-diketo-5-methylthiopentyl-1-phosphate enolase-phosphatases, involved in methionine salvage; found	-2.0	-2.6
YOR083W	WHI5	Repressor of G1 transcription that binds to SCB binding factor (SBF) at SCB target promoters in early G1; phosphorylation of Whi5p by the CDK,	-2.0	
YJR030C			-2.1	
YBL009W	ALK2	Protein kinase; accumulation and phosphorylation are periodic during the cell cycle; phosphorylated in response to DNA damage; contains	-2.1	-2.1
YBR202W	MCM7	Component of the hexameric MCM complex, which is important for priming origins of DNA replication in G1 and becomes an active ATP-	-2.1	-3.0
YIL117C	PRM5	Pheromone-regulated protein, predicted to have 1 transmembrane segment; induced during cell integrity signaling	-2.1	
YHL035C	VMR1	Protein of unknown function that may interact with ribosomes, based on co-purification experiments; member of the ATP-binding cassette (ABC)	-2.1	
YEL071W	DLD3	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and	-2.1	
YIL009W	FAA3	Long chain fatty acyl-CoA synthetase, activates imported fatty acids; green fluorescent protein (GFP)-fusion protein localizes to the cell	-2.1	
YMR292W	GOT1	Homodimeric protein that is packaged into COPII vesicles and cycles between the ER and Golgi; involved in secretory transport but not directly	-2.1	
YDR501W	PLM2	Forkhead Associated domain containing protein and putative transcription factor found associated with chromatin; target of SBF	-2.1	
YBR088C	POL30	Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta; may function as a docking site for other	-2.1	
YHL047C	ARN2	Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound	-2.2	
YPL265W	DIP5	Dicarboxylic amino acid permease, mediates high-affinity and high-capacity transport of L-glutamate and L-aspartate; also a transporter for	-2.2	-3.9
YOL012C	HTZ1	Histone variant H2AZ, exchanged for histone H2A in nucleosomes by the SWR1 complex; involved in transcriptional regulation through prevention	-2.2	-2.5
YDR113C	PDS1	Securin, inhibits anaphase by binding separin Esp1p; blocks cyclin destruction and mitotic exit, essential for meiotic progression and mitotic	-2.2	-2.0
YJR143C	PMT4	Protein O-mannosyltransferase, transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues;	-2.2	
YJL173C	RFA3	Subunit of heterotrimeric Replication Protein A (RPA), which is a highly conserved single-stranded DNA binding protein involved in DNA	-2.2	
YJL074C	SMC3	Subunit of the multiprotein cohesin complex required for sister chromatid cohesion in mitotic cells; also required, with Rec8p, for cohesion and	-2.2	
YGR205W			-2.2	
YOR381W-A			-2.2	
YOR317W	FAA1	Long chain fatty acyl-CoA synthetase, activates imported fatty acids with a preference for C12:0-C16:0 chain lengths; functions in long chain fatty	-2.2	-2.5
YER070W	RNR1	Major isoform of the large subunit of ribonucleotide-diphosphate reductase; the RNR complex catalyzes rate-limiting step in dNTP	-2.2	-2.3
YOR073W	SGO1	Component of the spindle checkpoint, involved in sensing lack of tension on mitotic chromosomes; protects centromeric Rec8p at meiosis I;	-2.2	-2.3

YGL012W	ERG4	C-24(28) sterol reductase, catalyzes the final step in ergosterol biosynthesis; mutants are viable, but lack ergosterol	-2.3	-2.0
YAR018C	KIN3	Nonessential protein kinase with unknown cellular role	-2.3	
YDL003W	MCD1	Essential subunit of the cohesin complex required for sister chromatid cohesion in mitosis and meiosis; apoptosis induces cleavage and	-2.3	
YGR177C	ATF2	Alcohol acetyltransferase, may play a role in steroid detoxification; forms volatile esters during fermentation, which is important for brewing and	-2.3	-2.3
YJR109C	CPA2	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor	-2.3	-2.0
YDR518W	EUG1	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the	-2.3	
YBR047W	FMP23	Putative protein of unknown function; proposed to be involved in iron or copper homeostasis; the authentic, non-tagged protein is detected in	-2.3	
YOR108W	LEU9	Alpha-isopropylmalate synthase II (2-isopropylmalate synthase), catalyzes the first step in the leucine biosynthesis pathway; the minor	-2.3	-4.3
YKL043W	PHD1	Transcriptional activator that enhances pseudohyphal growth; regulates expression of FLO11, an adhesin required for pseudohyphal filament	-2.3	-3.2
YIL121W	QDR2	Multidrug transporter of the major facilitator superfamily, required for resistance to quinidine, barban, cisplatin, and bleomycin; may have a	-2.3	-2.4
YNL121C	TOM70	Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially	-2.3	
YLR183C	TOS4	Forkhead Associated domain containing protein and putative transcription factor found associated with chromatin; target of SBF	-2.3	
YNL300W	TOS6	Glycosylphosphatidylinositol-dependent cell wall protein, expression is periodic and decreases in response to ergosterol perturbation or upon	-2.3	
YBR265W	TSC10	3-ketosphinganine reductase, catalyzes the second step in phytosphingosine synthesis, essential for growth in the absence of	-2.3	-3.3
YDR381W	YRA1	RNA binding protein required for export of poly(A) ⁺ mRNA from the nucleus; proposed to couple mRNA export with 3' end processing via its	-2.3	
YGL256W	ADH4	Alcohol dehydrogenase isoenzyme type IV, dimeric enzyme demonstrated to be zinc-dependent despite sequence similarity to iron-	-2.4	
YOR074C	CDC21	Thymidylate synthase, required for de novo biosynthesis of pyrimidine deoxyribonucleotides; expression is induced at G1/S	-2.4	
YPL127C	HHO1	Histone H1, a linker histone required for nucleosome packaging at restricted sites; suppresses DNA repair involving homologous	-2.4	
YDR528W	HLR1	Protein involved in regulation of cell wall composition and integrity and response to osmotic stress; overproduction suppresses a lysis sensitive	-2.4	-2.4
YJL051W	IRC8	Bud tip localized protein of unknown function; mRNA is targeted to the bud by a She2p dependent transport system; mRNA is cell cycle	-2.4	-2.3
YPR194C	OPT2	Oligopeptide transporter; member of the OPT family, with potential orthologs in <i>S. pombe</i> and <i>C. albicans</i> ; also plays a role in formation of	-2.4	-13.7
YGR221C	TOS2	Protein involved in localization of Cdc24p to the site of bud growth; may act as a membrane anchor; localizes to the bud neck and bud tip;	-2.4	-2.5
YOR381W	FRE3	Ferric reductase, reduces siderophore-bound iron prior to uptake by transporters; expression induced by low iron levels	-2.5	
YNR009W	NRM1	Transcriptional co-repressor of MBF (MCB binding factor)-regulated gene expression; Nrm1p associates stably with promoters via MBF to repress	-2.5	-3.8
YML052W	SUR7	Plasma membrane protein that localizes to furrow-like invaginations (MCC patches); component of eisosomes; associated with endocytosis,	-2.5	-3.5
YLR212C	TUB4	Gamma-tubulin, involved in nucleating microtubules from both the cytoplasmic and nuclear faces of the spindle pole body	-2.5	
YCL026C-A	FRM2	Protein of unknown function, involved in the integration of lipid signaling pathways with cellular homeostasis; expression induced in cells treated	-2.6	
YBL032W	HEK2	RNA binding protein involved in the asymmetric localization of ASH1 mRNA; represses translation of ASH1 mRNA, an effect reversed by	-2.6	
YPL250C	ICY2	Protein of unknown function; mobilized into polysomes upon a shift from a fermentable to nonfermentable carbon source; potential Cdc28p	-2.6	-2.6
YPL274W	SAM3	High-affinity S-adenosylmethionine permease, required for utilization of S-adenosylmethionine as a sulfur source; has similarity to S-	-2.6	-7.8
YJL047C-A			-2.6	-3.1
YLR049C			-2.6	-3.9
YPL189W	GUP2	Probable membrane protein with a possible role in proton symport of glycerol; member of the MBOAT family of putative membrane-bound O-	-2.6	

YHR175W-A			-2.7	
YNL018C			-2.7	
YOR028C	CIN5	Basic leucine zipper (bZIP) transcription factor of the yAP-1 family, mediates pleiotropic drug resistance and salt tolerance; nuclearly	-2.7	
YNR028W	CPR8	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; similarity	-2.7	-2.8
YHR143W	DSE2	Daughter cell-specific secreted protein with similarity to glucanases, degrades cell wall from the daughter side causing daughter to separate	-2.7	-5.1
YNL327W	EGT2	Glycosylphosphatidylinositol (GPI)-anchored cell wall endoglucanase required for proper cell separation after cytokinesis, expression is	-2.7	-3.3
YJL157C	FAR1	Cyclin-dependent kinase inhibitor that mediates cell cycle arrest in response to pheromone; also forms a complex with Cdc24p, Ste4p, and	-2.7	-5.3
YCL024W	KCC4	Protein kinase of the bud neck involved in the septin checkpoint, associates with septin proteins, negatively regulates Swe1p by	-2.7	-3.3
YNL301C	RPL18B	Protein component of the large (60S) ribosomal subunit, identical to Rpl18Ap and has similarity to rat L18 ribosomal protein	-2.7	-2.2
YOL014W			-2.8	
YDL198C	GGC1	Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the	-2.8	-3.1
YJR005C-A			-2.9	
YGR109C	CLB6	B-type cyclin involved in DNA replication during S phase; activates Cdc28p to promote initiation of DNA synthesis; functions in formation of	-2.9	-4.2
YOR010C	TIR2	Putative cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins; transcription is induced by cold shock and	-2.9	
YBR092C	PHO3	Constitutively expressed acid phosphatase similar to Pho5p; brought to the cell surface by transport vesicles; hydrolyzes thiamin phosphates in	-2.9	-3.7
YAR031W	PRM9	Pheromone-regulated protein with 3 predicted transmembrane segments and an FF sequence, a motif involved in COPII binding; member of	-2.9	
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	-2.9	
YJL056C	ZAP1	Zinc-regulated transcription factor; binds to zinc-responsive promoters to induce transcription of certain genes in presence of zinc, represses other	-2.9	
YGL117W			-3.0	-2.3
YNL034W			-3.0	
YNL078W	NIS1	Protein localized in the bud neck at G2/M phase; physically interacts with septins; possibly involved in a mitotic signaling network	-3.0	-2.7
YJR004C	SAG1	Alpha-agglutinin of alpha-cells, binds to Aga1p during agglutination, N-terminal half is homologous to the immunoglobulin superfamily and	-3.0	-5.0
YMR032W	HOF1	Bud neck-localized, SH3 domain-containing protein required for cytokinesis; regulates actomyosin ring dynamics and septin localization;	-3.1	-2.8
YBL044W			-3.2	-3.1
YDR354W	TRP4	Anthranilate phosphoribosyl transferase of the tryptophan biosynthetic pathway, catalyzes the phosphoribosylation of anthranilate, subject to the	-3.2	
YBR085W	AAC3	Mitochondrial inner membrane ADP/ATP translocator, exchanges cytosolic ADP for mitochondrially synthesized ATP; expressed under	-3.3	-3.0
YIL158W	AIM20	Putative protein of unknown function; overexpression causes a cell cycle delay or arrest; green fluorescent protein (GFP)-fusion protein localizes	-3.3	-3.2
YDR044W	HEM13	Coproporphyrinogen III oxidase, an oxygen requiring enzyme that catalyzes the sixth step in the heme biosynthetic pathway; transcription	-3.3	-2.0
YMR215W	GAS3	Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall	-3.4	-3.8
YOR387C			-3.6	
YDL241W			-3.7	
YPL241C	CIN2	GTPase-activating protein (GAP) for Cin4p; tubulin folding factor C involved in beta-tubulin (Tub2p) folding; mutants display increased	-3.7	-2.4
YMR030W-A			-3.8	-2.3

YMR230W-A			-4.0	-9.5
YMR317W			-4.0	
YNL066W	SUN4	Cell wall protein related to glucanases, possibly involved in cell wall septation; member of the SUN family	-4.0	-6.3
YMR006C	PLB2	Phospholipase B (lysophospholipase) involved in phospholipid metabolism; displays transacylase activity in vitro; overproduction	-4.2	-2.1
YJL078C	PRY3	Protein of unknown function	-4.2	-3.6
YER081W	SER3	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser33p	-4.2	
YHR214C-E			-4.3	-5.0
YOR315W	SFG1	Nuclear protein, putative transcription factor required for growth of superficial pseudohyphae (which do not invade the agar substrate) but	-4.3	-9.4
YBL002W	HTB2	Histone H2B, core histone protein required for chromatin assembly and chromosome function; nearly identical to HTB1; Rad6p-Bre1p-Lge1p	-4.5	
YJL217W	REE1	Cytoplasmic protein involved in the regulation of enolase (ENO1); mRNA expression is induced by calcium shortage, copper deficiency (via	-4.8	
YHR153C	SPO16	Meiosis-specific protein involved in synaptonemal complex assembly; implicated in regulation of crossover formation; required for sporulation	-4.8	-2.8
YBL029W			-5.0	-13.5
YKR093W	PTR2	Integral membrane peptide transporter, mediates transport of di- and tri-peptides; conserved protein that contains 12 transmembrane domains;	-5.0	
YGR234W	YHB1	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress	-5.0	-3.6
YNL058C			-5.3	
YLR348C	DIC1	Mitochondrial dicarboxylate carrier, integral membrane protein, catalyzes a dicarboxylate-phosphate exchange across the inner mitochondrial	-5.3	-2.0
YHL028W	WSC4	ER membrane protein involved in the translocation of soluble secretory proteins and insertion of membrane proteins into the ER membrane; may	-5.3	-24.4
YOR384W	FRE5	Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels; the authentic, non-tagged protein is detected in highly	-5.6	
YBL003C	HTA2	Histone H2A, core histone protein required for chromatin assembly and chromosome function; one of two nearly identical (see also HTA1)	-5.9	
YAR071W	PHO11	One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; induced by	-6.7	-6.5
YIL011W	TIR3	Cell wall mannoprotein of the Srp1p/Tip1p family of serine-alanine-rich proteins; expressed under anaerobic conditions and required for	-7.1	-4.1
YKL220C	FRE2	Ferric reductase and cupric reductase, reduces siderophore-bound iron and oxidized copper prior to uptake by transporters; expression induced	-7.7	
YAR073W	IMD1	Nonfunctional protein with homology to IMP dehydrogenase; probable pseudogene, located close to the telomere; is not expressed at	-8.3	
YHR216W	IMD2	Inosine monophosphate dehydrogenase, catalyzes the rate-limiting step in GTP biosynthesis, expression is induced by mycophenolic acid	-8.3	
YGL089C	MF(ALPHA)2	Mating pheromone alpha-factor, made by alpha cells; interacts with mating type a cells to induce cell cycle arrest and other responses	-9.1	-7.1
YGL258W	VEL1	Protein of unknown function; highly induced in zinc-depleted conditions and has increased expression in NAP1 deletion mutants	-9.1	
YJL218W			-10.6	-6.2
YDR534C	FIT1	Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of	-11.6	
YDL227C	HO	Site-specific endonuclease required for gene conversion at the MAT locus (homothallic switching) through the generation of a ds DNA break;	-16.7	-6.0