

Table S2 Genes down regulated in quercetin treated cells. *S. cerevisiae* BY4741 was grown to exponential phase in YPD medium and treated with 300 μ M of quercetin or equal volume of DMSO (control cells) for 15 min. Genes differentially regulated (quercetin vs control) were sorted into functional categories according to MIPS; some genes were listed in more than one category.

Gene name	Fold change	Gene Product
Amino acid metabolism		
<i>SRB6</i>	-2.1	part of Srb/mediator complex; transcription factor
<i>CIT2</i>	-1.0	citrate synthase
<i>MAK31</i>	-1.8	member of the Sm protein family
<i>DTD1</i>	-1.2	D-Tyr-tRNA(Tyr) deacylase
<i>LYS5</i>	-1.0	alpha aminoadipate reductase phosphopantetheinyl transferase
<i>YIL167W</i>	-1.3	questionable protein
<i>MET14</i>	-1.1	adenylylsulfate kinase
<i>MET1</i>	-1.1	S-adenosyl-L-methionine uroporphyrinogen III transmethylase
<i>ASP3-1</i>	-1.2	nitrogen catabolite-regulated cell-wall L-asparaginase II
<i>ASP3-2</i>	-1.0	nitrogen catabolite-regulated cell-wall L-asparaginase II
<i>ASP3-3</i>	-1.0	nitrogen catabolite-regulated cell-wall L-asparaginase II
<i>ASP3-4</i>	-1.2	nitrogen catabolite-regulated cell-wall L-asparaginase II
<i>ORT1</i>	-1.0	ornithine transporter of the mitochondrial inner membrane
<i>MET31</i>	-1.2	highly homologous to Met32p; transcriptional regulator of sulfur amino acid metabolism
Nucleotide/nucleoside/nucleobase metabolism		
<i>RIB1</i>	-0.9	GTP cyclohydrolase II
<i>DUT1</i>	-1.2	dUTP pyrophosphatase
<i>CDC36</i>	-1.1	basal transcription inhibitor; transcriptional regulator
<i>HPT1</i>	-1.8	hypoxanthine guanine phosphoribosyltransferase
<i>GNA1</i>	-1.2	glucosamine-phosphate N-acetyltransferase
<i>SLX9</i>	-0.9	protein of unknown function
<i>RRP46</i>	-1.2	3'->5' exoribonuclease
<i>CPD1</i>	-1.9	2',3'-cyclic nucleotide 3'-phosphodiesterase
<i>DAL7</i>	-1.5	malate synthase 2
<i>MRT4</i>	-1.3	mRNA turnover 4
<i>PUS5</i>	-1.8	RNA:pseudouridine (Psi)-synthase
<i>URA10</i>	-0.9	orotate phosphoribosyltransferase 2
<i>LSM7</i>	-1.6	snRNP protein
<i>DCP1</i>	-0.9	mRNA decapping enzyme
<i>SPS4</i>	-1.6	sporulation-specific protein
<i>FCY1</i>	-1.2	cytosine deaminase
Phosphate metabolism		
<i>DUT1</i>	-1.2	dUTP pyrophosphatase
<i>YPI1</i>	-1.0	PP1 phosphatase inhibitor
<i>DOG2</i>	-0.9	2-deoxyglucose-6-phosphate phosphatase
<i>MET14</i>	-1.1	adenylylsulfate kinase
<i>FBP1</i>	-0.9	fructose-1,6-bisphosphatase
<i>CTL1</i>	-1.3	RNA triphosphatase
Regulation of phosphate metabolism		
<i>YPI1</i>	-1.0	PP1 phosphatase inhibitor
C-compound and carbohydrate metabolism		
<i>ACS1</i>	-1.5	acetyl CoA synthetase
<i>LDB7</i>	-0.9	protein involved in mannosylphosphorylation of cell wall mannoproteins

Gene name	Fold change	Gene Product
<i>HAP3</i>	-1.3	transcriptional activator protein of CYC1 (component of HAP2/HAP3 heteromer)
<i>GAL10</i>	-1.2	UDP-glucose 4-epimerase
<i>SRB6</i>	-2.1	part of Srb/Mediator complex; transcription factor
<i>CIT2</i>	-1.0	citrate synthase
<i>OST4</i>	-0.9	oligosaccharyltransferase subunit
<i>SOR2</i>	-1.3	protein of unknown function, possible role in fructose or mannose metabolism
<i>NRG1</i>	-1.6	binds to UAS-1 in the STA1 promoter and can interact with Ssn6; transcriptional repressor
<i>SNF11</i>	-1.4	SWI/SNF global transcription activator complex component
<i>YDR248C</i>	-1.2	questionable protein
<i>GPI11</i>	-1.3	protein involved in glycosylphosphatidylinositol (GPI) biosynthesis
<i>ACN9</i>	-1.2	Protein of the mitochondrial intermembrane space, required for acetate utilization and gluconeogenesis
<i>FAU1</i>	-1.1	5,10-methenyltetrahydrofolate synthetase
<i>GNA1</i>	-1.2	glucosamine-phosphate N-acetyltransferase
<i>SNF6</i>	-0.9	chromatin remodeling Snf/Swi complex subunit
<i>DOG2</i>	-0.9	2-deoxyglucose-6-phosphate phosphatase
<i>DAL7</i>	-1.5	malate synthase 2
<i>GON7</i>	-1.4	protein proposed to be involved in the transfer of mannosylphosphate groups onto N-linked oligosaccharides
<i>SOR1</i>	-1.5	sorbitol dehydrogenase, sorbitol-induced
<i>KTI12</i>	-1.1	elongator associated protein
<i>YLR164W</i>	-1.1	strong similarity to succinate dehydrogenase membrane anchor subunit Sdh4p
<i>IDP3</i>	-1.0	NADP-dependent isocitrate dehydrogenase
<i>YNR071C</i>	-1.3	questionable protein
<i>RKI1</i>	-0.9	ribose-5-phosphate ketol-isomerase
<i>OST2</i>	-1.4	oligosaccharyltransferase epsilon subunit
<i>SPR1</i>	-1.1	exo-1,3-beta-glucanase, sporulation-specific
<i>YOR283W</i>	-0.9	questionable protein

Lipid, fatty acid and isoprenoid metabolism

<i>RER2</i>	-0.9	cis-prenyltransferase
<i>GPI11</i>	-1.3	protein involved in glycosylphosphatidylinositol (GPI) biosynthesis
<i>YLL049W</i>	-0.9	questionable protein
<i>ARV1</i>	-1.0	protein involved in sterol distribution
<i>IDP3</i>	-1.0	NADP-dependent isocitrate dehydrogenase
<i>SPO1</i>	-0.9	similar to phospholipase B
<i>GPI15</i>	-1.6	human Pig-H homolog
<i>CYB5</i>	-1.1	cytochrome b5
<i>YOL101C</i>	-0.9	questionable protein
<i>INO4</i>	-1.7	basic helix-loop-helix (bHLH) protein
<i>YPL095C</i>	-1.0	questionable protein
<i>PPT2</i>	-2.1	phosphopantetheine:protein transferase (PPTase)
<i>DAP1</i>	-1.5	sterol-binding protein (putative)

Metabolism of vitamins, cofactors, and prosthetic groups

<i>ACS1</i>	-1.5	acetyl CoA synthetase
<i>RIB1</i>	-0.9	GTP cyclohydrolase II
<i>PET18</i>	-2.2	protein required for respiratory growth and stability of the mitochondrial genome
<i>HEM3</i>	-0.9	phorphobilinogen deaminase (uroporphyrinogen synthase)
<i>FAU1</i>	-1.1	5,10-methenyltetrahydrofolate synthetase
<i>SNO3</i>	-0.9	protein is related with B(1) biosynthesis during the exponential phase

Gene name	Fold change	Gene Product
<i>LYS5</i>	-1.0	alpha amino adipate reductase phosphopantetheinyl transferase
<i>QCR9</i>	-1.0	ubiquinol cytochrome c oxidoreductase complex 7.3 kDa subunit 9
<i>FMC1</i>	-1.2	assembly factor of ATP synthase in heat stress
<i>MET1</i>	-1.1	S-adenosyl-L-methionine uroporphyrinogen III transmethylase
<i>IDP3</i>	-1.0	NADP-dependent isocitrate dehydrogenase
<i>BIO3</i>	-1.0	7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase
<i>ISU1</i>	-1.1	iron-sulfur cluster nifU-like protein
<i>PPT2</i>	-2.1	phosphopantetheine:protein transferase (PPTase)

Secondary metabolism

<i>KTI11</i>	-1.2	similar to Hemiascomycetous yeast protein
<i>MAK31</i>	-1.8	member of the Sm protein family
<i>HEM3</i>	-0.9	phorphobilinogen deaminase (uroporphyrinogen synthase)
<i>TSA2</i>	-1.0	thioredoxin-peroxidase
<i>YJR097W</i>	-1.5	protein that may function as a cochaperone
<i>MET1</i>	-1.1	S-adenosyl-L-methionine uroporphyrinogen III transmethylase

Energy

<i>ACS1</i>	-1.5	acetyl CoA synthetase
<i>NRG2</i>	-1.6	NRG1 homolog
<i>CIT2</i>	-1.0	citrate synthase
<i>COX9</i>	-2.0	cytochrome c oxidase subunit VIIa
<i>INH1</i>	-1.4	ATPase inhibitor
<i>PET100</i>	-1.5	cytochrome c oxidase-specific assembly factor
<i>YDR115W</i>	-1.4	questionable protein
<i>TIM11</i>	-1.7	mitochondrial F1F0-ATPase subunit e
<i>ACN9</i>	-1.2	Protein of the mitochondrial intermembrane space, required for acetate utilization and gluconeogenesis
<i>QCR7</i>	-1.1	ubiquinol cytochrome C oxidoreductase subunit 7
<i>UBC8</i>	-1.0	ubiquitin-conjugating enzyme; ubiquitin-protein ligase
<i>YPI1</i>	-1.0	PP1 phosphatase inhibitor
<i>QCR6</i>	-1.3	ubiquinol cytochrome C oxidoreductase subunit 6 (17 kDa)
<i>YGL226W</i>	-1.0	questionable protein
<i>QCR9</i>	-1.0	ubiquinol cytochrome c oxidoreductase complex 7.3 kDa subunit 9
<i>VMA10</i>	-1.2	vacuolar ATPase V1 domain subunit G (13 kDa)
<i>VMA22</i>	-1.9	required for V-ATPase activity
<i>DAL7</i>	-1.5	malate synthase 2
<i>CYC1</i>	-0.9	iso-1-cytochrome c
<i>COX17</i>	-1.5	cysteine-rich protein
<i>COX12</i>	-1.1	cytochrome c oxidase subunit VIb
<i>YLR164W</i>	-1.1	strong similarity to succinate dehydrogenase membrane anchor subunit Sdh4p
<i>FBP1</i>	-0.9	fructose-1,6-bisphosphatase
<i>COX8</i>	-1.0	cytochrome c oxidase chain VIII
<i>ATP18</i>	-1.7	ATP synthase associated protein
<i>YML087C</i>	-1.1	questionable protein
<i>COX14</i>	-1.2	mitochondrial membrane protein
<i>MRPS17</i>	-0.9	mitochondrial ribosomal protein of the small subunit
<i>COX7</i>	-2.2	cytochrome c oxidase subunit VII
<i>YMR299C</i>	-1.3	protein of unknown function; GFP-fusion protein localizes to the cytoplasm
<i>IDP3</i>	-1.0	NADP-dependent isocitrate dehydrogenase
<i>ATP19</i>	-1.2	ATP synthase subunit k homolog
<i>RKI1</i>	-0.9	ribose-5-phosphate ketol-isomerase
<i>YOR283W</i>	-0.9	questionable protein
<i>OYE3</i>	-1.8	NADPH dehydrogenase
<i>ATP15</i>	-1.3	ATP synthase epsilon subunit
<i>ATP20</i>	-1.5	ATP synthase subunit g homolog

Gene name	Fold change	Gene Product
<i>MRPL51</i>	-1.1	mitochondrial ribosomal protein of the large subunit
Cell cycle and DNA processing		
<i>POP5</i>	-1.3	RNase MRP subunit (putative); RNase P integral subunit
<i>HTA2</i>	-1.7	histone H2A
<i>KTI11</i>	-1.2	similar to Hemiascomycetous yeast protein
<i>HHF1</i>	-2.3	histone H4 (HHF1 and HHF2 code for identical proteins)
<i>HHT1</i>	-1.7	histone H3 (HHT1 and HHT2 code for identical proteins)
<i>POL30</i>	-1.1	proliferating Cell Nuclear Antigen (PCNA)
<i>NHP6B</i>	-1.2	11 kDa nonhistone chromosomal protein
<i>SLX1</i>	-1.3	subunit of a complex, with Slx4p, that hydrolyzes 5' branches from duplex DNA
<i>DAD3</i>	-1.3	outer kinetochore protein - part of Dam1 complex
<i>DPB3</i>	-1.1	DNA polymerase II C and C' subunits
<i>HMLALPHA2</i>	-2.7	mating type regulatory protein, silenced copy at HML
<i>HTL1</i>	-2.5	high-temperature lethal
<i>MATALPHA2</i>	-3.0	mating type regulatory protein, expressed copy at MAT locus
<i>APC11</i>	-1.2	anaphase promoting complex (APC) subunit
<i>IWR1</i>	-0.9	interacts with RNA Polymerase II
<i>MSH5</i>	-1.2	mutS homolog
<i>CDC36</i>	-1.1	basal transcription inhibitor; transcriptional regulator
<i>RAD57</i>	-1.2	RecA homolog; interacts with Rad 55p
<i>DAD1</i>	-1.7	Duo1 and Dam1 interacting; localized to intranuclear spindles and spindle pole bodies
<i>SNF11</i>	-1.4	SWI/SNF global transcription activator complex component
<i>TFB5</i>	-1.9	Component of general transcription and DNA repair factor TFIIF
<i>STN1</i>	-1.2	involved in telomere length regulation
<i>TAF10</i>	-1.2	TFIID subunit
<i>SPC19</i>	-1.2	spindle pole component
<i>HTA1</i>	-1.7	histone H2A (HTA1 and HTA2 code for nearly identical proteins)
<i>MCM21</i>	-0.9	Involved in minichromosome maintenance
<i>DAD4</i>	-1.7	outer kinetochore protein - part of Dam1 complex
<i>SEM1</i>	-2.6	Regulator of exocytosis and pseudohyphal differentiation
<i>DYN2</i>	-2.1	dynein light chain (putative)
<i>ADA2</i>	-1.4	general transcriptional adaptor or co-activator
<i>BIM1</i>	-2.0	binding to microtubules
<i>YER066W</i>	-1.2	questionable protein
<i>ISC10</i>	-1.7	meiosis-specific protein required for spore formation
<i>GNA1</i>	-1.2	glucosamine-phosphate N-acetyltransferase
<i>FAR7</i>	-1.0	protein involved in G1 cell cycle arrest in response to pheromone, in a pathway different from the Far1p-dependent pathway
<i>SPT4</i>	-3.1	transcription elongation protein
<i>SLX9</i>	-0.9	protein of unknown function
<i>SYF2</i>	-0.9	SYNthetic lethal with CDC40
<i>TRX2</i>	-1.0	thioredoxin
<i>CPD1</i>	-1.9	2',3'-cyclic nucleotide 3'-phosphodiesterase
<i>SNF6</i>	-0.9	chromatin remodeling Snf/Swi complex subunit
<i>LRP1</i>	-1.6	like rRNA Processing protein involved in regulation of DNA repair and recombination
<i>YNG2</i>	-1.2	NuA4 histone acetyltransferase complex component
<i>SPO12</i>	-1.5	sporulation protein
<i>SPO16</i>	-1.0	sporulation protein
<i>SSP1</i>	-1.2	essential for meiosis and spore formation
<i>EST3</i>	-1.8	Subunit of the telomerase
<i>REV7</i>	-1.5	DNA polymerase zeta (pol-zeta) subunit
<i>STS1</i>	-1.1	restores protein transport when overexpressed and rRNA stability to a sec23 mutation

Gene name	Fold change	Gene Product
<i>YIR024C</i>	-1.1	(putative) involved in cell cycle control
<i>YJL065C</i>	-1.0	subunit of ISW2/yCHRAC chromatin remodelling complex
<i>NNF1</i>	-1.3	spindle pole protein, required for accurate chromosome segregation
<i>MCM22</i>	-1.1	required for maintenance of chromosomes and minichromosomes
<i>MGM101</i>	-0.9	mitochondrial nucleoid protein
<i>DAD2</i>	-1.3	outer kinetochore protein - part of Dam1 complex
<i>TEN1</i>	-2.3	protein involved in Telomeric pathways in association with Stn1
<i>TRX1</i>	-1.0	thioredoxin
<i>VPS71</i>	-0.9	component of the Swr1p complex that incorporates Htz1p into chromatin, required for vacuolar protein sorting
<i>HUG1</i>	-1.3	protein involved in the Mec1p-mediated checkpoint pathway that responds to DNA damage or replication arrest
<i>MFT1</i>	-1.2	mitochondrial targeting protein
<i>TAF13</i>	-1.0	TFIID subunit
<i>IMP2</i>	-1.0	protease
<i>BUB2</i>	-0.9	protein required for cell cycle arrest in response to loss of microtubule function
<i>ABF2</i>	-1.0	HMG-1 homolog
<i>CIN4</i>	-1.0	GTP-binding protein
<i>TAF9</i>	-1.2	TFIID subunit
<i>SAP30</i>	-1.7	subunit of the histone deacetylase B complex
<i>JNM1</i>	-1.1	coiled-coil domain protein required for proper nuclear migration during mitosis
<i>YMR299C</i>	-1.3	protein of unknown function; GFP-fusion protein localizes to the cytoplasm
<i>SPO1</i>	-0.9	similar to phospholipase B
<i>HHF2</i>	-2.3	histone H4
<i>HHT2</i>	-1.4	histone H3
<i>NOP15</i>	-1.4	ribosome biogenesis
<i>GIM3</i>	-1.4	bovine prefoldin subunit 4 homolog (putative)
<i>KAR1</i>	-1.0	involved in spindle pole body duplication and karyogamy
<i>YNL213C</i>	-1.2	questionable protein
<i>NTG2</i>	-1.1	endonuclease III DNA base excision repair N-glycosylase
<i>HRT1</i>	-1.1	Skp1-Cullin-F-box ubiquitin protein ligase (SCF) subunit
<i>PSF3</i>	-1.3	a subunit of the GINS complex required for chromosomal DNA replication
<i>CIN5</i>	-1.1	transcriptional activator
<i>YNG1</i>	-1.0	histone acetyltransferase complex component
<i>SAS5</i>	-1.0	involved in silencing at telomeres, HML and HMR
<i>RFM1</i>	-1.0	DNA-binding protein
<i>SPS4</i>	-1.6	sporulation-specific protein
<i>SPC29</i>	-1.3	spindle pole body component
<i>SPP1</i>	-0.9	compass (complex proteins associated with Set1p) component
<i>MCM16</i>	-1.8	outer kinetochore protein
<i>DIB1</i>	-1.3	protein required for mitosis
Transcription		
<i>POP5</i>	-1.3	RNase MRP subunit (putative); RNase P integral subunit
<i>HTA2</i>	-1.7	histone H2A
<i>POP8</i>	-1.5	RNase P integral subunit; subunit of RNase MRP (putative)
<i>HAP3</i>	-1.3	transcriptional activator protein of CYC1 (component of HAP2/HAP3 heteromer)
<i>RRN10</i>	-1.5	upstream activation factor subunit
<i>LSM2</i>	-1.2	snRNA-associated protein, Sm class
<i>HHF1</i>	-2.3	histone H4 (HHF1 and HHF2 code for identical proteins)
<i>HHT1</i>	-1.7	histone H3 (HHT1 and HHT2 code for identical proteins)
<i>NRG2</i>	-1.6	NRG1 homolog

Gene name	Fold change	Gene Product
<i>NHP6B</i>	-1.2	11 kDa nonhistone chromosomal protein
<i>CBP6</i>	-1.2	translational activator of COB mRNA
<i>RPB5</i>	-1.1	25 kDa RNA polymerase subunit (common to polymerases I, II and III)
<i>POP7</i>	-1.4	RNase MRP subunit (putative); RNase P integral subunit
<i>NTC20</i>	-1.4	splicing factor
<i>SRB6</i>	-2.1	part of Srb/Mediator complex; transcription factor
<i>KRR1</i>	-0.9	Involved in cell division and spore germination
<i>HMLALPHA1</i>	-1.6	mating type regulatory protein, silenced copy at HML
<i>HMLALPHA2</i>	-2.7	mating type regulatory protein, silenced copy at HML
<i>SRD1</i>	-1.2	protein involved in the processing of pre-rRNA to mature rRNA
<i>PET18</i>	-2.2	protein required for respiratory growth and stability of the mitochondrial genome
<i>MATALPHA2</i>	-3.0	mating type regulatory protein, expressed copy at MAT locus
<i>MATALPHA1</i>	-1.5	mating type regulatory protein, expressed copy at MAT locus
<i>YCR087C-A</i>	-1.2	questionable protein
<i>HMRA1</i>	-2.0	mating type regulatory protein, silenced copy at HMR locus
<i>MSS2</i>	-1.1	cox2 pre-mRNA splicing factor
<i>CDC36</i>	-1.1	basal transcription inhibitor; transcriptional regulator
<i>NHP2</i>	-2.2	HMG-like protein
<i>NOP6</i>	-1.8	protein with similarity to hydrophilins, which are involved in the adaptive response to hyperosmotic conditions
<i>DTD1</i>	-1.2	D-Tyr-tRNA(Tyr) deacylase
<i>NRG1</i>	-1.6	binds to UAS-1 in the STA1 promoter and can interact with Ssn6; transcriptional repressor
<i>RPC11</i>	-1.4	TFIIS-like small Pol III subunit C11
<i>SNF11</i>	-1.4	SWI/SNF global transcription activator complex component
<i>TFB5</i>	-1.9	Component of general transcription and DNA repair factor TFIIF
<i>RRP8</i>	-1.1	nucleolar protein required for efficient processing of pre-rRNA at site A2; methyltransferase homolog
<i>RRP1</i>	-1.0	involved in processing rRNA precursor species to mature rRNAs
<i>CWC15</i>	-2.0	Protein involved in mRNA splicing
<i>TAF10</i>	-1.2	TFIID subunit
<i>HTA1</i>	-1.7	histone H2A (HTA1 and HTA2 code for nearly identical proteins)
<i>SRB7</i>	-1.2	RNA polymerase II holoenzyme/mediator subunit
<i>LSM6</i>	-1.2	snRNP protein
<i>NCB2</i>	-1.6	Negative Cofactor B2 is the beta subunit of a negative regulator of RNA polymerase II holoenzyme
<i>YDR412W</i>	-0.9	protein required for cell viability
<i>ADA2</i>	-1.4	general transcriptional adaptor or co-activator
<i>SMB1</i>	-1.1	associated with U1 snRNP as part of the Sm-core that is common to all spliceosomal snRNPs
<i>LSM4</i>	-1.0	U6 snRNA associated protein
<i>LSM5</i>	-2.0	snRNP protein
<i>BUR6</i>	-2.0	transcriptional regulator
<i>SMX2</i>	-1.3	snRNP G protein (human Sm-G homolog)
<i>LOC1</i>	-2.0	nuclear protein involved in asymmetric localization of ASH1 mRNA
<i>CGR1</i>	-2.3	coiled-coil protein
<i>RPB9</i>	-1.3	RNA polymerase II core subunit
<i>POP6</i>	-1.4	RNase P integral subunit; subunit of RNase MRP (putative)
<i>SPT4</i>	-3.1	transcription elongation protein
<i>SMD1</i>	-1.1	homolog of human core snRNP protein D1, involved in snRNA maturation
<i>PRP38</i>	-1.1	RNA splicing factor
<i>RRP46</i>	-1.2	3'->5' exoribonuclease
<i>SYF2</i>	-0.9	SYnthetic lethal with CDC40
<i>CPD1</i>	-1.9	2',3'-cyclic nucleotide 3'-phosphodiesterase
<i>YGR251W</i>	-1.2	protein required for cell viability

Gene name	Fold change	Gene Product
<i>PXR1</i>	-1.3	possible telomerase regulator or RNA-binding protein
<i>SNF6</i>	-0.9	chromatin remodeling Snf/Swi complex subunit
<i>BCD1</i>	-0.9	box C/D snoRNA accumulation
<i>SRB2</i>	-1.5	RNA polymerase II holoenzyme/mediator subunit
<i>NOP10</i>	-1.3	H/ACA-box snoRNPs component
<i>LRP1</i>	-1.6	like rRNA Processing protein involved in regulation of DNA repair and recombination
<i>YHR085W</i>	-1.2	protein of unknown function, essential for viability, may be involved in rRNA processing
<i>GAR1</i>	-1.4	small nucleolar RNP protein
<i>RPC10</i>	-1.6	RNA polymerase II subunit
<i>IMP3</i>	-0.9	U3 snoRNP protein
<i>IST3</i>	-2.1	U2 snRNP associated protein
<i>MSL1</i>	-1.2	U2 snRNP component
<i>YAP5</i>	-1.5	transcription factor
<i>RPC17</i>	-1.2	RNA polymerase III subunit C17
<i>TAD2</i>	-0.9	tRNA-specific adenosine deaminase subunit
<i>ASF1</i>	-1.1	anti-silencing protein that causes depression of silent loci when overexpressed
<i>RPB4</i>	-1.0	RNA polymerase II fourth largest subunit
<i>RPA34</i>	-1.5	RNA polymerase I subunit A34.5
<i>LSM8</i>	-2.1	snRNP protein
<i>RPA12</i>	-1.0	RNA polymerase I A12.2 subunit
<i>YJR141W</i>	-1.3	protein required for cell viability
<i>MRT4</i>	-1.3	mRNA turnover 4
<i>UTP11</i>	-1.0	U3 snoRNP protein
<i>YKR022C</i>	-1.3	protein required for cell viability
<i>YLR016C</i>	-1.3	questionable protein
<i>YLR022C</i>	-1.0	protein required for cell viability
<i>FYV7</i>	-2.3	protein involved in processing the 35S rRNA primary transcript to generate the 20S and 27SA2 pre-rRNA transcripts
<i>YLR145W</i>	-2.2	protein required for cell viability
<i>SMD3</i>	-1.1	core snRNP protein
<i>PUS5</i>	-1.8	RNA:pseudouridine (Psi)-synthase
<i>PDR8</i>	-1.1	zinc finger transcription factor
<i>SMD2</i>	-0.9	U1 snRNP protein of the Sm class
<i>YHC1</i>	-1.7	U1 snRNP protein required for pre-mRNA splicing
<i>TAD3</i>	-0.9	tRNA-specific adenosine deaminase subunit
<i>YLR405W</i>	-0.9	dihydrouridine synthase 4
<i>TSR2</i>	-1.3	twenty S rRNA accumulation
<i>LSM3</i>	-2.5	snRNP protein
<i>TRM9</i>	-0.9	mcm5U/mcm5s2U tRNA carboxyl methyltransferase
<i>MFT1</i>	-1.2	mitochondrial targeting protein
<i>TAF13</i>	-1.0	TFIID subunit
<i>YML107C</i>	-1.3	protein of unknown function; GFP-fusion protein localizes to the nuclear periphery
<i>DAT1</i>	-1.2	datin, oligo(dA)/oligo(dT)-binding protein
<i>SEN15</i>	-1.2	tetrameric tRNA splicing endonuclease 15kDa subunit
<i>CTL1</i>	-1.3	RNA triphosphatase
<i>TAF9</i>	-1.2	TFIID subunit
<i>SAP30</i>	-1.7	subunit of the histone deacetylase B complex
<i>RLP7</i>	-1.3	nucleolar protein related to ribosomal protein L7
<i>SPO1</i>	-0.9	similar to phospholipase B
<i>HHF2</i>	-2.3	histone H4
<i>HHT2</i>	-1.4	histone H3
<i>RPC19</i>	-1.2	RNA polymerases I (A) and III (C) subunit
<i>LSM7</i>	-1.6	snRNP protein

Gene name	Fold change	Gene Product
<i>RPB11</i>	-1.2	RNA polymerase II core subunit
<i>YOL101C</i>	-0.9	questionable protein
<i>INO4</i>	-1.7	basic helix-loop-helix (bHLH) protein
<i>HRT1</i>	-1.1	Skp1-Cullin-F-box ubiquitin protein ligase (SCF) subunit
<i>DCP1</i>	-0.9	mRNA decapping enzyme
<i>YOR004W</i>	-1.2	protein required for cell viability
<i>CIN5</i>	-1.1	transcriptional activator
<i>BUD21</i>	-1.5	U3 snoRNP protein
<i>SPP2</i>	-1.7	required for final stages of spliceosome maturation
<i>SME1</i>	-1.0	spliceosomal snRNA-associated Sm core protein required for mRNA splicing, also likely associated with telomerase TLC1 RNA
<i>RPB10</i>	-1.9	RNA polymerase II core subunit
<i>SAS5</i>	-1.0	involved in silencing at telomeres, HML and HMR
<i>RPB8</i>	-0.9	DNA-directed RNA polymerase I, II, III 16 KD subunit
<i>YOR287C</i>	-1.7	protein required for cell viability
<i>RRS1</i>	-1.2	regulator for ribosome synthesis
<i>MBF1</i>	-1.9	multiprotein bridging factor
<i>MET31</i>	-1.2	transcriptional regulator of sulfur amino acid metabolism
<i>YPL047W</i>	-1.4	questionable protein
<i>SPP1</i>	-0.9	compass (complex proteins associated with Set1p) component
<i>TIF6</i>	-1.0	translation initiation factor 6 (eIF6)
<i>BRR1</i>	-0.9	spliceosomal snRNP component
<i>DIB1</i>	-1.3	protein required for mitosis
<i>RDS3</i>	-2.0	protein required for cell viability
<i>SNT309</i>	-1.5	protein complex component associated with the splicing factor Prp19p
<i>YPR143W</i>	-1.3	protein required for cell viability
<i>RPO26</i>	-1.5	RNA polymerases I, II, and III subunit

Protein synthesis

<i>ECM1</i>	-1.7	putative transmembrane domain protein involved in cell wall biogenesis
<i>CBP6</i>	-1.2	translational activator of COB mRNA
<i>MRPL37</i>	-1.3	mitochondrial ribosomal protein of the large subunit
<i>MRPL27</i>	-1.7	mitochondrial ribosomal protein of the large subunit
<i>KRR1</i>	-0.9	Involved in cell division and spore germination
<i>MRPL32</i>	-1.7	ribosomal protein (YmL32)
<i>IMG2</i>	-1.1	mitochondrial ribosomal protein of the small subunit
<i>DTD1</i>	-1.2	D-Tyr-tRNA(Tyr) deacylase
<i>YDR115W</i>	-1.4	questionable protein
<i>YDR185C</i>	-1.1	questionable protein
<i>RPL27B</i>	-0.9	ribosomal protein L27B
<i>SLF1</i>	-1.1	La motif-containing proteins that modulate mRNA translation
<i>NOP16</i>	-1.4	ribosome biogenesis
<i>RSM18</i>	-1.1	mitochondrial ribosome small subunit component
<i>RPS24A</i>	-1.0	ribosomal protein S24A
<i>RPL23B</i>	-0.9	ribosomal protein L23B (L17aB) (YL32)
<i>RPL22B</i>	-1.6	ribosomal protein L22B (L1c) (rp4) (YL31)
<i>LOC1</i>	-2.0	nuclear protein involved in asymmetric localization of ASH1 mRNA
<i>RPL29</i>	-0.9	ribosomal protein L29 (YL43)
<i>CGR1</i>	-2.3	coiled-coil protein
<i>MRPL25</i>	-1.3	mitochondrial ribosomal protein of the large subunit
<i>YGR201C</i>	-1.0	questionable protein
<i>RSM27</i>	-2.0	mitochondrial ribosome small subunit component
<i>RPL27A</i>	-1.0	ribosomal protein L27A
<i>IMP3</i>	-0.9	U3 snoRNP protein
<i>PET130</i>	-1.1	protein required for respiratory growth
<i>MRPL49</i>	-0.9	mitochondrial ribosomal protein of the large subunit

Gene name	Fold change	Gene Product
<i>RPS21B</i>	-1.7	ribosomal protein S21B (S26B) (YS25)
<i>RPL39</i>	-1.3	ribosomal protein L39 (L46) (YL40)
<i>RPL43B</i>	-1.0	ribosomal protein L43B
<i>MRP17</i>	-1.5	ribosomal protein MRP17
<i>MRT4</i>	-1.3	mRna turnover 4
<i>MRPL31</i>	-1.0	mitochondrial ribosomal protein of the large subunit
<i>RPS27A</i>	-1.0	ribosomal protein S27A (rp61) (YS20)
<i>RPS21A</i>	-1.2	ribosomal protein S21A (S26A) (YS25)
<i>RPL37A</i>	-1.3	ribosomal protein L37A (L43) (YL35)
<i>YLR221C</i>	-0.9	riboSome Assembly
<i>RPS28B</i>	-1.0	ribosomal protein S28B (S33B) (YS27)
<i>RPS30A</i>	-1.1	ribosomal protein S30A
<i>MRPL15</i>	-1.4	mitochondrial ribosomal protein of the large subunit
<i>RPL38</i>	-1.0	ribosomal protein L38
<i>RPS29A</i>	-1.1	ribosomal protein S29A (S36A) (YS29)
<i>MRPL39</i>	-1.2	mitochondrial ribosomal protein of the large subunit
<i>TRM9</i>	-0.9	mcm5U/mcm5s2U tRNA carboxyl methyltransferase
<i>RPS18B</i>	-0.9	ribosomal protein S18B
<i>MRPS8</i>	-1.2	mitochondrial ribosomal protein of the small subunit
<i>MRPS17</i>	-0.9	mitochondrial ribosomal protein of the small subunit
<i>MRPL44</i>	-1.3	mitochondrial ribosomal protein of the large subunit
<i>TIF11</i>	-1.2	translation initiation factor eIF1A
<i>MRPL33</i>	-1.6	mitochondrial ribosomal protein of the large subunit
<i>RLP7</i>	-1.3	nucleolar protein related to ribosomal protein L7
<i>NOP15</i>	-1.4	ribosome biogenesis
<i>SUI1</i>	-1.7	translation initiation factor eIF1
<i>MRPL50</i>	-1.2	mitochondrial ribosomal protein of the large subunit, not essential for mitochondrial translation
<i>RSM19</i>	-1.0	mitochondrial ribosome small subunit component
<i>RPS28A</i>	-1.3	ribosomal protein S28A (S33A) (YS27)
<i>RPS30B</i>	-1.3	ribosomal protein S30B
<i>RPL33B</i>	-1.2	ribosomal protein L33B (L37B) (rp47) (YL37)
<i>RRS1</i>	-1.2	regulator for ribosome synthesis
<i>TIF6</i>	-1.0	translation initiation factor 6 (eIF6)
<i>MRPL51</i>	-1.1	mitochondrial ribosomal protein of the large subunit
<i>YPR143W</i>	-1.3	protein required for cell viability
<i>MRP2</i>	-0.9	mitochondrial ribosomal protein, small subunit
Protein fate		
<i>PEX22</i>	-1.6	product of gene unknown
<i>LDB7</i>	-0.9	protein involved in mannosylphosphorylation of cell wall mannoproteins
<i>PRE7</i>	-0.9	proteasome subunit
<i>KTI11</i>	-1.2	similar to Hemiascomycetous yeast protein
<i>RER2</i>	-0.9	cis-prenyltransferase
<i>MRS5</i>	-1.0	involved in mitochondrial biogenesis
<i>ATG14</i>	-1.5	required for autophagy
<i>YSY6</i>	-3.4	protein that participates in secretory pathway
<i>UBS1</i>	-1.0	general positive regulator of CDC34
<i>DER1</i>	-1.1	endoplasmic reticulum membrane protein, required for the protein degradation process associated with the ER, involved in the retrograde transport of misfolded or unassembled proteins
<i>ATG12</i>	-2.3	component of the autophagic system
<i>SHG1</i>	-1.5	compass (complex proteins associated with Set1p) component
<i>MAK31</i>	-1.8	member of the Sm protein family
<i>YCR060W</i>	-1.5	questionable protein
<i>APC11</i>	-1.2	anaphase promoting complex (APC) subunit
<i>PEX19</i>	-1.2	40 kDa farnesylated protein associated with peroxisomes

Gene name	Fold change	Gene Product
<i>COX9</i>	-2.0	cytochrome c oxidase subunit VIIa
<i>SRP14</i>	-1.4	signal recognition particle subunit
<i>MSS2</i>	-1.1	cox2 pre-mRNA splicing factor
<i>OST4</i>	-0.9	oligosaccharyltransferase subunit
<i>TFB5</i>	-1.9	Component of general transcription and DNA repair factor TFIIH
<i>SSS1</i>	-1.6	ER protein-translocase complex subunit
<i>RUB1</i>	-1.3	ubiquitin-like protein
<i>TAF10</i>	-1.2	TFIID subunit
<i>UBC1</i>	-1.2	ubiquitin-conjugating enzyme
<i>CSN9</i>	-2.7	COP9 signalosome (CSN) subunit
<i>YDR185C</i>	-1.1	questionable protein
<i>GPI11</i>	-1.3	protein involved in glycosylphosphatidylinositol (GPI) biosynthesis
<i>TIM11</i>	-1.7	mitochondrial F1F0-ATPase subunit e
<i>SEM1</i>	-2.6	Regulator of exocytosis and pseudohyphal differentiation
<i>ADA2</i>	-1.4	general transcriptional adaptor or co-activator
<i>YDR459C</i>	-1.2	likely functions in pathway(s) outside Ras
<i>FPR2</i>	-1.0	FKBP13 (FK506 binding protein) peptidyl-prolyl cis-trans isomerase (PPIase)
<i>QCR7</i>	-1.1	ubiquinol cytochrome C oxidoreductase subunit 7
<i>GIM4</i>	-2.0	bovine prefoldin subunit 2 homolog (putative)
<i>UBC8</i>	-1.0	ubiquitin-conjugating enzyme; ubiquitin-protein ligase
<i>TIM9</i>	-1.8	essential subunit of the TIM22-complex for mitochondrial protein import
<i>SBH2</i>	-1.5	Sbh1p homolog
<i>PET117</i>	-1.5	protein required for assembly of cytochrome c oxidase
<i>YPT1</i>	-0.9	GTP-binding protein; ras homolog
<i>YPI1</i>	-1.0	PP1 phosphatase inhibitor
<i>LYS5</i>	-1.0	alpha aminoacidate reductase phosphopantetheinyl transferase
<i>BRR6</i>	-1.5	nuclear envelope protein
<i>SMD1</i>	-1.1	homolog of human core snRNP protein D1, involved in snRNA maturation
<i>VMA21</i>	-1.7	protein involved in vacuolar H-ATPase assembly or function
<i>TRX2</i>	-1.0	thioredoxin
<i>PEX21</i>	-1.3	peroxin
<i>MRS11</i>	-1.4	subunit of the Tim22-complex
<i>VMA22</i>	-1.9	required for V-ATPase activity
<i>WSS1</i>	-1.6	weak suppressor of smt3
<i>SSP1</i>	-1.2	essential for meiosis and spore formation
<i>URM1</i>	-1.5	ubiquitin-like protein
<i>YRB2</i>	-0.9	nuclear protein that interacts with Gsp1p and Crm1p
<i>FMC1</i>	-1.2	assembly factor of ATP synthase in heat stress
<i>IST3</i>	-2.1	U2 snRNP associated protein
<i>MSL1</i>	-1.2	U2 snRNP component
<i>STS1</i>	-1.1	restores protein transport when overexpressed and rRNA stability to a sec23 mutation
<i>YJL104W</i>	-0.9	presequence translocase-associated motor, constituent of the mitochondrial import motor PAM
<i>PF1D1</i>	-1.3	bovine prefoldin subunit 1 homolog (putative)
<i>GON7</i>	-1.4	protein proposed to be involved in the transfer of mannosylphosphate groups onto N-linked oligosaccharides
<i>SPC1</i>	-2.5	homolog of the SPC12 subunit of mammalian signal peptidase complex
<i>APS2</i>	-1.0	clathrin associated protein complex small subunit
<i>YJR097W</i>	-1.5	protein that may function as a cochaperone
<i>TIM8</i>	-1.0	mitochondrial protein import machinery subunit
<i>VPS24</i>	-1.3	involved in secretion
<i>VPH2</i>	-1.0	25.2 kDa protein involved in assembly of vacuolar H(+) ATPase
<i>SRP21</i>	-1.7	signal recognition particle component
<i>DID2</i>	-1.2	class E vacuolar-protein sorting and endocytosis factor

Gene name	Fold change	Gene Product
<i>COX17</i>	-1.5	cysteine-rich protein
<i>ATG10</i>	-1.5	protein-conjugating enzyme
<i>COX12</i>	-1.1	cytochrome c oxidase subunit VIb
<i>TRX1</i>	-1.0	thioredoxin
<i>SRN2</i>	-1.1	suppressor of rna1-1 mutation
<i>APS1</i>	-1.0	clathrin associated protein complex small subunit
<i>YKE2</i>	-1.1	Gim complex component
<i>YLR243W</i>	-1.1	protein required for cell viability
<i>UBC12</i>	-1.7	ubiquitin-conjugating enzyme
<i>VPS71</i>	-0.9	component of the Swr1p complex that incorporates Htz1p into chromatin, required for vacuolar protein sorting
<i>MFT1</i>	-1.2	mitochondrial targeting protein
<i>COX14</i>	-1.2	mitochondrial membrane protein
<i>IMP2</i>	-1.0	protease
<i>TAF9</i>	-1.2	TFIID subunit
<i>COX7</i>	-2.2	cytochrome c oxidase subunit VII
<i>SAP30</i>	-1.7	subunit of the histone deacetylase B complex
<i>GOT1</i>	-1.2	membrane protein
<i>GPI15</i>	-1.6	human Pig-H homolog
<i>TOM7</i>	-0.9	translocase of the outer mitochondrial membrane
<i>YPT53</i>	-1.0	GTP-binding protein; rab family
<i>GIM3</i>	-1.4	bovine prefoldin subunit 4 homolog (putative)
<i>ATX1</i>	-1.4	copper binding homeostasis protein (putative)
<i>HUB1</i>	-1.5	ubiquitin-like modifier
<i>HRT1</i>	-1.1	Skp1-Cullin-F-box ubiquitin protein ligase (SCF) subunit
<i>YSP3</i>	-1.0	subtilisin-like protease III
<i>HSP10</i>	-1.6	heat shock protein 10
<i>PEP12</i>	-1.0	syntaxin (T-SNARE), vacuolar
<i>TOM6</i>	-2.1	mitochondrial outer membrane import receptor subunit, 6 kD
<i>YNG1</i>	-1.0	histone acetyltransferase complex component
<i>ARF3</i>	-1.1	GTP-binding ADP-ribosylation factor
<i>OST2</i>	-1.4	oligosaccharyltransferase epsilon subunit
<i>SAS5</i>	-1.0	involved in silencing at telomeres, HML and HMR
<i>MGE1</i>	-0.9	GrpE homolog
<i>NAT5</i>	-2.4	N-acetyltransferase
<i>ARL3</i>	-0.9	ADP-ribosylation factor-like protein, member of the arf-sar family in the ras superfamily
<i>VPS28</i>	-1.0	protein involved in vacuolar traffic
<i>SPP1</i>	-0.9	compass (complex proteins associated with Set1p) component
<i>PPT2</i>	-2.1	phosphopantetheine:protein transferase (PPTase)
<i>ATG5</i>	-1.6	Involved in autophagy
<i>TFP3</i>	-1.1	vacuolar ATPase V0 domain subunit c' (17 kDa) vacuolar H(+) ATPase 17 kDa subunit C
<i>MAK3</i>	-1.1	N-acetyltransferase
<i>BRR1</i>	-0.9	spliceosomal snRNP component

Regulation of metabolism and protein function

<i>NRG2</i>	-1.6	NRG1 homolog
<i>POL30</i>	-1.1	proliferating Cell Nuclear Antigen (PCNA)
<i>HMLALPHA1</i>	-1.6	mating type regulatory protein, silenced copy at HML
<i>HMLALPHA2</i>	-2.7	mating type regulatory protein, silenced copy at HML
<i>MATALPHA2</i>	-3.0	mating type regulatory protein, expressed copy at MAT locus
<i>MATALPHA1</i>	-1.5	mating type regulatory protein, expressed copy at MAT locus
<i>HMRA1</i>	-2.0	mating type regulatory protein, silenced copy at HMR locus
<i>INH1</i>	-1.4	ATPase inhibitor
<i>NCB2</i>	-1.6	Negative Cofactor B2 is the beta subunit of a negative regulator of RNA polymerase II holoenzyme

Gene name	Fold change	Gene Product
<i>ADA2</i>	-1.4	general transcriptional adaptor or co-activator
<i>BUR6</i>	-2.0	transcriptional regulator
<i>YPI1</i>	-1.0	PP1 phosphatase inhibitor
<i>PEX21</i>	-1.3	peroxin
<i>YNG2</i>	-1.2	NuA4 histone acetyltransferase complex component
<i>SPL2</i>	-1.7	suppressor of <i>plc1-delta</i>
<i>KTI12</i>	-1.1	elongator associated protein
<i>BUB2</i>	-0.9	protein required for cell cycle arrest in response to loss of microtubule function
<i>MBF1</i>	-1.9	multiprotein bridging factor
<i>ERI1</i>	-1.2	ER-associated Ras Inhibitor

Cellular transport, transport facilities and transport routes

<i>PEX22</i>	-1.6	product of gene unknown
<i>YBR043C</i>	-1.0	protein of unknown function, may have a role in drug resistance
<i>MRS5</i>	-1.0	involved in mitochondrial biogenesis
<i>YMC2</i>	-1.0	mitochondrial carrier protein
<i>YSY6</i>	-3.4	protein that participates in secretory pathway
<i>UBS1</i>	-1.0	general positive regulator of <i>CDC34</i>
<i>ATG12</i>	-2.3	component of the autophagic system
<i>TRS20</i>	-1.9	trapp subunit of 20 kDa
<i>YPT10</i>	-1.0	similar to Rab proteins and other small GTP-binding proteins
<i>CTP1</i>	-1.2	citrate transporter
<i>GRX1</i>	-1.1	glutaredoxin
<i>TRX3</i>	-0.9	thioredoxin
<i>PEX19</i>	-1.2	40 kDa farnesylated protein associated with peroxisomes
<i>COX9</i>	-2.0	cytochrome c oxidase subunit VIIa
<i>SRP14</i>	-1.4	signal recognition particle subunit
<i>MSS2</i>	-1.1	<i>cox2</i> pre-mRNA splicing factor
<i>INH1</i>	-1.4	ATPase inhibitor
<i>SSS1</i>	-1.6	ER protein-translocase complex subunit
<i>UBC1</i>	-1.2	ubiquitin-conjugating enzyme
<i>TIM11</i>	-1.7	mitochondrial F1F0-ATPase subunit e
<i>SEM1</i>	-2.6	Regulator of exocytosis and pseudohyphal differentiation
<i>DYN2</i>	-2.1	dynein light chain (putative)
<i>TIM9</i>	-1.8	essential subunit of the TIM22-complex for mitochondrial protein import
<i>SBH2</i>	-1.5	Sbh1p homolog
<i>YPT1</i>	-0.9	GTP-binding protein; ras homolog
<i>LOC1</i>	-2.0	nuclear protein involved in asymmetric localization of <i>ASH1</i> mRNA
<i>ERV14</i>	-0.9	14 kDa protein found on ER-derived vesicles
<i>BRR6</i>	-1.5	nuclear envelope protein
<i>VMA7</i>	-1.2	vacuolar ATPase V1 domain subunit F (14 kDa)
<i>LST7</i>	-1.1	required for amino acid permease transport from the Golgi to the cell surface
<i>YGR131W</i>	-1.7	questionable protein
<i>TRX2</i>	-1.0	thioredoxin
<i>PEX21</i>	-1.3	peroxin
<i>MRS11</i>	-1.4	subunit of the Tim22-complex
<i>VMA10</i>	-1.2	vacuolar ATPase V1 domain subunit G (13 kDa)
<i>BET1</i>	-1.6	membrane protein required for vesicular transport between the endoplasmic reticulum and Golgi complex
<i>YIL040W</i>	-1.0	protein of unknown function, localizes to the endoplasmic reticulum
<i>YRB2</i>	-0.9	nuclear protein that interacts with Gsp1p and Crm1p
<i>QDR1</i>	-0.9	multidrug resistance transporter
<i>FLX1</i>	-0.9	FAD carrier protein
<i>STS1</i>	-1.1	restores protein transport when overexpressed and rRNA stability to a <i>sec23</i> mutation

Gene name	Fold change	Gene Product
<i>SYS1</i>	-1.0	multicopy suppressor of ypt6 null mutation
<i>YJL104W</i>	-0.9	presequence translocase-associated motor, constituent of the mitochondrial import motor PAM
<i>NCE101</i>	-1.4	involved in secretion of proteins that lack classical secretory signal sequences
<i>CYC1</i>	-0.9	iso-1-cytochrome c
<i>APS2</i>	-1.0	clathrin associated protein complex small subunit
<i>TIM8</i>	-1.0	mitochondrial protein import machinery subunit
<i>SFT1</i>	-1.5	v-SNARE
<i>VPS24</i>	-1.3	involved in secretion
<i>SRP21</i>	-1.7	signal recognition particle component
<i>MTR2</i>	-1.8	mRNA transport regulator
<i>DID2</i>	-1.2	class E vacuolar-protein sorting and endocytosis factor
<i>BET3</i>	-0.9	transport protein particle (TRAPP) component
<i>COX17</i>	-1.5	cysteine-rich protein
<i>ATG10</i>	-1.5	protein-conjugating enzyme
<i>YLR004C</i>	-1.0	questionable protein
<i>YLR016C</i>	-1.3	questionable protein
<i>COX12</i>	-1.1	cytochrome c oxidase subunit VIb
<i>TRX1</i>	-1.0	thioredoxin
<i>SRN2</i>	-1.1	suppressor of rna1-1 mutation
<i>ZRT2</i>	-0.9	low affinity zinc transport protein
<i>APS1</i>	-1.0	clathrin associated protein complex small subunit
<i>ARV1</i>	-1.0	protein involved in sterol distribution
<i>COX8</i>	-1.0	cytochrome c oxidase chain VIII
<i>ERV25</i>	-1.0	vesicle coat component
<i>VPS71</i>	-0.9	component of the Swr1p complex that incorporates Htz1p into chromatin, required for vacuolar protein sorting
<i>MFT1</i>	-1.2	mitochondrial targeting protein
<i>ATP18</i>	-1.7	ATP synthase associated protein
<i>YML107C</i>	-1.3	protein of unknown function; GFP-fusion protein localizes to the nuclear periphery
<i>VPS20</i>	-0.9	vacuolar protein sorting (putative)
<i>GFD1</i>	-1.2	protein of the nuclear pore complex
<i>COX7</i>	-2.2	cytochrome c oxidase subunit VII
<i>GOT1</i>	-1.2	membrane protein
<i>JNM1</i>	-1.1	coiled-coil domain protein required for proper nuclear migration during mitosis
<i>YMR299C</i>	-1.3	protein of unknown function; GFP-fusion protein localizes to the cytoplasm
<i>NCE103</i>	-1.4	carbonic anhydrase-like protein
<i>TOM7</i>	-0.9	translocase of the outer mitochondrial membrane
<i>YPT53</i>	-1.0	GTP-binding protein; rab family
<i>CYB5</i>	-1.1	cytochrome b5
<i>ATX1</i>	-1.4	copper binding homeostasis protein (putative)
<i>ATP19</i>	-1.2	ATP synthase subunit k homolog
<i>PEP12</i>	-1.0	syntaxin (T-SNARE), vacuolar
<i>TOM6</i>	-2.1	mitochondrial outer membrane import receptor subunit, 6 kD
<i>ARF3</i>	-1.1	GTP-binding ADP-ribosylation factor
<i>ORT1</i>	-1.0	Mitochondrial ornithine carrier - member of the mitochondrial carrier family
<i>MGE1</i>	-0.9	GrpE homolog
<i>RET3</i>	-0.9	vesicle coat component
<i>ARL3</i>	-0.9	ADP-ribosylation factor-like protein, member of the arf-sar family in the ras superfamily
<i>VPS28</i>	-1.0	protein involved in vacuolar traffic
<i>PPT2</i>	-2.1	phosphopantetheine:protein transferase (PPTase)
<i>ATG5</i>	-1.6	Involved in autophagy
<i>OYE3</i>	-1.8	NADPH dehydrogenase

Gene name	Fold change	Gene Product
<i>TFP3</i>	-1.1	vacuolar ATPase V0 domain subunit c' (17 kDa) vacuolar H(+) ATPase 17 kDa subunit C
<i>ATP15</i>	-1.3	ATP synthase epsilon subunit
<i>ATP20</i>	-1.5	ATP synthase subunit g homolog
Cellular communication /Signal transduction mechanism		
<i>MFA1</i>	-2.0	a-factor mating pheromone precursor
<i>STE18</i>	-1.6	G protein gamma subunit; coupled to mating factor receptor
<i>MFA2</i>	-1.7	a-factor mating pheromone precursor
<i>ZEO1</i>	-2.1	Mid2p-interacting protein, modulates the PKC1-MPK1 cell integrity pathway
<i>ERI1</i>	-1.2	ER-associated Ras Inhibitor
Cell rescue, defense and virulence		
<i>YBR043C</i>	-1.0	protein of unknown function, may have a role in drug resistance
<i>GPX2</i>	-1.4	phospholipid hydroperoxide glutathione peroxidase
<i>GRX1</i>	-1.1	glutaredoxin
<i>YCR060W</i>	-1.5	questionable protein
<i>TRX3</i>	-0.9	thioredoxin
<i>NOP6</i>	-1.8	protein with similarity to hydrophilins, which are involved in the adaptive response to hyperosmotic conditions
<i>RAD57</i>	-1.2	RecA homolog; interacts with Rad 55p
<i>NRG1</i>	-1.6	binds to UAS-1 in the STA1 promoter and can interact with Ssn6; transcriptional repressor
<i>PET100</i>	-1.5	cytochrome c oxidase-specific assembly factor
<i>CTA1</i>	-1.8	catalase A
<i>TSA2</i>	-1.0	thioredoxin-peroxidase
<i>FPR2</i>	-1.0	FKBP13 (FK506 binding protein) peptidyl-prolyl cis-trans isomerase (PPIase)
<i>TIM9</i>	-1.8	essential subunit of the TIM22-complex for mitochondrial protein import
<i>YER187W</i>	-2.1	questionable protein
<i>SNO3</i>	-0.9	protein is related with B(1) biosynthesis during the exponential phase
<i>TRX2</i>	-1.0	thioredoxin
<i>MRS11</i>	-1.4	subunit of the Tim22-complex
<i>DOG2</i>	-0.9	2-deoxyglucose-6-phosphate phosphatase
<i>CUP1-1</i>	-2.0	copper binding metallothionein
<i>CUP1-2</i>	-2.1	copper binding metallothionein
<i>VMA22</i>	-1.9	required for V-ATPase activity
<i>LRP1</i>	-1.6	like rRNA Processing protein involved in regulation of DNA repair and recombination
<i>SPL2</i>	-1.7	suppressor of plc-1-delta
<i>EST3</i>	-1.8	Subunit of the telomerase
<i>QDR1</i>	-0.9	multidrug resistance transporter
<i>ASF1</i>	-1.1	anti-silencing protein that causes depression of silent loci when overexpressed
<i>RPB4</i>	-1.0	RNA polymerase II fourth largest subunit
<i>PFD1</i>	-1.3	bovine prefoldin subunit 1 homolog (putative)
<i>GON7</i>	-1.4	protein proposed to be involved in the transfer of mannosylphosphate groups onto N-linked oligosaccharides
<i>KTI12</i>	-1.1	elongator associated protein
<i>YKR049C</i>	-1.0	protein localized to the mitochondria
<i>RPS21A</i>	-1.2	ribosomal protein S21A (S26A) (YS25)
<i>TRX1</i>	-1.0	thioredoxin
<i>ASP3-1</i>	-1.2	nitrogen catabolite-regulated cell-wall L-asparaginase II
<i>ASP3-2</i>	-1.0	nitrogen catabolite-regulated cell-wall L-asparaginase II
<i>ASP3-3</i>	-1.0	nitrogen catabolite-regulated cell-wall L-asparaginase II
<i>ASP3-4</i>	-1.2	nitrogen catabolite-regulated cell-wall L-asparaginase II

Gene name	Fold change	Gene Product
<i>PDR8</i>	-1.1	zinc finger transcription factor
<i>TRM9</i>	-0.9	mcm5U/mcm5s2U tRNA carboxyl methyltransferase
<i>HUG1</i>	-1.3	protein involved in the Mec1p-mediated checkpoint pathway that responds to DNA damage or replication arrest
<i>SIP18</i>	-1.1	salt-Induced Protein
<i>HOR7</i>	-1.2	hyperosmolarity-responsive gene
<i>ATX1</i>	-1.4	copper binding homeostasis protein (putative)
<i>ZEO1</i>	-2.1	Mid2p-interacting protein, modulates the PKC1-MPK1 cell integrity pathway
<i>HSP10</i>	-1.6	heat shock protein 10
<i>CIN5</i>	-1.1	transcriptional activator
<i>MGE1</i>	-0.9	GrpE homolog
<i>RFM1</i>	-1.0	DNA-binding protein
<i>ARR2</i>	-1.9	arsenate reductase

Interaction with the environment

<i>YBL028C</i>	-2.1	questionable protein
<i>SRB6</i>	-2.1	part of Srb/Mediator complex; transcription factor
<i>HMLALPHA1</i>	-1.6	mating type regulatory protein, silenced copy at HML
<i>HMLALPHA2</i>	-2.7	mating type regulatory protein, silenced copy at HML
<i>MATALPHA2</i>	-3.0	mating type regulatory protein, expressed copy at MAT locus
<i>MATALPHA1</i>	-1.5	mating type regulatory protein, expressed copy at MAT locus
<i>HMRA2</i>	-3.0	mating type regulatory protein, silenced copy at HMR locus
<i>HMRA1</i>	-2.0	mating type regulatory protein, silenced copy at HMR locus
<i>CDC36</i>	-1.1	basal transcription inhibitor; transcriptional regulator
<i>RAD57</i>	-1.2	RecA homolog; interacts with Rad 55p
<i>NRG1</i>	-1.6	binds to UAS-1 in the STA1 promoter and can interact with Ssn6; transcriptional repressor
<i>SNF11</i>	-1.4	SWI/SNF global transcription activator complex component
<i>CSN9</i>	-2.7	COP9 signalosome (CSN) subunit
<i>MFA1</i>	-2.0	a-factor mating pheromone precursor
<i>SLF1</i>	-1.1	La motif-containing proteins that modulate mRNA translation
<i>FAR7</i>	-1.0	protein involved in G1 cell cycle arrest in response to pheromone, in a pathway different from the Far1p-dependent pathway
<i>AGA2</i>	-1.4	a-agglutinin adhesion subunit
<i>VMA7</i>	-1.2	vacuolar ATPase V1 domain subunit F (14 kDa)
<i>SNF6</i>	-0.9	chromatin remodeling Snf/Swi complex subunit
<i>VMA10</i>	-1.2	vacuolar ATPase V1 domain subunit G (13 kDa)
<i>VMA22</i>	-1.9	required for V-ATPase activity
<i>SPL2</i>	-1.7	suppressor of plc1-delta
<i>STE18</i>	-1.6	G protein gamma subunit; coupled to mating factor receptor
<i>VPH2</i>	-1.0	25.2 kDa protein involved in assembly of vacuolar H(+) ATPase
<i>COX17</i>	-1.5	cysteine-rich protein
<i>ZRT2</i>	-0.9	low affinity zinc transport protein
<i>KAR5</i>	-1.1	coiled-coil membrane protein
<i>SAP30</i>	-1.7	subunit of the histone deacetylase B complex
<i>MFA2</i>	-1.7	a-factor mating pheromone precursor
<i>KAR1</i>	-1.0	involved in spindle pole body duplication and karyogamy
<i>ATX1</i>	-1.4	copper binding homeostasis protein (putative)
<i>HUB1</i>	-1.5	ubiquitin-like modifier
<i>YOL101C</i>	-0.9	questionable protein
<i>CIN5</i>	-1.1	transcriptional activator
<i>ISU1</i>	-1.1	iron-sulfur cluster nifU-like protein
<i>TFP3</i>	-1.1	vacuolar ATPase V0 domain subunit c' (17 kDa) vacuolar H(+) ATPase 17 kDa subunit C
<i>ATP15</i>	-1.3	ATP synthase epsilon subunit
<i>RDS3</i>	-2.0	protein required for cell viability

Gene name	Fold change	Gene Product
Transposable elements, viral and plasmid proteins		
<i>MAK31</i>	-1.8	member of the Sm protein family
<i>RTT102</i>	-0.9	regulator of Ty1 Transposition
Cell fate		
<i>NHP6B</i>	-1.2	11 kDa nonhistone chromosomal protein
<i>SPR6</i>	-1.3	sporulation-specific protein
<i>ASF1</i>	-1.1	anti-silencing protein that causes depression of silent loci when overexpressed
<i>YKL082C</i>	-0.9	required for normal pre-rRNA Processing
<i>KTI12</i>	-1.1	elongator associated protein
<i>DAD2</i>	-1.3	outer kinetochore protein - part of Dam1 complex
<i>BUB2</i>	-0.9	protein required for cell cycle arrest in response to loss of microtubule function
<i>SAP30</i>	-1.7	subunit of the histone deacetylase B complex
<i>YMR269W</i>	-2.2	protein possibly involved in protein synthesis
<i>HUB1</i>	-1.5	ubiquitin-like modifier
Development (Systemic)		
<i>HMLALPHA1</i>	-1.6	mating type regulatory protein, silenced copy at HML
<i>HMLALPHA2</i>	-2.7	mating type regulatory protein, silenced copy at HML
<i>MATALPHA2</i>	-3.0	mating type regulatory protein, expressed copy at MAT locus
<i>MATALPHA1</i>	-1.5	mating type regulatory protein, expressed copy at MAT locus
<i>HMRA1</i>	-2.0	mating type regulatory protein, silenced copy at HMR locus
<i>AGA2</i>	-1.4	a-agglutinin adhesion subunit
<i>KAR5</i>	-1.1	coiled-coil membrane protein
<i>KAR1</i>	-1.0	involved in spindle pole body duplication and karyogamy
<i>HUB1</i>	-1.5	ubiquitin-like modifier
Biogenesis of cellular components		
<i>ACS1</i>	-1.5	acetyl CoA synthetase
<i>ECM1</i>	-1.7	putative transmembrane domain protein involved in cell wall biogenesis
<i>LDB7</i>	-0.9	protein involved in mannosylphosphorylation of cell wall mannoproteins
<i>RER2</i>	-0.9	cis-prenyltransferase
<i>MRS5</i>	-1.0	involved in mitochondrial biogenesis
<i>ATG12</i>	-2.3	component of the autophagic system
<i>SHG1</i>	-1.5	compass (complex proteins associated with Set1p) component
<i>YPT10</i>	-1.0	similar to Rab proteins and other small GTP-binding proteins
<i>MRPL37</i>	-1.3	mitochondrial ribosomal protein of the large subunit
<i>MRPL27</i>	-1.7	mitochondrial ribosomal protein of the large subunit
<i>CTP1</i>	-1.2	citrate transporter
<i>MRPL32</i>	-1.7	ribosomal protein (YmL32)
<i>PET18</i>	-2.2	protein required for respiratory growth and stability of the mitochondrial genome
<i>IMG2</i>	-1.1	mitochondrial ribosomal protein of the small subunit
<i>PEX19</i>	-1.2	40 kDa farnesylated protein associated with peroxisomes
<i>RAD57</i>	-1.2	RecA homolog; interacts with Rad 55p
<i>DAD1</i>	-1.7	Duo1 and Dam1 interacting; localized to intranuclear spindles and spindle pole bodies
<i>STN1</i>	-1.2	involved in telomere length regulation
<i>YDR115W</i>	-1.4	questionable protein
<i>TAF10</i>	-1.2	TFIID subunit
<i>SPC19</i>	-1.2	spindle pole component
<i>DYN2</i>	-2.1	dynein light chain (putative)
<i>ADA2</i>	-1.4	general transcriptional adaptor or co-activator
<i>GIM4</i>	-2.0	bovine prefoldin subunit 2 homolog (putative)

Gene name	Fold change	Gene Product
<i>TIM9</i>	-1.8	essential subunit of the TIM22-complex for mitochondrial protein import
<i>BIM1</i>	-2.0	binding to microtubules
<i>RSM18</i>	-1.1	mitochondrial ribosome small subunit component
<i>SPR6</i>	-1.3	sporulation-specific protein
<i>MDM39</i>	-1.2	spore wall formation. Mitochondrial distribution and morphology
<i>CGR1</i>	-2.3	coiled-coil protein
<i>BRR6</i>	-1.5	nuclear envelope protein
<i>MRPL25</i>	-1.3	mitochondrial ribosomal protein of the large subunit
<i>TRX2</i>	-1.0	thioredoxin
<i>RSM27</i>	-2.0	mitochondrial ribosome small subunit component
<i>PEX21</i>	-1.3	peroxin
<i>MRS11</i>	-1.4	subunit of the Tim22-complex
<i>EST3</i>	-1.8	Subunit of the telomerase
<i>YRB2</i>	-0.9	nuclear protein that interacts with Gsp1p and Crm1p
<i>SYS1</i>	-1.0	multicopy suppressor of ypt6 null mutation
<i>MRPL49</i>	-0.9	mitochondrial ribosomal protein of the large subunit
<i>YJL104W</i>	-0.9	presequence translocase-associated motor, constituent of the mitochondrial import motor PAM
<i>RPA34</i>	-1.5	RNA polymerase I subunit A34.5
<i>PFD1</i>	-1.3	bovine prefoldin subunit 1 homolog (putative)
<i>GON7</i>	-1.4	protein proposed to be involved in the transfer of mannosylphosphate groups onto N-linked oligosaccharides
<i>ABM1</i>	-2.0	protein of unknown function, required for normal microtubule organization
<i>MRP17</i>	-1.5	ribosomal protein MRP17
<i>YKL082C</i>	-0.9	required for normal pre-rRNA Processing
<i>MRPL31</i>	-1.0	mitochondrial ribosomal protein of the large subunit
<i>DAD2</i>	-1.3	outer kinetochore protein - part of Dam1 complex
<i>TEN1</i>	-2.3	protein involved in Telomeric pathways in association with Stn1
<i>TRX1</i>	-1.0	thioredoxin
<i>YKE2</i>	-1.1	Gim complex component
<i>MRPL15</i>	-1.4	mitochondrial ribosomal protein of the large subunit
<i>MRPL39</i>	-1.2	mitochondrial ribosomal protein of the large subunit
<i>BUB2</i>	-0.9	protein required for cell cycle arrest in response to loss of microtubule function
<i>KAR5</i>	-1.1	coiled-coil membrane protein
<i>ABF2</i>	-1.0	HMG-1 homolog
<i>CIN4</i>	-1.0	GTP-binding protein
<i>MRPS8</i>	-1.2	mitochondrial ribosomal protein of the small subunit
<i>MRPS17</i>	-0.9	mitochondrial ribosomal protein of the small subunit
<i>MRPL44</i>	-1.3	mitochondrial ribosomal protein of the large subunit
<i>TAF9</i>	-1.2	TFIID subunit
<i>MRPL33</i>	-1.6	mitochondrial ribosomal protein of the large subunit
<i>JNM1</i>	-1.1	coiled-coil domain protein required for proper nuclear migration during mitosis
<i>YMR299C</i>	-1.3	protein of unknown function; GFP-fusion protein localizes to the cytoplasm
<i>GIM3</i>	-1.4	bovine prefoldin subunit 4 homolog (putative)
<i>KAR1</i>	-1.0	involved in spindle pole body duplication and karyogamy
<i>YNL213C</i>	-1.2	questionable protein
<i>MRPL50</i>	-1.2	mitochondrial ribosomal protein of the large subunit, not essential for mitochondrial translation
<i>RSM19</i>	-1.0	mitochondrial ribosome small subunit component
<i>MDM12</i>	-1.2	mitochondrial outer membrane protein
<i>ZEO1</i>	-2.1	Mid2p-interacting protein, modulates the PKC1-MPK1 cell integrity pathway
<i>HSP10</i>	-1.6	heat shock protein 10
<i>YNG1</i>	-1.0	histone acetyltransferase complex component
<i>SPC29</i>	-1.3	spindle pole body component

Gene name	Fold change	Gene Product
<i>SPP1</i>	-0.9	compass (complex proteins associated with Set1p) component
<i>ATG5</i>	-1.6	Involved in autophagy
<i>YPL250C</i>	-1.3	Protein that interacts with the cytoskeleton and is involved in chromatin organization and nuclear transport
<i>MRPL51</i>	-1.1	mitochondrial ribosomal protein of the large subunit
<i>MRP2</i>	-0.9	mitochondrial ribosomal protein, small subunit
Cell type differentiation		
<i>NRG2</i>	-1.6	NRG1 homolog
<i>NHP6B</i>	-1.2	11 kDa nonhistone chromosomal protein
<i>SRB6</i>	-2.1	part of Srb/Mediator complex; transcription factor
<i>BUD23</i>	-1.0	protein involved in bud-site selection
<i>NRG1</i>	-1.6	binds to UAS-1 in the STA1 promoter and can interact with Ssn6; transcriptional repressor
<i>UBC1</i>	-1.2	ubiquitin-conjugating enzyme
<i>SEM1</i>	-2.6	Regulator of exocytosis and pseudohyphal differentiation
<i>EMI1</i>	-1.5	early meiotic induction
<i>SPO73</i>	-1.4	meiosis-specific protein of unknown function, required for spore wall formation during sporulation
<i>SPR6</i>	-1.3	sporulation-specific protein
<i>ISC10</i>	-1.7	meiosis-specific protein required for spore formation
<i>ERV14</i>	-0.9	14 kDa protein found on ER-derived vesicles
<i>SPO12</i>	-1.5	sporulation protein
<i>SPO16</i>	-1.0	sporulation protein
<i>SSP1</i>	-1.2	essential for meiosis and spore formation
<i>YKL082C</i>	-0.9	required for normal pre-rRNA Processing
<i>DAD2</i>	-1.3	outer kinetochore protein - part of Dam1 complex
<i>BUD20</i>	-1.8	protein involved in bud-site selection
<i>ADY4</i>	-0.9	component of the meiotic outer plaque
<i>BUB2</i>	-0.9	protein required for cell cycle arrest in response to loss of microtubule function
<i>SAP30</i>	-1.7	subunit of the histone deacetylase B complex
<i>SPO1</i>	-0.9	similar to phospholipase B
<i>SPR1</i>	-1.1	exo-1,3-beta-glucanase, sporulation-specific
<i>YOR304C-A</i>	-1.1	protein of unknown function; GFP-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck
<i>SPS4</i>	-1.6	sporulation-specific protein
Unclassified proteins		
<i>YAL037W</i>	-1.3	questionable protein
<i>YAL044W-A</i>	-1.0	similar to pombe uvi31, putative DNA repair protein
<i>YAR023C</i>	-1.3	putative integral membrane protein, member of DUP240 gene family
<i>YAR069C</i>	-1.0	questionable protein
<i>YBL029C-A</i>	-1.4	protein of unknown function; GFP-fusion protein localizes to the cell periphery
<i>MOH1</i>	-0.9	questionable protein
<i>YBL059W</i>	-1.1	questionable protein
<i>YBL107C</i>	-1.4	questionable protein
<i>YBL108C-A</i>	-1.1	questionable protein
<i>YBR062C</i>	-1.2	questionable protein
<i>YBR262C</i>	-2.1	protein localized to the mitochondria
<i>YCL056C</i>	-1.7	protein of unknown function; GFP-fusion protein localizes to the cytoplasm
<i>YCR007C</i>	-1.4	putative integral membrane protein, member of DUP240 gene family
<i>YCR016W</i>	-1.0	questionable protein
<i>YCR022C</i>	-1.1	questionable protein
<i>YCR097W-A</i>	-1.6	questionable protein
<i>YCR102C</i>	-1.2	questionable protein

Gene name	Fold change	Gene Product
<i>YDL099W</i>	-1.1	protein of unknown function; GFP-fusion protein localizes to the cytoplasm
<i>YDL114W-A</i>	-1.7	questionable protein
<i>YDL121C</i>	-1.2	questionable protein
<i>YDL133W</i>	-1.3	questionable protein
<i>YDL156W</i>	-1.1	questionable protein
<i>YDL157C</i>	-1.1	questionable protein
<i>YDL159W-A</i>	-1.1	questionable protein
<i>YDL177C</i>	-1.6	questionable protein
<i>YDL240C-A</i>	-1.4	questionable protein
<i>YDL247W-A</i>	-1.7	questionable protein
<i>DOS2</i>	-1.1	protein of unknown function, GFP-fusion protein localizes to the cytoplasm
<i>SHU2</i>	-1.7	suppressor of hydroxy-urea sensitivity
<i>YDR210W</i>	-1.4	protein of unknown function; GFP-fusion protein localizes to the cell periphery
<i>BSC2</i>	-1.3	transcript encoded by this ORF shows a high level of stop codon bypass
<i>PHM6</i>	-2.2	protein of unknown function, expression is regulated by phosphate levels
<i>YDR336W</i>	-1.0	questionable protein
<i>YDR339C</i>	-1.2	protein required for cell viability
<i>YDR357C</i>	-1.2	protein of unknown function; GFP-fusion protein localizes to the cytoplasm
<i>BCP1</i>	-0.9	questionable protein
<i>YDR379C-A</i>	-1.2	questionable protein
<i>YDR381C-A</i>	-2.1	questionable protein
<i>NKP1</i>	-1.3	non-essential kinetochore protein
<i>CWC21</i>	-1.2	component of a complex containing Cef1p, putatively involved in pre-mRNA splicing
<i>YDR532C</i>	-1.5	questionable protein
<i>YEL018W</i>	-1.2	stable stoichiometric subunit of the NuA4 complex
<i>YEL028W</i>	-1.3	questionable protein
<i>IES6</i>	-1.7	protein that associates with the INO80 chromatin remodeling complex under low-salt conditions
<i>YEL048C</i>	-2.1	questionable protein
<i>RMD6</i>	-1.9	required for meiotic nuclear division
<i>YEL073C</i>	-0.9	questionable protein
<i>YER030W</i>	-1.5	questionable protein
<i>YER039C-A</i>	-1.1	questionable protein
<i>YER071C</i>	-0.9	protein of unknown function; GFP-fusion protein localizes to the cytoplasm
<i>IES5</i>	-1.1	protein that associates with the INO80 chromatin remodeling complex under low-salt conditions
<i>YER093C-A</i>	-1.3	questionable protein
<i>YER121W</i>	-1.7	questionable protein
<i>YER137C</i>	-1.7	questionable protein
<i>YER182W</i>	-1.2	protein localized to the mitochondria
<i>YFR026C</i>	-1.6	questionable protein
<i>YFR043C</i>	-1.1	questionable protein
<i>YGL050W</i>	-1.1	questionable protein
<i>YGL080W</i>	-0.9	protein localized to the mitochondria
<i>YGL108C</i>	-1.3	protein of unknown function; GFP-fusion protein localizes to the cell periphery
<i>YGL220W</i>	-1.4	questionable protein
<i>YGR021W</i>	-1.1	questionable protein
<i>YGR035C</i>	-1.8	protein of unknown function, potential Cdc28p substrate
<i>YGR042W</i>	-1.2	questionable protein
<i>YGR153W</i>	-1.0	questionable protein
<i>YGR154C</i>	-0.9	questionable protein
<i>YGR168C</i>	-1.3	questionable protein
<i>YGR206W</i>	-1.1	questionable protein
<i>YGR243W</i>	-1.9	protein localized to mitochondria

Gene name	Fold change	Gene Product
<i>YHL013C</i>	-1.0	questionable protein
<i>YHL042W</i>	-1.2	questionable protein
<i>YHL045W</i>	-1.2	questionable protein
<i>FYV4</i>	-0.9	protein of unknown function, required for survival upon exposure to K1 killer toxin
<i>YHR132W-A</i>	-0.9	questionable protein
<i>YHR162W</i>	-1.0	questionable protein
<i>KRE27</i>	-1.3	killer toxin resistant
<i>YIL029C</i>	-1.8	questionable protein
<i>YIL089W</i>	-1.0	questionable protein
<i>YIL127C</i>	-2.0	questionable protein
<i>YIL158W</i>	-1.5	questionable protein
<i>YIL161W</i>	-1.6	questionable protein
<i>YIL165C</i>	-1.4	questionable protein
<i>SDL1</i>	-1.7	L-serine dehydratase
<i>YJL049W</i>	-1.1	questionable protein
<i>ICS3</i>	-1.3	protein of unknown function
<i>YJL118W</i>	-0.9	questionable protein
<i>YJL122W</i>	-1.3	questionable protein
<i>YJL156W-A</i>	-1.3	questionable protein
<i>YJR011C</i>	-1.1	questionable protein
<i>YJR012C</i>	-1.1	protein required for cell viability
<i>YAE1</i>	-1.6	essential protein of unknown function
<i>YJR079W</i>	-1.0	questionable protein
<i>YJR082C</i>	-1.6	stable subunit of the NuA4 complex
<i>YJR085C</i>	-1.3	questionable protein
<i>YKL018C-A</i>	-1.4	questionable protein
<i>YKL061W</i>	-1.0	questionable protein
<i>YKL133C</i>	-1.0	questionable protein
<i>YKL137W</i>	-1.1	questionable protein
<i>YKR075C</i>	-1.5	questionable protein
<i>YLL014W</i>	-2.3	questionable protein
<i>YLR036C</i>	-0.9	questionable protein
<i>YLR051C</i>	-1.4	protein required for cell viability
<i>YLR065C</i>	-1.1	questionable protein
<i>YLR073C</i>	-1.4	questionable protein
<i>YLR099W-A</i>	-1.2	questionable protein
<i>YLR104W</i>	-1.5	questionable protein
<i>YLR108C</i>	-1.0	questionable protein
<i>YLR112W</i>	-1.4	questionable protein
<i>YLR126C</i>	-1.1	questionable protein
<i>QRI5</i>	-2.4	mitochondrial protein of unknown function
<i>YLR211C</i>	-1.2	questionable protein
<i>YLR218C</i>	-1.1	questionable protein
<i>YLR254C</i>	-1.2	questionable protein
<i>TMA7</i>	-1.9	protein putative involved in cytoplasmic ribosome function
<i>YLR281C</i>	-1.5	questionable protein
<i>YLR346C</i>	-1.6	protein of unknown function; expression regulated by PDR1
<i>YLR363W-A</i>	-1.5	questionable protein
<i>YLR376C</i>	-1.4	platinum sensitivity protein
<i>YLR408C</i>	-1.6	questionable protein
<i>YLR456W</i>	-1.5	questionable protein
<i>YLR460C</i>	-1.1	questionable protein
<i>YML011C</i>	-1.0	questionable protein
<i>YML053C</i>	-1.0	questionable protein
<i>YML108W</i>	-1.5	protein of unknown function localised to cytoplasm and nucleus
<i>YML119W</i>	-0.9	questionable protein

Gene name	Fold change	Gene Product
<i>YMR003W</i>	-1.3	questionable protein
<i>YMR040W</i>	-2.5	questionable protein
<i>YMR071C</i>	-1.1	integral membrane protein
<i>YMR114C</i>	-2.3	questionable protein
<i>YMR132C</i>	-1.3	questionable protein
<i>ICY1</i>	-1.0	Protein that interacts with the cytoskeleton and is involved in chromatin organization and nuclear transport
<i>YNL024C</i>	-1.4	putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family
<i>YNL046W</i>	-1.9	questionable protein
<i>YNL056W</i>	-1.1	questionable protein
<i>YNL100W</i>	-0.9	questionable protein
<i>YNL122C</i>	-1.2	questionable protein
<i>YNL149C</i>	-1.2	protein required for cell viability
<i>YNL157W</i>	-1.1	questionable protein
<i>YNL211C</i>	-2.1	questionable protein
<i>YNR004W</i>	-0.9	questionable protein
<i>YNR020C</i>	-1.4	questionable protein
<i>YNR024W</i>	-2.1	questionable protein
<i>YNR040W</i>	-1.0	questionable protein
<i>YOL014W</i>	-1.5	questionable protein
<i>YOR012W</i>	-1.2	questionable protein
<i>YOR013W</i>	-1.4	questionable protein
<i>YOR052C</i>	-1.3	questionable protein
<i>FYV12</i>	-1.6	protein required for survival upon exposure to K1 killer toxin
<i>IES4</i>	-1.1	protein that associates with the INO80 chromatin remodeling complex under low-salt conditions
<i>YOR252W</i>	-1.5	questionable protein
<i>YOR305W</i>	-1.5	questionable protein
<i>YOR318C</i>	-1.2	questionable protein
<i>YPL039W</i>	-1.8	questionable protein
<i>YPL071C</i>	-1.9	questionable protein
<i>YPL108W</i>	-1.3	questionable protein
<i>YPL144W</i>	-0.9	questionable protein
<i>YPL267W</i>	-1.2	questionable protein
<i>YPR074W-A</i>	-2.2	questionable protein