

Table S1 Genes up 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		
"DUR1,2"	3.0	urea amidolyase (contains urea carboxylase and allophanate hydrolase)
SHM1	2.0	"Serine hydroxymethyltransferase, mitochondrial"
ILV6	2.6	"Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria"
ILV1	2.0	threonine deaminase
THR1	2.1	homoserine kinase
APE2	3.4	aminopeptidase yscII
ECM38	2.2	gamma-glutamyltransferase homolog
CAR2	2.7	ornithine aminotransferase
GCV2	2.3	glycine cleavage system P subunit glycine decarboxylase complex P subunit glycine synthase P subunit
GAD1	2.2	glutamate decarboxylase
ZWF1	3.3	glucose-6-phosphate dehydrogenase
ARG1	2.0	arginosuccinate synthetase
GDH1	2.0	NADP-specific glutamate dehydrogenase
Nucleotide/nucleoside/nucleobase metabolism		
CDC19	2.6	pyruvate kinase
FUI1	2.0	uridine permease
MEC1	2.4	"Required for mitotic growth, DNA repair and mitotic recombination, regulates phosphorylation of Rad53p, required for dmc1 arrest and meiotic recombination, homolog of fission yeast Rad3 and human ATR"
"DUR1,2"	3.0	urea amidolyase (contains urea carboxylase and allophanate hydrolase)
SDS24	2.1	"Similar to <i>S. pombe</i> SDS23, suppresses DIS2, localized to the nucleus"
SHM1	2.0	"Serine hydroxymethyltransferase, mitochondrial"
GDA1	2.5	guanosine diphosphatase of Golgi membrane
KEM1	2.2	5'-3' exonuclease
"ADE5,7"	2.1	aminoimidazole ribotide synthetase glycinamide ribotide synthetase
CYR1	2.5	adenylate cyclase
URA2	2.5	aspartate transcarbamylase carbamoyl phosphate synthetase glutamine amidotransferase
JSN1	2.1	benomyl dependent tubulin mutant
DCS1	1.9	"Non-essential hydrolase involved in mRNA decapping, may function in a feedback mechanism to regulate deadenylation, contains pyrophosphatase activity and Ja HIT (histidine triad) Jmotif; interacts with neutral trehalase Nth1pJJ"
ADE17	2.6	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase/IMP cyclohydrolase
SRV2	2.4	70 kDa adenylate cyclase-associated protein
IRA2	2.3	GTPase activating protein highly homologous to Ira1p neurofibromin homolog
PYK2	2.6	"Pyruvate kinase, glucose-repressed isoform"
Phosphate metabolism		
CDC19	2.6	pyruvate kinase
SEC18	2.1	ATPase NSF protein involved in protein transport between ER and Golgi

Gene Name	Fold change	Gene product
<i>MEC1</i>	2.4	"Required for mitotic growth, DNA repair and mitotic recombination, regulates phosphorylation of Rad53p, required for dmc1 arrest and meiotic recombination, homolog of fission yeast Rad3 and human ATR"
<i>GLK1</i>	3.0	glucokinase
<i>TPS2</i>	2.2	trehalose-6-phosphate phosphatase
<i>KIN1</i>	2.0	Serine/threonine protein kinase
<i>PDR15</i>	2.0	multidrug resistance transporter (putative)
<i>GDA1</i>	2.5	guanosine diphosphatase of Golgi membrane
<i>GAL83</i>	2.0	Glucose repression protein
<i>PTC2</i>	2.1	protein phosphatase type 2C
<i>CHD1</i>	2.3	transcriptional regulator
<i>HXK1</i>	5.2	hexokinase I (PI) (also called hexokinase A)
<i>PIL1</i>	2.4	Phosphorylation Inhibited by Long chain base
<i>THR1</i>	2.1	homoserine kinase
<i>KSP1</i>	2.6	Serine/threonine kinase similar to casein kinase II and other serine/threonine protein kinases
<i>SCH9</i>	2.1	cAMP-dependent protein kinase homolog suppressor of cdc25ts
<i>TPK1</i>	2.0	cAMP-dependent protein kinase catalytic subunit (putative)
<i>SSC1</i>	2.4	mitochondrial matrix protein involved in protein import Endo.Sccl endonuclease subunit
<i>HSP104</i>	2.4	heat shock protein 104
<i>YBT1</i>	2.1	"Yeast bile transporter, similar to mammalian bile transporter"
<i>DAK1</i>	2.0	dihydroxyacetone kinase (putative)
<i>YNR047W</i>	2.1	questionable protein
<i>INP53</i>	2.0	inositol polyphosphate 5-phosphatase
<i>PYK2</i>	2.6	"Pyruvate kinase, glucose-repressed isoform"

C-compound and carbohydrate metabolism

<i>CDC19</i>	2.6	pyruvate kinase
<i>TPS1</i>	2.6	trehalose-6-phosphate synthase/phosphatase complex 56 kDa synthase subunit
<i>PYC2</i>	2.5	pyruvate carboxylase
<i>SHM1</i>	2.0	"Serine hydroxymethyltransferase, mitochondrial"
<i>ILV6</i>	2.6	"Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria"
<i>GLK1</i>	3.0	glucokinase
<i>SRB8</i>	2.7	activation mediator subcomplex of RNA polymerase I holoenzyme
<i>GPD1</i>	2.1	glycerol-3-phosphate dehydrogenase
<i>BSC1</i>	4.0	Bypass of Stop Codon transcript encoded by this ORF shows a high level of stop codon bypass
<i>NTH1</i>	2.3	neutral trehalase
<i>TPS2</i>	2.2	trehalose-6-phosphate phosphatase
<i>ADR1</i>	2.7	positive transcriptional regulator
<i>SSN2</i>	2.2	transcription factor
<i>EMI2</i>	2.7	Early Meiotic Induction
<i>GAL83</i>	2.0	Glucose repression protein
<i>HXK1</i>	5.2	hexokinase I (PI) (also called hexokinase A)
<i>CWH41</i>	2.1	glucosidase I
<i>PYC1</i>	2.5	pyruvate carboxylase
<i>DIE2</i>	2.3	glucosyltransferase
<i>ENO1</i>	2.1	enolase I
<i>GRE3</i>	2.0	aldose reductase
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>KGD1</i>	2.4	alpha-ketoglutarate dehydrogenase
<i>SUC2</i>	2.6	invertase (sucrose hydrolyzing enzyme)
<i>PMT4</i>	2.0	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase

Gene Name	Fold change	Gene product
<i>GFA1</i>	3.2	glucoseamine-6-phosphate synthase glutamine_fructose-6-phosphate amidotransferase
<i>SDH1</i>	2.2	succinate dehydrogenase flavoprotein subunit
<i>GPI13</i>	2.0	ER membrane localized phosphoryltransferase that adds phosphoethanolamine onto the third mannose residue of the glycosylphosphatidylinositol (GPI) anchor precursor; similar to human PIG-O protein
<i>PDC5</i>	2.3	pyruvate decarboxylase
<i>GSY2</i>	2.2	glycogen synthase (UDP-glucose-starch glucosyltransferase)
<i>ECM38</i>	2.2	gamma-glutamyltransferase homolog
<i>FKS1</i>	2.6	"1,3-beta-D-glucan synthase"
<i>DAK1</i>	2.0	dihydroxyacetone kinase (putative)
<i>TSL1</i>	4.7	similar to TPS3 gene product trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit
<i>PGM2</i>	4.1	phosphoglucomutase
<i>ADE17</i>	2.6	5-aminimidazole-4-carboxamide ribonucleotide (AICAR) transformylase/IMP cyclohydrolase
<i>GCV2</i>	2.3	glycine cleavage system P subunit glycine decarboxylase complex P subunit glycine synthase P subunit
<i>YMR237W</i>	2.1	questionable protein
<i>TPS3</i>	3.1	trehalose-6-phosphate synthase/phosphatase complex 115 kDa regulatory subunit
<i>LAT1</i>	2.5	pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase component (E2)
<i>ZWF1</i>	3.3	glucose-6-phosphate dehydrogenase
<i>YOL155C</i>	2.1	ORF
<i>LSC1</i>	2.0	"alpha subunit of succinyl-CoA ligase (synthetase; ATP-forming), a mitochondrial enzyme of the TCA cycle"
<i>KRE5</i>	2.2	"appears to function early in (1,6)-beta-D-glucan synthesis pathway"
<i>PYK2</i>	2.6	"Pyruvate kinase, glucose-repressed isoform"
<i>GPH1</i>	7.0	glycogen phosphorylase

Lipid, fatty acid and isoprenoid metabolism

<i>SWH1</i>	2.6	Similar to mammalian oxysterol-binding protein
<i>SHM1</i>	2.0	"Serine hydroxymethyltransferase, mitochondrial"
<i>GPD1</i>	2.1	glycerol-3-phosphate dehydrogenase
<i>GPI13</i>	2.0	ER membrane localized phosphoryltransferase that adds phosphoethanolamine onto the third mannose residue of the glycosylphosphatidylinositol (GPI) anchor precursor; similar to human PIG-O protein
<i>HMG2</i>	2.1	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme
<i>YML059C</i>	2.1	questionable protein
<i>DAK1</i>	2.0	dihydroxyacetone kinase (putative)
<i>INP53</i>	2.0	inositol polyphosphate 5-phosphatase
<i>NCR1</i>	2.1	transmembrane protein (putative)
<i>FAS2</i>	2.0	fatty acid synthase alpha subunit
<i>PLC1</i>	2.0	phosphoinositide-specific phospholipase C

Metabolism of vitamins, cofactors, and prosthetic groups

<i>PYC2</i>	2.5	pyruvate carboxylase
<i>SHM1</i>	2.0	"Serine hydroxymethyltransferase, mitochondrial"
<i>BPL1</i>	2.2	biotin:apoprotein ligase
<i>PYC1</i>	2.5	pyruvate carboxylase
<i>ECM38</i>	2.2	gamma-glutamyltransferase homolog
<i>GCV2</i>	2.3	glycine cleavage system P subunit glycine decarboxylase complex P subunit glycine synthase P subunit
<i>FAS2</i>	2.0	fatty acid synthase alpha subunit

Secondary metabolism

<i>ENO1</i>	2.1	enolase I
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Gene Name	Fold change	Gene product
<i>GRE3</i>	2.0	aldose reductase
<i>GPI13</i>	2.0	ER membrane localized phosphoryltransferase that adds phosphoethanolamine onto the third mannose residue of the glycosylphosphatidylinositol (GPI) anchor precursor; similar to human PIG-O protein
<i>ARG1</i>	2.0	arginosuccinate synthetase

Energy

<i>CDC19</i>	2.6	pyruvate kinase
<i>TPS1</i>	2.6	trehalose-6-phosphate synthase/phosphatase complex 56 kDa synthase subunit
<i>PYC2</i>	2.5	pyruvate carboxylase
<i>GLK1</i>	3.0	glucokinase
<i>NTH1</i>	2.3	neutral trehalase
<i>TPS2</i>	2.2	trehalose-6-phosphate phosphatase
<i>PDA1</i>	2.2	pyruvate dehydrogenase alpha subunit (E1 alpha)
<i>HXK1</i>	5.2	hexokinase I (PI) (also called hexokinase A)
<i>PYC1</i>	2.5	pyruvate carboxylase
<i>SOL4</i>	2.8	6-phosphogluconolactonase
<i>ENO1</i>	2.1	enolase I
<i>KGD1</i>	2.4	alpha-ketoglutarate dehydrogenase
<i>RAV1</i>	2.1	Regulator of (H ⁺)-ATPase in vacuolar membrane
<i>ATP2</i>	2.4	F(1)F(0)-ATPase complex beta subunit
<i>SDH1</i>	2.2	succinate dehydrogenase flavoprotein subunit
<i>CSF1</i>	2.2	Protein required for fermentation at low temperature
<i>PDC5</i>	2.3	pyruvate decarboxylase
<i>GSY2</i>	2.2	glycogen synthase (UDP-glucose-starch glucosyltransferase)
<i>FKS1</i>	2.6	"1,3-beta-D-glucan synthase"
<i>TSL1</i>	4.7	similar to TPS3 gene product trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit
<i>PGM2</i>	4.1	phosphoglucomutase
<i>MYO5</i>	2.0	myosin I
<i>TPS3</i>	3.1	trehalose-6-phosphate synthase/phosphatase complex 115 kDa regulatory subunit
<i>LAT1</i>	2.5	pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase component (E2)
<i>ZWF1</i>	3.3	glucose-6-phosphate dehydrogenase
<i>CYT1</i>	2.0	cytochrome c1
<i>LSC1</i>	2.0	"alpha subunit of succinyl-CoA ligase (synthetase; ATP-forming), a mitochondrial enzyme of the TCA cycle"
<i>KRE5</i>	2.2	"appears to function early in (1,6)-beta-D-glucan synthesis pathway"
<i>PYK2</i>	2.6	"Pyruvate kinase, glucose-repressed isoform"
<i>GDH1</i>	2.0	NADP-specific glutamate dehydrogenase
<i>GPH1</i>	7.0	glycogen phosphorylase

Cell cycle and DNA processing

<i>SWH1</i>	2.6	Similar to mammalian oxysterol-binding protein
<i>RPG1</i>	2.2	translation initiation factor eIF3 subunit
<i>MEC1</i>	2.4	"Required for mitotic growth, DNA repair and mitotic recombination, regulates phosphorylation of Rad53p, required for dmc1 arrest and meiotic recombination, homolog of fission yeast Rad3 and human ATR"
<i>SDS24</i>	2.1	"Similar to S. pombe SDS23, suppresses DIS2, localized to the nucleus"
<i>BUD3</i>	2.2	"Protein involved in bud-site selection and required for axial budding pattern; localizes with septins to bud neck in mitosis and may constitute ""axial landmark"" for next round of budding"
<i>SSD1</i>	2.0	Product of gene unknown
<i>TOM1</i>	2.0	"hct-domain-containing protein, containing kinase motifs similar to Rsp5"

Gene Name	Fold change	Gene product
<i>SEC3</i>	2.0	"Profilin synthetic lethal protein, has region of coiled-coil structure; subunit of the Exocyst complex--the Exocyst complex contains the gene products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SEC15 and EXO70 and is required for exocytosis"
<i>PTC2</i>	2.1	protein phosphatase type 2C
<i>RSP5</i>	2.5	involved in ubiquitin-mediated protein degradation
<i>CHD1</i>	2.3	transcriptional regulator
<i>KEM1</i>	2.2	5'-3' exonuclease
<i>SAE2</i>	2.2	Involved in meiotic recombination and chromosome metabolism
<i>SCH9</i>	2.1	cAMP-dependent protein kinase homolog suppressor of cdc25ts
<i>SIM1</i>	2.1	(putative) involved in control of DNA replication
<i>PAN1</i>	2.6	Involved in actin organization and endocytosis
<i>CYR1</i>	2.5	adenylate cyclase
<i>NET1</i>	2.0	Nucleolar protein involved in exit from mitosis
<i>SCP160</i>	2.2	"May be required during cell division for faithful partitioning of the ER-nuclear envelope membranes, involved in control of mitotic chromosome transmission"
<i>JSN1</i>	2.1	benomyl dependent tubulin mutant
<i>ECM38</i>	2.2	gamma-glutamyltransferase homolog
<i>MSC1</i>	2.2	"Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; msc1 mutants are defective in directing meiotic recombination events to homologous chromatids"
<i>FAR11</i>	2.5	"Protein involved in G1 cell cycle arrest in response to pheromone, in a pathway different from the Far1p-dependent pathway; interacts with Far3p, Far7p, Far8p, Far9p, and Far10p"
<i>APC1</i>	2.1	ubiquitin ligase subunit
<i>ATG2</i>	2.1	peripheral membrane protein
<i>BNI1</i>	2.0	"formin, involved in spindle orientation"
<i>NFI1</i>	2.0	chromatin protein
<i>WTM1</i>	2.0	transcriptional modulator
<i>PLC1</i>	2.0	phosphoinositide-specific phospholipase C
Transcription		
<i>SRB8</i>	2.7	activation mediator subcomplex of RNA polymerase I holoenzyme
<i>TUP1</i>	2.0	"glucose repression regulatory protein, exhibits similarity to beta subunits of G proteins"
<i>STP4</i>	2.3	Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
<i>ADR1</i>	2.7	positive transcriptional regulator
<i>NPL3</i>	3.6	contains RNA recognition motif nuclear shuttling protein
<i>SSN2</i>	2.2	transcription factor
<i>GAL83</i>	2.0	Glucose repression protein
<i>CHD1</i>	2.3	transcriptional regulator
<i>PAB1</i>	2.5	poly(A) binding protein
<i>ARC1</i>	2.0	"Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Ygl245wp), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids"
<i>KEM1</i>	2.2	5'-3' exonuclease
<i>SOL4</i>	2.8	6-phosphogluconolactonase
<i>MGA1</i>	2.1	similar to heat shock transcription factor
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>TAO3</i>	2.2	Identified in a hunt for mutants that activate OCH1 transcription
<i>NET1</i>	2.0	Nucleolar protein involved in exit from mitosis
<i>TPK1</i>	2.0	cAMP-dependent protein kinase catalytic subunit (putative)
<i>JSN1</i>	2.1	benomyl dependent tubulin mutant
<i>GSP1</i>	2.1	GTP-binding protein
<i>WTM1</i>	2.0	transcriptional modulator

Gene Name	Fold change	Gene product
Protein synthesis		
<i>RPG1</i>	2.2	translation initiation factor eIF3 subunit
<i>EFT2</i>	1.9	translation elongation factor 2 (EF-2)
<i>PAB1</i>	2.5	poly(A) binding protein
<i>FRS2</i>	2.0	phenylalanine-tRNA ligase subunit
<i>ARC1</i>	2.0	"Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Ygl245wp), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids"
<i>YGR054W</i>	2.5	yeast homolog of mammalian eIF2A
<i>MES1</i>	2.3	methionine-tRNA ligase
<i>DED81</i>	2.2	asparaginyl-tRNA synthetase
<i>APE2</i>	3.4	aminopeptidase yscII
<i>EAP1</i>	2.3	functionally analogous to mammalian 4E-BPs functional and limited sequence similarity to CAF20
<i>DPS1</i>	2.7	aspartyl-tRNA synthetase
<i>EFT1</i>	2.1	translation elongation factor 2 (EF-2)
<i>CAM1</i>	2.5	calcium and phospholipid binding protein homologous to translation elongation factor 1-gamma (EF-1gamma)
Protein fate		
<i>SLA1</i>	2.3	cytoskeletal protein binding protein
<i>MEC1</i>	2.4	"Required for mitotic growth, DNA repair and mitotic recombination, regulates phosphorylation of Rad53p, required for dmc1 arrest and meiotic recombination, homolog of fission yeast Rad3 and human ATR"
<i>SSE2</i>	2.8	HSP70 family SSE1 homolog
<i>SDS24</i>	2.1	"Similar to S. pombe SDS23, suppresses DIS2, localized to the nucleus"
<i>APE3</i>	2.1	aminopeptidase yscIII
<i>YCL044C</i>	2.4	questionable protein
<i>ABP1</i>	2.6	actin binding protein
<i>BPL1</i>	2.2	biotin:apoprotein ligase
<i>KIN1</i>	2.0	Serine/threonine protein kinase
<i>NPL3</i>	3.6	contains RNA recognition motif nuclear shuttling protein
<i>TOM1</i>	2.0	"hect-domain-containing protein, containing kinase motifs similar to Rsp5"
<i>GDA1</i>	2.5	guanosine diphosphatase of Golgi membrane
<i>PRB1</i>	2.3	vacuolar protease B
<i>GAL83</i>	2.0	Glucose repression protein
<i>PTC2</i>	2.1	protein phosphatase type 2C
<i>KAP123</i>	2.2	karyopherin beta 4
<i>RSP5</i>	2.5	involved in ubiquitin-mediated protein degradation
<i>BLM3</i>	2.0	involved in protecting the cell against bleomycin damage
<i>CHC1</i>	2.3	Clathrin heavy chain
<i>UBR1</i>	2.3	ubiquitin-protein ligase
<i>DIE2</i>	2.3	glucosyltransferase
<i>ECM29</i>	2.0	ExtraCellular Mutant
<i>KSP1</i>	2.6	Serine/threonine kinase similar to casein kinase II and other serine/threonine protein kinases
<i>SCH9</i>	2.1	cAMP-dependent protein kinase homolog suppressor of cdc25ts
<i>SEC24</i>	2.5	vesicle coat component
<i>PAN1</i>	2.6	Involved in actin organization and endocytosis
<i>TPK1</i>	2.0	cAMP-dependent protein kinase catalytic subunit (putative)
<i>SSC1</i>	2.4	mitochondrial matrix protein involved in protein import Endo.Sccl endonuclease subunit
<i>PMT4</i>	2.0	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
<i>APE2</i>	3.4	aminopeptidase yscII
<i>HSP104</i>	2.4	heat shock protein 104

Gene Name	Fold change	Gene product
<i>GPI13</i>	2.0	ER membrane localized phosphoryltransferase that adds phosphoethanolamine onto the third mannose residue of the glycosylphosphatidylinositol (GPI) anchor precursor; similar to human PIG-O protein
<i>VPS13</i>	2.6	homologous to human COH1
<i>UBR2</i>	2.1	ubiquitin-protein ligase (E3)
<i>YPS1</i>	2.0	GPI-anchored aspartic protease
<i>ECM38</i>	2.2	gamma-glutamyltransferase homolog
<i>SEC61</i>	2.5	membrane component of ER protein translocation apparatus
<i>STE23</i>	2.0	involved in a-factor processing
<i>YML059C</i>	2.1	questionable protein
<i>TOM40</i>	2.4	forms the outer membrane import channel mitochondrial outer membrane protein
<i>UBP15</i>	2.5	deubiquitinating enzyme (putative)
<i>APC1</i>	2.1	ubiquitin ligase subunit
<i>ATG2</i>	2.1	peripheral membrane protein
<i>YNR047W</i>	2.1	questionable protein
<i>STI1</i>	2.2	heat shock protein also induced by canavanine and entry into stationary phase
<i>VPS17</i>	2.3	Peripheral membrane protein required for vacuolar protein sorting
<i>NFI1</i>	2.0	chromatin protein
<i>KRE5</i>	2.2	"appears to function early in (1,6)-beta-D-glucan synthesis pathway"
<i>BRO1</i>	2.2	BCK1-like resistance to osmotic shock
<i>SEC16</i>	2.7	vesicle coat component
<i>SSE1</i>	2.2	HSP70 family SSA1 SSE2 homolog
<i>PEP4</i>	2.2	vacuolar proteinase A
<i>FAS2</i>	2.0	fatty acid synthase alpha subunit
<i>APM1</i>	2.2	clathrin associated protein complex medium subunit

Regulation of metabolism and protein function

<i>IRA1</i>	2.0	GTPase activating protein (GAP)
<i>ILV6</i>	2.6	"Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria"
<i>SEC7</i>	2.0	guanine nucleotide exchange protein for ARF
<i>PTC2</i>	2.1	protein phosphatase type 2C
<i>BLM3</i>	2.0	involved in protecting the cell against bleomycin damage
<i>PIL1</i>	2.4	Phosphorylation Inhibited by Long chain base
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>SSC1</i>	2.4	mitochondrial matrix protein involved in protein import Endo.Sccl endonuclease subunit
<i>TSL1</i>	4.7	similar to TPS3 gene product trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit
<i>IRA2</i>	2.3	GTPase activating protein highly homologous to Ira1p neurofibromin homolog
<i>STI1</i>	2.2	heat shock protein also induced by canavanine and entry into stationary phase
<i>WTM1</i>	2.0	transcriptional modulator

Cellular transport, transport facilities and transport routes

<i>SLA1</i>	2.3	cytoskeletal protein binding protein
<i>FUI1</i>	2.0	uridine permease
<i>EDE1</i>	2.9	EH domain protein involved in endocytosis
<i>SEC18</i>	2.1	ATPase NSF protein involved in protein transport between ER and Golgi
<i>VMA2</i>	2.1	vacuolar ATPase V1 domain subunit B (60 kDa)
<i>SDS24</i>	2.1	"Similar to S. pombe SDS23, suppresses DIS2, localized to the nucleus"
<i>GLK1</i>	3.0	glucokinase
<i>STP4</i>	2.3	Involved in pre-tRNA splicing and in uptake of branched-chain amino acids

Gene Name	Fold change	Gene product
<i>COP1</i>	2.0	coatomer complex gamma-alpha-COP alpha subunit
<i>SEC7</i>	2.0	guanine nucleotide exchange protein for ARF
<i>RVS167</i>	2.0	cytoskeletal protein (putative)
<i>PDR15</i>	2.0	multidrug resistance transporter (putative)
<i>NPL3</i>	3.6	contains RNA recognition motif nuclear shuttling protein
<i>NHX1</i>	2.1	Na ⁺ /H ⁺ exchanger
<i>TOM1</i>	2.0	"hect-domain-containing protein, containing kinase motifs similar to Rsp5"
<i>SEC3</i>	2.0	"Profilin synthetic lethal protein, has region of coiled-coil structure; subunit of the Exocyst complex--the Exocyst complex contains the gene products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SEC15 and EXO70 and is required for exocytosis"
<i>KAP123</i>	2.2	karyopherin beta 4
<i>PAB1</i>	2.5	poly(A) binding protein
<i>DNF1</i>	2.1	Potential aminophospholipid translocase
<i>RET2</i>	1.9	coatomer (COPI) complex delta subunit
<i>ARC1</i>	2.0	"Protein that binds tRNA and methionyl- and glutamyl-tRNA synthetases (Mes1p and Ygl245wp), delivering tRNA to them, stimulating catalysis, and ensuring their localization to the cytoplasm; also binds quadruplex nucleic acids"
<i>CHC1</i>	2.3	Clathrin heavy chain
<i>NEO1</i>	2.1	P-type ATPase
<i>SEC24</i>	2.5	vesicle coat component
<i>PAN1</i>	2.6	Involved in actin organization and endocytosis
<i>SCP160</i>	2.2	"May be required during cell division for faithful partitioning of the ER-nuclear envelope membranes, involved in control of mitotic chromosome transmission"
<i>SSC1</i>	2.4	mitochondrial matrix protein involved in protein import Endo.Sccl endonuclease subunit
<i>MIR1</i>	2.2	Product of gene unknown
<i>ECM27</i>	2.3	ExtraCellular Mutant
<i>ATP2</i>	2.4	F(1)F(0)-ATPase complex beta subunit
<i>SDH1</i>	2.2	succinate dehydrogenase flavoprotein subunit
<i>GAP1</i>	2.6	general amino acid permease
<i>VPS13</i>	2.6	homologous to human COH1
<i>YBT1</i>	2.1	"Yeast bile transporter, similar to mammalian bile transporter"
<i>GSP1</i>	2.1	GTP-binding protein
<i>VRP1</i>	2.7	proline-rich protein verprolin
<i>SEC61</i>	2.5	membrane component of ER protein translocation apparatus
<i>HXT2</i>	2.1	high affinity hexose transporter-2
<i>MYO5</i>	2.0	myosin I
<i>SSO2</i>	2.1	t-SNARE
<i>TOM40</i>	2.4	forms the outer membrane import channel mitochondrial outer membrane protein
<i>ATG2</i>	2.1	peripheral membrane protein
<i>BNI1</i>	2.0	"formin, involved in spindle orientation"
<i>SEC21</i>	2.0	PEST sequence-containing protein non-clathrin coat protein
<i>PHO91</i>	2.0	Low-affinity phosphate transporter
<i>CYT1</i>	2.0	cytochrome c1
<i>INP53</i>	2.0	inositol polyphosphate 5-phosphatase
<i>VPS17</i>	2.3	Peripheral membrane protein required for vacuolar protein sorting
<i>GSP2</i>	2.1	GTP-binding protein Gsp1p homolog
<i>NCR1</i>	2.1	transmembrane protein (putative)
<i>SVL3</i>	2.1	"Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck"
<i>BRO1</i>	2.2	BCK1-like resistance to osmotic shock
<i>SEC16</i>	2.7	vesicle coat component
<i>APM1</i>	2.2	clathrin associated protein complex medium subunit

Gene Name	Fold change	Gene product
Cellular communication/Signal transduction mechanism		
<i>IRA1</i>	2.0	GTPase activating protein (GAP)
<i>GAL83</i>	2.0	Glucose repression protein
<i>PTC2</i>	2.1	protein phosphatase type 2C
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>CYR1</i>	2.5	adenylate cyclase
<i>TPK1</i>	2.0	cAMP-dependent protein kinase catalytic subunit (putative)
<i>GIS3</i>	2.0	GIG3 suppressor
<i>SRV2</i>	2.4	70 kDa adenylyl cyclase-associated protein
<i>BNI1</i>	2.0	"formin, involved in spindle orientation"
<i>IRA2</i>	2.3	GTPase activating protein highly homologous to <i>Ira1p</i> neurofibromin homolog
<i>INP53</i>	2.0	inositol polyphosphate 5-phosphatase
<i>BRO1</i>	2.2	BCK1-like resistance to osmotic shock
<i>PLC1</i>	2.0	phosphoinositide-specific phospholipase C
Cell rescue, defense and virulence		
<i>IST2</i>	2.5	"Plasma membrane protein that may be involved in osmotolerance, localizes to the mother cell in small-budded cells and to the bud in medium- and large-budded cells; mRNA is transported to the bud tip by an actomyosin-driven process"
<i>TPS1</i>	2.6	trehalose-6-phosphate synthase/phosphatase complex 56 kDa synthase subunit
<i>MEC1</i>	2.4	"Required for mitotic growth, DNA repair and mitotic recombination, regulates phosphorylation of Rad53p, required for <i>dmc1</i> arrest and meiotic recombination, homolog of fission yeast <i>Rad3</i> and human <i>ATR</i> "
<i>SSE2</i>	2.8	HSP70 family <i>SSE1</i> homolog
<i>GPD1</i>	2.1	glycerol-3-phosphate dehydrogenase
<i>NTH1</i>	2.3	neutral trehalase
<i>TPS2</i>	2.2	trehalose-6-phosphate phosphatase
<i>SED1</i>	3.5	cell surface glycoprotein (putative)
<i>SSD1</i>	2.0	Product of gene unknown
<i>RVS167</i>	2.0	cytoskeletal protein (putative)
<i>NHX1</i>	2.1	Na ⁺ /H ⁺ exchanger
<i>PRB1</i>	2.3	vacuolar protease B
<i>PTC2</i>	2.1	protein phosphatase type 2C
<i>RSP5</i>	2.5	involved in ubiquitin-mediated protein degradation
<i>BLM3</i>	2.0	involved in protecting the cell against bleomycin damage
<i>PIL1</i>	2.4	Phosphorylation Inhibited by Long chain base
<i>MGA1</i>	2.1	similar to heat shock transcription factor
<i>GRE3</i>	2.0	aldose reductase
<i>SCH9</i>	2.1	cAMP-dependent protein kinase homolog suppressor of <i>cdc25ts</i>
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>SSC1</i>	2.4	mitochondrial matrix protein involved in protein import <i>Endo.Sccl</i> endonuclease subunit
<i>HSP104</i>	2.4	heat shock protein 104
<i>VRP1</i>	2.7	proline-rich protein verprolin
<i>DAK1</i>	2.0	dihydroxyacetone kinase (putative)
<i>TSL1</i>	4.7	similar to <i>TPS3</i> gene product trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit
<i>MYO5</i>	2.0	myosin I
<i>GAD1</i>	2.2	glutamate decarboxylase
<i>TPS3</i>	3.1	trehalose-6-phosphate synthase/phosphatase complex 115 kDa regulatory subunit
<i>YNL190W</i>	2.0	questionable protein
<i>ZWF1</i>	3.3	glucose-6-phosphate dehydrogenase
<i>BNI1</i>	2.0	"formin, involved in spindle orientation"

Gene Name	Fold change	Gene product
<i>STI1</i>	2.2	heat shock protein also induced by canavanine and entry into stationary phase
<i>BRO1</i>	2.2	BCK1-like resistance to osmotic shock
<i>SSE1</i>	2.2	HSP70 family SSA1 SSE2 homolog
<i>PEP4</i>	2.2	vacuolar proteinase A

Interaction with the environment

<i>VMA2</i>	2.1	vacuolar ATPase V1 domain subunit B (60 kDa)
<i>IRA1</i>	2.0	GTPase activating protein (GAP)
<i>GPD1</i>	2.1	glycerol-3-phosphate dehydrogenase
<i>NHX1</i>	2.1	Na ⁺ /H ⁺ exchanger
<i>GAL83</i>	2.0	Glucose repression protein
<i>PTC2</i>	2.1	protein phosphatase type 2C
<i>PIL1</i>	2.4	Phosphorylation Inhibited by Long chain base
<i>SCH9</i>	2.1	cAMP-dependent protein kinase homolog suppressor of cdc25ts
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>CYR1</i>	2.5	adenylate cyclase
<i>PRY3</i>	2.6	"Pathogen Related in Sc, contains homology to the plant PR-1 class of pathogen related proteins. The protein sequence is over 60% identical with the Pry2p & Pry3p over 145 resid. PRY1 is >35% identical (50% similar) to tobacco PR-1c protein."
<i>SCP160</i>	2.2	"May be required during cell division for faithful partitioning of the ER-nuclear envelope membranes, involved in control of mitotic chromosome transmission"
<i>RAV1</i>	2.1	Regulator of (H ⁺)-ATPase in vacuolar membrane
<i>MIR1</i>	2.2	Product of gene unknown
<i>ATP2</i>	2.4	F(1)F(0)-ATPase complex beta subunit
<i>GFA1</i>	3.2	glucoseamine-6-phosphate synthase glutamine_fructose-6-phosphate amidotransferase
<i>STE23</i>	2.0	involved in a-factor processing
<i>MYO5</i>	2.0	myosin I
<i>FAR11</i>	2.5	"Protein involved in G1 cell cycle arrest in response to pheromone, in a pathway different from the Far1p-dependent pathway; interacts with Far3p, Far7p, Far8p, Far9p, and Far10p"
<i>BNI1</i>	2.0	"formin, involved in spindle orientation"
<i>PHO91</i>	2.0	Low-affinity phosphate transporter
<i>YNR047W</i>	2.1	questionable protein
<i>BRO1</i>	2.2	BCK1-like resistance to osmotic shock
<i>SSE1</i>	2.2	HSP70 family SSA1 SSE2 homolog

Transposable elements, viral and plasmid proteins

<i>YDR170W-A</i>	2.4	Ty ORF
<i>YDR210W-A</i>	2.9	TyA Gag protein; the main structural constituent of virus-like particles (VLPs)
<i>YDR261W-A</i>	2.4	TyA Gag protein; the main structural constituent of virus-like particles (VLPs)
<i>YGR161W-A</i>	2.1	TyA Gag protein; the main structural constituent of virus-like particles (VLPs)
<i>YLR410W-A</i>	2.8	TyA Gag protein; the main structural constituent of virus-like particles (VLPs)
<i>YOR192C-A</i>	2.8	TyA Gag protein; the main structural constituent of virus-like particles (VLPs)
<i>YOR343W-A</i>	3.0	TyA Gag protein; the main structural constituent of virus-like particles (VLPs)
<i>YOR343W-B</i>	3.3	"TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are required for retrotransposition"

Cell fate

<i>SLA1</i>	2.3	cytoskeletal protein binding protein
<i>ABP1</i>	2.6	actin binding protein
<i>WHI4</i>	2.2	RNA binding protein (putative) WHI3 homolog

Gene Name	Fold change	Gene product
<i>SSD1</i>	2.0	Product of gene unknown
<i>RVS167</i>	2.0	cytoskeletal protein (putative)
<i>SCH9</i>	2.1	cAMP-dependent protein kinase homolog suppressor of <i>cdc25ts</i>
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>SIM1</i>	2.1	(putative) involved in control of DNA replication
<i>TAO3</i>	2.2	Identified in a hunt for mutants that activate <i>OCH1</i> transcription
<i>ATP2</i>	2.4	F(1)F(0)-ATPase complex beta subunit
<i>VRP1</i>	2.7	proline-rich protein verprolin
<i>SSO2</i>	2.1	t-SNARE
<i>SRV2</i>	2.4	70 kDa adenylyl cyclase-associated protein
<i>WHI3</i>	2.0	RNA binding protein (putative)
<i>BNI1</i>	2.0	"formin, involved in spindle orientation"
<i>STI1</i>	2.2	heat shock protein also induced by canavanine and entry into stationary phase
<i>NFI1</i>	2.0	chromatin protein
<i>KRE5</i>	2.2	"appears to function early in (1,6)-beta-D-glucan synthesis pathway"
<i>SVL3</i>	2.1	"Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck"
<i>SSE1</i>	2.2	HSP70 family SSA1 SSE2 homolog
<i>PLC1</i>	2.0	phosphoinositide-specific phospholipase C

Biogenesis of cellular components

<i>SLA1</i>	2.3	cytoskeletal protein binding protein
<i>YCL044C</i>	2.4	questionable protein
<i>ABP1</i>	2.6	actin binding protein
<i>SED1</i>	3.5	cell surface glycoprotein (putative)
<i>ADR1</i>	2.7	positive transcriptional regulator
<i>SSD1</i>	2.0	Product of gene unknown
<i>RVS167</i>	2.0	cytoskeletal protein (putative)
<i>TOM1</i>	2.0	"hect-domain-containing protein, containing kinase motifs similar to Rsp5"
<i>CWH41</i>	2.1	glucosidase I
<i>ECM29</i>	2.0	ExtraCellular Mutant
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>SIM1</i>	2.1	(putative) involved in control of DNA replication
<i>PAN1</i>	2.6	Involved in actin organization and endocytosis
<i>BBC1</i>	2.8	shows synthetic fitness defect with <i>bni1</i> mutants and associates with the Bee1p-Vrp1p-Myo3/5p complex
<i>MHP1</i>	2.5	microtubule-associated protein (MAP) (putative)
<i>NET1</i>	2.0	Nucleolar protein involved in exit from mitosis
<i>ECM27</i>	2.3	ExtraCellular Mutant
<i>CWP1</i>	3.4	cell wall mannoprotein
<i>GFA1</i>	3.2	glucoseamine-6-phosphate synthase glutamine_ fructose-6-phosphate amidotransferase
<i>SDH1</i>	2.2	succinate dehydrogenase flavoprotein subunit
<i>ECM4</i>	2.4	ExtraCellular Mutant
<i>MMM1</i>	2.4	mitochondrial outer membrane protein
<i>GSP1</i>	2.1	GTP-binding protein
<i>ECM38</i>	2.2	gamma-glutamyltransferase homolog
<i>VRP1</i>	2.7	proline-rich protein verprolin
<i>FKS1</i>	2.6	"1,3-beta-D-glucan synthase"
<i>MYO5</i>	2.0	myosin I
<i>SSO2</i>	2.1	t-SNARE
<i>SRV2</i>	2.4	70 kDa adenylyl cyclase-associated protein
<i>ATG2</i>	2.1	peripheral membrane protein
<i>BNI1</i>	2.0	"formin, involved in spindle orientation"
<i>YOL155C</i>	2.1	ORF

Gene Name	Fold change	Gene product
<i>DFG16</i>	2.1	"Probable multiple transmembrane protein, involved in invasive growth upon nitrogen starvation"
<i>INP53</i>	2.0	inositol polyphosphate 5-phosphatase
<i>NFI1</i>	2.0	chromatin protein
<i>GSP2</i>	2.1	GTP-binding protein Gsp1p homolog
<i>SVL3</i>	2.1	"Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck"
<i>APM1</i>	2.2	clathrin associated protein complex medium subunit
<i>PLC1</i>	2.0	phosphoinositide-specific phospholipase C

Cell type differentiation

<i>SLA1</i>	2.3	cytoskeletal protein binding protein
<i>IRA1</i>	2.0	GTPase activating protein (GAP)
<i>BUD3</i>	2.2	"Protein involved in bud-site selection and required for axial budding pattern; localizes with septins to bud neck in mitosis and may constitute ""axial landmark"" for next round of budding"
<i>ABP1</i>	2.6	actin binding protein
<i>SPO71</i>	2.0	"Meiosis-specific protein of unknown function, required for spore wall formation during sporulation; dispensible for both nuclear divisions during meiosis"
<i>SSD1</i>	2.0	Product of gene unknown
<i>RVS167</i>	2.0	cytoskeletal protein (putative)
<i>EMI2</i>	2.7	Early Meiotic Induction
<i>PRB1</i>	2.3	vacuolar protease B
<i>SEC3</i>	2.0	"Profilin synthetic lethal protein, has region of coiled-coil structure; subunit of the Exocyst complex--the Exocyst complex contains the gene products encoded by SEC3, SEC5, SEC6, SEC8, SEC10, SEC15 and EXO70 and is required for exocytosis"
<i>GAL83</i>	2.0	Glucose repression protein
<i>RSP5</i>	2.5	involved in ubiquitin-mediated protein degradation
<i>KEM1</i>	2.2	5'-3' exonuclease
<i>MGA1</i>	2.1	similar to heat shock transcription factor
<i>BCY1</i>	2.0	cAMP-dependent protein kinase regulatory subunit
<i>TAO3</i>	2.2	Identified in a hunt for mutants that activate OCH1 transcription
<i>PAN1</i>	2.6	Involved in actin organization and endocytosis
<i>CYR1</i>	2.5	adenylate cyclase
<i>TPK1</i>	2.0	cAMP-dependent protein kinase catalytic subunit (putative)
<i>VRP1</i>	2.7	proline-rich protein verprolin
<i>MYO5</i>	2.0	myosin I
<i>SSO2</i>	2.1	t-SNARE
<i>SRV2</i>	2.4	70 kDa adenylyl cyclase-associated protein
<i>WHI3</i>	2.0	RNA binding protein (putative)
<i>ATG2</i>	2.1	peripheral membrane protein
<i>BNI1</i>	2.0	"formin, involved in spindle orientation"
<i>DFG16</i>	2.1	"Probable multiple transmembrane protein, involved in invasive growth upon nitrogen starvation"
<i>NFI1</i>	2.0	chromatin protein
<i>SVL3</i>	2.1	"Protein of unknown function, mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck"
<i>PEP4</i>	2.2	vacuolar proteinase A
<i>PLC1</i>	2.0	phosphoinositide-specific phospholipase C

Unclassified proteins

<i>YAL053W</i>	2.2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
<i>YBR108W</i>	2.3	questionable protein
<i>YCL045C</i>	2.1	questionable protein

Gene Name	Fold change	Gene product
<i>SYP1</i>	2.1	Suppressor of Yeast Profilin deletion
<i>YCR061W</i>	2.7	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern
<i>YEL043W</i>	2.3	questionable protein
<i>ZRG8</i>	2.5	Zinc regulated gene
<i>SCY1</i>	2.0	Suppressor of GTPase mutant
<i>YHR087W</i>	3.8	questionable protein
<i>YHR214W-A</i>	2.0	questionable protein
<i>YIL169C</i>	2.4	questionable protein
<i>YKR018C</i>	2.3	questionable protein
<i>YLR162W</i>	2.1	questionable protein
<i>YLR187W</i>	2.1	"Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck"
<i>YML072C</i>	2.1	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery
<i>YMR086W</i>	2.2	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery
<i>YMR196W</i>	2.2	questionable protein
<i>YMR247C</i>	2.1	questionable protein
<i>YNL321W</i>	2.1	not essential for vegetative growth
<i>CUE5</i>	2.0	"Protein containing a CUE domain that binds ubiquitin, which may facilitate intramolecular monoubiquitination; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern"
<i>YOR066W</i>	2.0	questionable protein
<i>YPL137C</i>	2.1	questionable protein
<i>YPL184C</i>	2.1	questionable protein