

**Up regulated genes in WT cells following 0.1% MMS exposure for 60 minutes**

<b>Gene name</b>	<b>Average Fold Change</b>	<b>S.E.M.</b>	<b>Description</b>
<b>Cell Stress</b>			
<i>GSH1</i>	3.96	0.41	gamma-glutamylcysteine synthetase
<i>DDR2</i>	3.66	0.51	Multistress response protein
<i>GSH2</i>	2.62	0.08	Glutathione Synthetase
<i>DAK1</i>	2.75	0.28	putative dihydroxyacetone kinase
<i>GRE2</i>	5.67	0.53	induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants
<i>GRE3</i>	2.78	0.33	Aldo-keto reductase
<i>GLR1</i>	3.24	0.23	Glutathione oxidoreductase
<i>GLO1</i>	3.46	0.22	lactoylglutathione lyase (glyoxalase I)
<i>HSF1</i>	4.22	0.51	heat shock transcription factor
<i>HSP104</i>	5.00	0.49	heat shock protein 104
<i>HSP78</i>	8.56	1.16	Mitochondrial heat shock protein 78 kDa
<i>HSP42</i>	8.03	0.63	Similar to HSP26; expression is regulated by stress conditions
<i>SSE2</i>	3.55	0.15	HSP70 family member, highly homologous to Sse1p
<i>YHB1</i>	4.49	0.15	Flavo-hemoglobin, may play a role in the oxidative stress response
<i>TSL1</i>	7.25	0.84	subunit of trehalose-6-phosphate synthase\phosphatase complex
<i>TPS2</i>	4.90	0.28	Trehalose-6-phosphate phosphatase
<i>TPS1</i>	6.66	0.63	56 kD synthase subunit of trehalose-6-phosphate synthase\phosphatase complex
<i>TPS3</i>	3.48	0.18	115 kD regulatory subunit of trehalose-6-phosphate synthase\phosphatase complex
<i>GRX4</i>	3.67	0.43	similarity to Legionella glutaredoxin-like protein
<i>POS5</i>	4.99	0.84	similarity to Utr1p and YEL041w
<i>GPX2</i>	4.11	0.66	Probable glutathione peroxidase
<i>GTT2</i>	16.04	3.66	Glutathione transferase
<i>WHI2</i>	3.05	0.19	Protein required for full activation of the general stress response, possibly through Msn2p dephosphorylation
<i>DOT5</i>	2.27	0.09	Nuclear thiol peroxidase
<i>NTH1</i>	8.43	0.87	Neutral trehalase, required for thermotolerance and may mediate resistance to other cellular stresses
<i>NTH2</i>	4.11	0.30	Neutral trehalase, required for thermotolerance and may mediate resistance to other cellular stresses
<i>ZTA1</i>	9.03	1.22	Homolog to quinone oxidoreductase (E. coli)
<b>DNA Repair/ Replication</b>			
<i>THP1</i>	2.71	0.27	Null mutant is viable and shows transcription-

			associated hyper-recombination and transcription elongation impairment
<i>RAD2</i>	4.21	0.71	homolog of XPG protein, copurifies with TFIIH, mRNA is induced by DNA damage and meiosis
<i>RAD7</i>	3.10	0.42	Nucleotide excision repair protein
<i>RAD26</i>	2.64	0.43	DNA-dependent ATPase, homologous to human Cockayne syndrome B gene
<i>RAD54</i>	4.37	1.58	Required for X-ray damage repair, mitotic recombination, and full meiotic recombination
<i>HSM3</i>	11.76	4.90	Hsm3p may be a member of the yeast MutS homolog family
<i>IMP2'</i>	4.02	0.51	Transcriptional activator involved in maintenance of ion homeostasis and protection against DNA damage caused by bleomycin and other oxidants
<i>DCC1</i>	2.82	0.34	Defective in sister Chromatid Cohesion, DNA replication factor C complex
<i>DDI1</i>	6.00	0.88	DNA damage-inducible
<b>Signal Transduction</b>			
<i>BCY1</i>	3.69	0.47	regulatory subunit of cAMP-dependent protein kinase
<i>TPK2</i>	3.00	0.18	cAMP-dependent protein kinase catalytic subunit
<i>PTC4</i>	3.34	0.68	Probable phosphoprotein phosphatase
<i>PTC5</i>	2.28	0.14	similarity to ser/thr protein phosphatases
<i>NPR1</i>	2.56	0.24	protein kinase homolog
<i>MDG1</i>	2.99	0.24	multicopy suppressor of <i>bem1</i> mutation, may be involved in G-protein mediated signal transduction
<i>PSK1</i>	3.97	0.55	Serine/threonine kinase
<i>TPD3</i>	3.90	0.53	protein phosphatase 2A regulatory subunit A
<i>GPA2</i>	3.25	0.27	alpha subunit of the heterotrimeric G protein, has signaling role in response to nutrients
<i>PPH21</i>	3.81	0.09	serine-threonine protein phosphatase 2A
<i>PDE1</i>	3.74	0.30	3',5'-Cyclic-nucleotide phosphodiesterase, cAMP-mediated signaling
<i>MKK2</i>	3.89	0.57	protein kinase
<i>YPK1</i>	4.20	0.24	Serine/threonine protein kinase with similarity to protein kinase C, is 90% identical to Ypk2p
<i>SLT2</i>	3.91	0.28	putative protein kinase
<i>GPA1</i>	2.42	0.12	Involved in the mating pheromone signal transduction pathway
<i>BEM4</i>	3.69	0.37	Involved in polarity establishment and bud emergence
<i>RRD2</i>	6.52	0.54	Resistant to Rapamycin Deletion 2, protein phosphatase type 2A, regulator, osmotic response
<i>YPL150W</i>	2.39	0.18	YPL150W similarity to ser/thr protein kinases
<i>RIM11</i>	3.61	0.45	Serine/threonine protein kinase, phosphorylates the mitotic activator IME1

<i>CMK2</i>	6.09	0.70	Calmodulin-dependent protein kinase
<i>PPZ1</i>	2.68	0.28	serine-threonine phosphatase Z
<i>CMP2</i>	8.58	1.94	Catalytic A subunit of calcineurin, type 2B protein serine/threonine phosphatase
<i>YAK1</i>	9.11	1.15	Serine-threonine protein kinase
<i>RTG2</i>	2.65	0.27	Protein involved in interorganelle communication between mitochondria, peroxisomes, and nucleus
<i>PTK2</i>	3.15	0.21	Putative serine/threonine protein kinase that enhances spermine uptake
<i>PAM1</i>	2.44	0.13	coiled-coil protein multicopy suppressor of loss of PP2A
<i>PPZ2</i>	10.67	1.15	serine-threonine phosphatase Z
<i>STE50</i>	3.73	0.38	involved in pheromone signal transduction pathway
<i>STE5</i>	2.87	0.35	signal transduction during conjugation with cellular fusion
<i>STE11</i>	3.82	0.43	Ser/Thr protein kinase; MEKK homolog
<i>AFR1</i>	3.59	0.51	coordinates regulation of alpha-factor receptor signalling and induction of morphogenesis
<i>RCK2</i>	2.40	0.04	Serine/threonine protein kinase
<i>VPS34</i>	3.27	0.25	phosphatidylinositol 3-kinase
<i>PPM1</i>	4.31	0.35	carboxy methyl transferase for protein phosphatase 2A catalytic subunit
<i>KIN1</i>	5.02	1.26	Serine/threonine protein kinase
<i>AOS1</i>	2.14	0.03	Nuclear protein that acts as a heterodimer with Uba2p to activate Smt3p (SUMO) before its conjugation to proteins (sumoylation), which may play a role in protein targeting
<i>TAP42</i>	3.22	0.39	42 kDa protein that physically associates with the PP2A and SIT4 protein phosphatase catalytic subunits
<i>YPI1</i>	3.05	0.21	Inhibitor of the type I protein phosphatase Glc7p, which is involved in regulation of a variety of metabolic processes
<b>Chromatin Maintenance</b>			
<i>SIF2</i>	4.35	0.43	Sir4p-Interacting Factor, chromatin silencing at telomere
<i>PHO23</i>	3.28	0.32	involved in transcriptional regulation of PHO5, histone deacetylase activity, chromatin modification
<i>GOD1</i>	2.40	0.11	Component of the NuA4 histone acetyltransferase complex
<b>Transcription</b>			
<i>POB3</i>	3.65	0.21	Binds to catalytic subunit of DNA polymerase alpha
<i>CST6</i>	3.13	0.23	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family

<i>RIM101</i>	2.39	0.06	transcriptional activator required for entry into meiosis
<i>SNF6</i>	2.86	0.19	Involved in global regulation of transcription
<i>SIN4</i>	5.01	2.20	component of RNA polymerase II holoenzyme\mediator complex
<i>TFG2</i>	2.95	0.31	transcription initiation factor TFIIF middle subunit
<i>CAF16</i>	3.47	0.30	ABC ATPase, regulation of transcription, DNA-dependent
<i>AFT2</i>	3.51	0.72	Activator of Iron (Fe) Transcription
<i>CAD1</i>	3.60	0.14	Transcriptional activator involved in resistance to 1,10-phenanthroline
<i>CTK3</i>	2.68	0.22	CTD kinase-I gamma subunit
<i>RTG3</i>	3.79	0.24	bHLH/Zip transcription factor which regulates CIT2 gene expression
<i>YRR1</i>	3.34	0.52	transcription factor
<i>UGA3</i>	21.89	10.78	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
<i>GTS1</i>	6.20	0.51	specific RNA polymerase II transcription factor
<i>HMLALPHA1</i>	2.72	0.22	transcription factor involved in the regulation of the alpha-specific genes
<i>EAF3</i>	2.37	0.12	histone acetylation, regulation of transcription from Pol II promoter
<i>URE2</i>	3.37	0.50	Nitrogen catabolite repression regulator that acts by inhibition of GLN3 in good nitrogen source
<i>NOT5</i>	3.00	0.26	member of the NOT complex, a global negative regulator of transcription
<i>PHO85</i>	3.02	0.32	negative transcriptional regulator, protein kinase homolog
<i>SIP3</i>	2.40	0.21	Interacts with SNF1 protein kinase, transcription cofactor activity
<b>Nucleotide Metabolism</b>			
<i>ADE16</i>	2.77	0.12	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase\IMP cyclohydrolase
<i>ADE1</i>	5.00	0.50	phosphoribosyl amino imidazolesuccinocarboxamide synthetase
<i>ADE2</i>	9.74	3.55	phosphoribosylamino-imidazole-carboxylase
<i>ADE12</i>	4.16	0.35	adenylosuccinate synthetase
<i>ADE17</i>	10.22	0.67	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase\IMP cyclohydrolase
<i>URA10</i>	13.71	10.12	Orotate phosphoribosyltransferase 2
<i>MTD1</i>	4.30	0.31	NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase, purine base biosynthesis
<i>APA2</i>	6.09	0.70	5',5'-P-1,P-4-tetraphosphate phosphorylase II
<i>THI6</i>	2.70	0.17	TMP pyrophosphorylase, hydroxyethylthiazole kinase

---

<b>Degradation</b>			
<i>RPT4</i>	2.90	0.25	component of the 26S proteasome cap subunit
<i>PUP1</i>	2.42	0.32	putative proteasome subunit
<i>PRE2</i>	2.77	0.05	proteasome subunit
<i>PRE8</i>	2.87	0.11	proteasome component Y7
<i>PRB1</i>	3.92	0.28	vacuolar protease B
<i>RPN3</i>	2.66	0.26	component of the regulatory module of the 26S proteasome, homologous to human p58 subunit
<i>RPN6</i>	3.33	0.07	Subunit of the regulatory particle of the proteasome
<i>RPN5</i>	3.07	0.17	Subunit of the regulatory particle of the proteasome
<i>RPT3</i>	3.84	0.19	probable 26S protease subunit and member of the CDC48/PAS1/SEC18 family of ATPases
<i>RPT2</i>	3.38	0.25	Probable 26S protease subunit and member of CDC48/PAS1/SEC18 family of ATPases
<i>DAP2</i>	2.89	0.37	Dipeptidyl aminopeptidase B (DPAP B)
<i>LAP4</i>	17.02	3.78	vacuolar aminopeptidase ysc1
<i>LAP3</i>	2.90	0.20	Aminopeptidase of cysteine protease family
<i>YPS1</i>	2.57	0.21	GPI-anchored aspartic protease
<i>YPS6</i>	5.99	1.78	GPI-anchored aspartic protease
<i>UBI4</i>	9.07	1.47	Ubiquitin
<i>UFD4</i>	3.44	0.39	Ubiquitin Fusion Degradation
<i>UFD1</i>	2.90	0.33	ubiquitin fusion degradation protein
<i>UFD2</i>	3.07	0.31	ubiquitin fusion degradation protein
<i>UBA4</i>	3.00	0.32	moeB, thiF, UBA1
<i>ULA1</i>	4.87	0.28	Required for activation of RUB1together with UBA3
<i>UBC8</i>	4.62	0.45	ubiquitin-conjugating enzyme; ubiquitin-protein ligase
<i>UBP6</i>	2.76	0.26	encodes putative deubiquitinating enzyme
<i>UBP2</i>	3.59	0.75	Ubiquitin-specific protease
<i>DOA1</i>	3.10	0.18	WD repeat protein required for ubiquitin-mediated protein degradation
<i>HUL5</i>	4.34	0.53	similarity to human human E6-associated protein
<i>HUL4</i>	3.74	0.43	similarity to human E6-associated protein
<i>PRE3</i>	2.31	0.10	Subunit of 20S proteasome
<i>PBN1</i>	2.79	0.14	Protease B Non-derepressible
<i>SCL1</i>	2.54	0.15	Proteasome subunit YC7alpha/Y8
<i>NPL4</i>	4.09	0.35	Forms a complex with Cdc48p and Ufd1p that recognizes ubiquitinated proteins in the ER and delivers them to the proteasome for degradation
<i>TUL1</i>	3.19	0.23	Transmembrane Ubiquitin Ligase
<i>RTT101</i>	2.70	0.27	Cullin family member; subunit of a complex containing ubiquitin ligase activity
<i>QRI8</i>	2.30	0.17	ubiquitin conjugating enzyme
<b>Mitochondrial Maintenance</b>			
<i>MASI</i>	3.05	0.22	mitochondrial processing protease subunit

---

<i>MRS4</i>	5.90	0.58	mitochondrial carrier protein, homologous to Mrs3p
<i>MRP8</i>	4.48	0.93	mitochondrial ribosomal protein
<i>OM45</i>	4.89	0.84	45-kDa mitochondrial outer membrane protein
<i>PET54</i>	5.01	0.95	Protein required for splicing of the COX1 intron
<i>PDX1</i>	3.21	0.43	Protein X component of mitochondrial pyruvate dehydrogenase complex
<i>MSP1</i>	2.91	0.16	40 kDa putative membrane-spanning ATPase
<i>STF2</i>	4.62	0.54	ATPase stabilizing factor
<i>COX15</i>	2.26	0.06	cytochrome oxidase assembly factor
<i>MDM34</i>	2.82	0.26	Mitochondrial outer membrane protein
<i>CYC7</i>	3.22	0.29	iso-2-cytochrome c
<i>DIN7</i>	2.50	0.14	Mitochondrial nuclease functioning in DNA repair and replication
<i>COQ4</i>	3.46	0.29	Involved in ubiquinone biosynthesis
<i>IDP1</i>	3.11	0.10	Mitochondrial form of NADP-specific isocitrate dehydrogenase
<i>YHM1</i>	3.40	0.16	high copy suppressor of <i>abf2</i> ; putative mitochondrial carrier protein
<i>NCA2</i>	2.76	0.22	Regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase
<i>YMC1</i>	2.34	0.10	putative mitochondrial carrier protein
<i>ORT1</i>	10.20	0.48	mitochondrial integral membrane protein
<i>PET8</i>	5.63	2.82	Member of family of mitochondrial carrier proteins
<i>FIS1</i>	2.86	0.33	Mitochondrial outer membrane protein involved in membrane fission
<i>COX20</i>	2.65	0.33	Mitochondrial inner membrane protein, required for processing of Cox2p and its assembly into cytochrome c oxidase
<i>MCR1</i>	3.68	0.31	NADH-cytochrome b5 reductase
<i>PET18</i>	2.82	0.29	Protein required for respiratory growth and stability of the mitochondrial genome
<i>CIT1</i>	3.45	0.43	citrate synthase. Nuclear encoded mitochondrial protein.
<i>COQ3</i>	4.22	0.18	O-methyltransferase, catalyzes two different O-methylation steps in Coenzyme Q biosynthesis
<i>ISAI</i>	2.72	0.15	Iron Sulfur Assembly -- mitochondrial matrix
<i>CRD1</i>	4.50	0.27	Cardiolipin synthase; produces cardiolipin, which is an important constituent of mitochondrial membranes
<i>ODC2</i>	3.99	0.65	Mitochondrial inner membrane transporter
<i>YIMI</i>	3.34	0.38	mitochondrial inner membrane protease
<i>SAM50</i>	3.16	0.14	Essential component of the Sorting and Assembly Machinery of the mitochondrial outer membrane
<b>Cell Cycle</b>			
<i>CDC20</i>	2.74	0.22	beta-transducin homolog
<i>CDC53</i>	2.97	0.20	Acts together with Cdc4p and Cdc34p to control the

			G1-S phase transition
<i>CDC10</i>	2.76	0.31	conserved potential GTP-binding protein
<i>CDC28</i>	2.69	0.17	protein kinase catalytic subunit
<i>CDC73</i>	2.58	0.17	Accessory factor associated with RNA polymerase II
<i>PCL5</i>	4.66	0.36	G1/S cyclin (weak)
<i>PCL6</i>	4.53	1.66	PHO85 cyclin
<i>HRT1</i>	2.54	0.21	protein binding, ubiquitin-protein ligase activity, G1/S and G2/M transition of mitotic cell cycle
<i>SGT1</i>	3.54	0.51	subunit of SCF ubiquitin ligase complex; essential regulator of cell
<i>APC9</i>	2.51	0.12	subunit of the anaphase promoting complex (APC)
<i>TFS1</i>	13.54	2.02	Suppressor of cdc25
<i>CAK1</i>	2.51	0.14	Cyclin-dependent kinase-activating kinase
<b>Cell Growth/ Maintenance</b>			
<i>SMY1</i>	2.47	0.13	kinesin heavy chain homolog, but is not believed to act as a kinesin, colocalizes with Myo2p
<i>ARC19</i>	3.06	0.25	Arp Complex Subunit
<i>ARC15</i>	2.73	0.52	Arp Complex Subunit
<i>ARC35</i>	2.95	0.28	Arp Complex Subunit
<i>ARC18</i>	2.66	0.14	Arp2/3 Complex Subunit
<i>ARP6</i>	3.66	0.25	Actin-related protein
<i>TWF1</i>	3.35	0.30	Twinfilin A, an actin monomer sequestering protein
<i>END3</i>	5.00	0.31	Required for endocytosis and organization of the cytoskeleton
<i>ADY3</i>	6.03	1.72	Protein required for spore wall formation
<i>HMRA2</i>	4.35	0.39	mating hormone a2
<i>PEX2</i>	2.99	0.18	Part of the RING finger complex of the peroxisomal import machinery
<i>PEX21</i>	3.29	0.40	Peroxin; Pex18p and Pex21p are partially functionally redundant
<i>PEX14</i>	2.99	0.08	Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins
<i>PEX3</i>	4.00	0.28	48-kDa peroxisomal integral membrane protein
<i>PEX5</i>	7.83	2.84	Essential for import of proteins with SKL-like import signal into peroxisomal matrix
<i>PEX10</i>	3.28	0.46	Part of the RING finger complex of the peroxisomal import machinery
<i>VID30</i>	5.27	1.84	vacuole import and degradation; TOR inhibitor
<i>SHE2</i>	2.27	0.15	Required for mother cell-specific HO expression
<i>BIK1</i>	2.41	0.10	Microtubule-binding protein
<i>NGR1</i>	2.48	0.20	negative growth regulatory protein
<i>CAP1</i>	4.49	0.32	capping - addition of actin subunits
<i>SRP72</i>	2.42	0.16	part of the signal recognition particle (SRP) ribonucleoprotein (RNP) complex that functions in

			protein targeting to the ER membrane
<i>VPS35</i>	2.52	0.37	Protein involved in vacuolar sorting
<i>VPS45</i>	5.97	1.15	Protein of the Sec1p family essential for vacuolar protein sorting
<i>VPS28</i>	2.52	0.15	soluble, hydrophilic protein involved in transport of precursors for soluble vacuolar hydrolases from the late endosome to the vacuole
<i>VPS30</i>	3.76	0.33	Required for sorting and delivery of soluble hydrolases to the vacuole.
<i>VPS17</i>	3.51	0.53	Peripheral membrane protein required for vacuolar protein sorting
<i>VPS33</i>	9.22	3.78	Vacuolar sorting protein essential for vacuolar morphogenesis and function
<i>CAP2</i>	3.43	0.45	capping - addition of actin subunits
<i>SEC6</i>	2.94	0.30	cytoplasmic protein involved in fusion of post-Golgi vesicles with the plasma membrane
<i>SEC18</i>	2.31	0.18	cytoplasmic protein involved in protein transport between ER and Golgi; ATPase
<i>SEC17</i>	2.53	0.09	peripheral membrane protein required for vesicular transport between ER and Golgi
<i>ENT1</i>	5.89	0.54	Epsin-like protein involved in endocytosis and actin patch assembly and functionally redundant with Ent2p
<i>APL2</i>	3.30	0.43	Beta-adaptin, large subunit of the clathrin-associated protein (AP-1) complex
<i>APL4</i>	2.31	0.09	Gamma-adaptin, large subunit of the clathrin-associated protein (AP) complex
<i>RVS161</i>	2.81	0.22	Reduced viability on starvation protein RVS161
<i>RGPI</i>	3.00	0.33	Reduced growth phenotype
<i>ATG19</i>	3.66	0.11	Protein involved in the cytoplasm-to-vacuole targeting pathway and in autophagy
<i>APM1</i>	3.17	0.29	medium subunit of the clathrin-associated protein complex
<i>APG7</i>	3.57	0.30	autophagy
<i>APM2</i>	4.46	0.81	Similar to clathrin coat proteins
<i>SLA2</i>	3.21	0.11	Protein involved in membrane cytoskeleton assembly
<i>TLG2</i>	2.80	0.17	tSNARE that affects a Late Golgi compartment
<i>YAP1801</i>	5.68	0.60	Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
<i>MVP1</i>	4.05	0.37	Protein required for sorting proteins to the vacuole
<i>SCD5</i>	4.23	0.44	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1
<i>VTI1</i>	6.76	0.48	Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p
<i>PEP8</i>	10.18	0.78	Plays a role in delivery of proteins to the vacuole
<i>PEP12</i>	8.52	2.74	integral membrane protein; c-terminal TMD; located in endosome

<i>EXO70</i>	12.07	2.03	component of Exocyst complex; required for exocytosis
<i>ERO1</i>	4.83	1.33	Glycoprotein required for oxidative protein folding in the endoplasmic reticulum
<i>EMP46</i>	7.48	3.53	Integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles
<i>YPT52</i>	2.31	0.09	rab5-like GTPase involved in vacuolar protein sorting and endocytosis
<i>ENT3</i>	4.71	0.51	involved in clathrin recruitment and traffic between the Golgi and endosomes
<i>APS3</i>	6.78	1.19	functions in transport of alkaline phosphatase to the vacuole
<i>TRS120</i>	2.44	0.20	targeting complex (TRAPP) component involved in ER to Golgi membrane traffic
<i>DON1</i>	4.89	1.68	Meiosis-specific component of the spindle pole body
<i>ENT5</i>	2.74	0.12	involved in clathrin recruitment and traffic between the Golgi and endosomes
<i>SAC6</i>	2.82	0.17	fibrin homolog (actin-filament bundling protein)
<i>STP22</i>	3.36	0.49	Ste pseudorevertant; required for vacuolar targeting of temperature-sensitive plasma membrane proteins
<i>GIP1</i>	26.20	6.46	Glc7 interacting protein which is required for spore formation
<i>AUT7</i>	4.36	0.22	Form a protein complex with Aut2p, to mediate attachment of autophagosomes to microtubules
<i>LAS17</i>	3.10	0.14	Actin assembly factor
<i>GSP2</i>	4.59	0.82	GTP binding protein involved in the maintenance of nuclear organization
<i>UFE1</i>	2.60	0.26	endoplasmic reticulum t-SNARE, coprecipitates with Sec20p, Tip1p. and Sec22p
<i>AUT1</i>	5.49	1.21	Protein involved in autophagocytosis during starvation
<i>GLC8</i>	3.94	0.58	Regulates activity of protein phosphatase 1, Glc7p
<i>CRNI</i>	2.44	0.16	Coronin, cortical actin cytoskeletal component
<b>Metabolism</b>			
<i>SDH2</i>	2.62	0.25	Succinate dehydrogenase
<i>AYT1</i>	4.59	1.09	trichothecene 3-O-acetyltransferase activity
<i>UGP1</i>	2.85	0.04	Uridinephosphoglucose pyrophosphorylase
<i>UGA2</i>	4.71	1.35	involved in utilization of GABA as a nitrogen source
<i>RIB5</i>	8.10	0.94	Riboflavin synthase alpha-chain
<i>ARA1</i>	2.63	0.34	D-arabinose dehydrogenase
<i>ADH5</i>	8.71	1.71	alcohol dehydrogenase isoenzyme V
<i>RBK1</i>	3.19	0.14	ribokinase
<i>GLK1</i>	6.57	1.84	Glucokinase
<i>AAD4</i>	8.22	2.18	Hypothetical aryl-alcohol dehydrogenase
<i>QRI1</i>	2.35	0.15	UDP-N-acetylglucosamine pyrophosphorylase
<i>BDH1</i>	3.80	0.70	similarity to alcohol/sorbitol dehydrogenase

<i>DOG2</i>	2.67	0.19	2-deoxyglucose-6-phosphate phosphatase
<i>GPH1</i>	4.26	0.19	Glycogen phosphorylase
<i>GDB1</i>	2.76	0.46	similarity to human 4-alpha-glucanotransferase/amylo-1,6-glucosidase
<i>MAL33</i>	16.19	4.46	Maltose fermentation regulatory protein
<i>GSY1</i>	7.08	0.47	Glycogen synthase
<i>GSY2</i>	7.66	1.17	Glycogen synthase
<i>FBP26</i>	13.03	8.10	Fructose-2,6-bisphosphatase
<i>XKS1</i>	6.10	0.67	xylulokinase
<i>GLC3</i>	6.75	1.01	1,4-glucan-6-(1,4-glucano)-transferase
<i>DPP1</i>	2.54	0.12	Diacylglycerol Pyrophosphate Phosphatase
<i>DPL1</i>	2.55	0.18	dihydrosphingosine phosphate lyase
<i>OSH2</i>	2.58	0.19	Member of an oxysterol-binding protein family with overlapping, redundant functions in sterol metabolism
<i>OSH6</i>	4.03	0.94	Member of an oxysterol-binding protein family with overlapping, redundant functions in sterol metabolism
<i>YDC1</i>	4.09	0.46	Yeast dihydro-ceramidase
<i>PDX3</i>	3.78	0.12	pyridoxine (pyridoxiamine) phosphate oxidase
<i>MCT1</i>	5.19	0.68	malonyl-CoA:ACP transferase
<i>TGL2</i>	9.03	4.02	TriGlyceride Lipase
<i>HEM12</i>	2.44	0.18	uroporphyrinogen decarboxylase
<i>FOL3</i>	3.02	0.35	dihydrofolate synthase activity
<i>SPE1</i>	2.27	0.13	Ornithine decarboxylase
<i>FAD1</i>	3.91	0.34	FAD synthetase
<i>AAD16</i>	17.60	3.59	strong similarity to aryl-alcohol dehydrogenases
<i>RIB1</i>	5.30	0.26	GTP cyclohydrolase II
<i>GDH2</i>	5.79	0.74	NAD-dependent glutamate dehydrogenase
<i>AAT2</i>	2.35	0.13	Cytosolic aspartate aminotransferase
<i>GCV2</i>	5.06	0.39	Glycine decarboxylase complex, glycine synthase, Glycine cleavage system
<i>GAD1</i>	10.75	1.29	glutamate decarboxylase
<i>PGM2</i>	21.42	3.32	Phosphoglucomutase
<i>ALD3</i>	4.40	0.81	Aldehyde Dehydrogenase (NAD(P)+)
<i>ALD2</i>	4.43	1.36	aldehyde dehydrogenase, (NAD(P)+), likely cytosolic
<i>EC11</i>	10.26	3.88	Peroxisomal enoyl-CoA hydratase
<i>ACF2</i>	2.64	0.23	glucan-hydrolyzing protein that acts on 1,3-beta linkages
<i>BNA1</i>	5.76	1.71	3-hydroxyanthranilic acid dioxygenase
<i>PNC1</i>	4.70	0.46	NAD(+) salvage pathway gene
<i>GCV1</i>	10.28	1.27	Required for metabolizing glycine as a nitrogen source
<i>EHT1</i>	4.90	0.36	alcohol acyl transferase
<i>DGA1</i>	2.83	0.32	Diacylglycerol acyltransferase
<i>GCY1</i>	34.79	8.07	Similar to mammalian aldo\keto reductases
<i>ARE2</i>	12.77	3.89	Acyl-CoA cholesterol acyltransferase
<i>CHS1</i>	3.40	0.31	chitin synthase 1
<i>ZWF1</i>	3.38	0.15	Glucose-6-phosphate dehydrogenase

<i>TGL3</i>	2.84	0.20	Triacylglycerol lipase of the lipid particle
<i>SNZ1</i>	19.42	1.60	Snooze: stationary phase-induced gene family, vitamin B6 metabolism
<i>YGL157W</i>	2.57	0.22	Oxidoreductase
<i>YDR531W</i>	2.66	0.10	Pantothenate kinase catalyzes the first committed step in the universal biosynthetic pathway leading to CoA.
<b>Amino Acid Metabolism</b>			
<i>MET17</i>	2.41	0.02	O-Acetylhomoserine-O-Acetylserine Sulfhydrylase
<i>MET1</i>	5.17	1.43	siroheme synthase
<i>MET10</i>	3.81	0.15	subunit of assimilatory sulfite reductase
<i>MET16</i>	6.14	0.76	3 phosphoadenylylsulfate reductase
<i>MET22</i>	4.83	0.49	3 (2 )5 -bisphosphate nucleotidase
<i>MET2</i>	8.65	3.97	homoserine O-trans-acetylase
<i>HIS5</i>	16.67	1.35	histidinol-phosphate aminotransferase
<i>HIS1</i>	5.64	0.40	ATP phosphoribosyltransferase
<i>HIS4</i>	71.51	28.43	histidinol dehydrogenase
<i>HIS7</i>	6.63	0.67	glutamine amidotransferase:cyclase
<i>LYS1</i>	7.91	1.62	saccharopine dehydrogenase
<i>LYS5</i>	3.79	0.19	aminoadipate-semialdehyde dehydrogenase small subunit (alpha-aminoadipate reductase)
<i>LYS21</i>	3.53	0.13	homocitrate synthase
<i>TRP3</i>	5.63	0.45	anthranilate synthase Component II and indole-3-phosphate (multifunctional enzyme)
<i>TRP5</i>	2.24	0.08	tryptophan synthetase
<i>TRP2</i>	3.97	0.67	anthranilate synthase Component I
<i>TRP4</i>	5.37	0.82	anthranilate phosphoribosyl transferase
<i>SER33</i>	2.37	0.11	serine family amino acid biosynthesis
<i>SER1</i>	3.45	0.15	phosphoserine transaminase
<i>ARG2</i>	5.73	1.27	Acetylglutamate Synthase, arginine biosynthesis
<i>ARG3</i>	29.58	7.37	Ornithine carbamoyltransferase
<i>ARG4</i>	18.26	2.39	argininosuccinate lyase
<i>ARG5,6</i>	17.05	1.77	N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate kinase
<i>ARG1</i>	31.08	4.15	arginosuccinate synthetase
<i>ARG8</i>	5.90	1.69	Acetylornithine aminotransferase
<i>LEU4</i>	3.80	0.17	alpha-isopropylmalate synthase
<i>SHM2</i>	3.57	0.19	serine hydroxymethyltransferase
<i>ASN2</i>	3.83	1.33	asparagine synthetase
<i>ARO9</i>	11.77	1.29	aromatic amino acid aminotransferase II
<i>ARO10</i>	21.18	6.95	Phenylpyruvate decarboxylase, leucine catabolism, phenylalanine catabolism
<i>ARO1</i>	3.52	0.30	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids

<i>ARO3</i>	4.48	0.43	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis
<i>ARO4</i>	2.44	0.14	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis
<i>CPA1</i>	5.74	0.31	Carbamoyl phosphate synthetase, arginine specific
<i>CPA2</i>	8.15	0.93	carbamyl phosphate synthetase
<i>ECM40</i>	9.91	0.43	acetylornithine acetyltransferase, arginine biosynthesis
<i>STR3</i>	8.44	1.34	cystathionine beta-lyase activity, methionine biosynthesis
<i>HOM3</i>	4.68	0.56	First step in common pathway for methionine and threonine biosynthesis
<b>RNA Processing</b>			
<i>PAP1</i>	2.78	0.51	poly(A) polymerase, mRNA polyadenylation
<i>NAB2</i>	3.08	0.10	nuclear polyadenylated RNA binding protein
<i>CEG1</i>	3.54	0.25	mRNA guanylyltransferase (mRNA capping enzyme)
<i>RNA14</i>	3.69	0.67	component of the cleavage and polyadenylation factor CF I involved in pre-mRNA 3'-end processing
<i>RSE1</i>	2.74	0.23	RNA splicing and ER to Golgi transport
<i>YSH1</i>	2.17	0.04	subunit of Polyadenylation factor I (PF I)
<i>PRP4</i>	3.12	0.39	Splicing factor, component of the U4/U6-U5 snRNP complex
<i>YTH1</i>	2.97	0.33	cleavage/polyadenylation specificity factor activity
<i>BRR1</i>	2.92	0.10	Protein involved in snRNP biogenesis
<i>EDC2</i>	2.83	0.17	Enhancer of mRNA Decapping
<i>CTL1</i>	4.53	0.61	RNA 5'-triphosphatase
<i>PRP3</i>	3.38	0.56	essential splicing factor
<i>PRP40</i>	3.79	0.54	Splicing component that associates with the yeast U1 small nuclear ribonucleoprotein particle
<i>CLP1</i>	4.07	0.50	CLeavage/Polyadenylation factor IA subunit
<i>RNY1</i>	24.09	1.69	similarity to ribonucleases
<i>PRP42</i>	3.86	0.67	U1 snRNP protein
<i>PAN3</i>	3.74	0.65	subunit of Pab1p-dependent poly(A) ribonuclease
<i>PTI1</i>	12.32	2.91	pre-mRNA cleavage factor activity
<i>PFS2</i>	3.05	0.29	Polyadenylation Factor I subunit 2
<i>NGL2</i>	2.98	0.10	correct 3'-end formation of 5.8S rRNA at site E is strictly dependent on Ngl2p
<i>DCS1</i>	5.03	0.48	Non-essential hydrolase involved in mRNA decapping
<b>Ribosomal Proteins</b>			
<i>RPL15B</i>	2.97	0.35	Ribosomal protein L15B

<b>Transport</b>			
<i>ADP1</i>	2.72	0.07	Active transport ATPase
<i>AGP1</i>	2.79	0.09	broad substrate range permease which transports asparagine and glutamine with intermediate specificity
<i>COT1</i>	2.49	0.15	Vacuolar transporter that mediates zinc transport into the vacuole
<i>YCF1</i>	2.87	0.21	Metal resistance protein with similarity to human cystic fibrosis protein CFTR and multidrug resistance proteins
<i>AVT4</i>	2.69	0.48	Vacuolar transporter
<i>SMF3</i>	6.65	2.94	Putative metal transporter
<i>NUP84</i>	3.76	0.38	Protein with homology to mammalian Nup107p
<i>ENB1</i>	5.61	0.76	Siderophore transporter for enterobactin
<i>FLR1</i>	5.07	1.28	Major Facilitator Transporter
<i>MNR2</i>	3.92	0.30	magnesium ion transporter activity
<i>ATR1</i>	38.53	12.31	Multidrug efflux pump of the major facilitator superfamily
<i>EDE1</i>	2.25	0.10	USO1 homolog ( <i>S. cerevisiae</i> ), cytoskeletal-related transport protein, Ca <sup>++</sup> binding
<i>BPT1</i>	2.36	0.17	bile pigment transporter
<i>PXA2</i>	8.03	2.14	peroxisomal ABC transporter 2
<i>TPN1</i>	4.12	0.45	transport of pyridoxine
<i>PDR16</i>	2.55	0.25	involved in pleiotropic drug resistance by controlling lipids in various cellular compartments
<i>CTR3</i>	2.26	0.08	Copper Transporter
<b>Unknown</b>			
---	3.05	0.42	non-annotated SAGE orf Found reverse in NC_001143 between 638531 and 638722. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	8.84	3.59	non-annotated SAGE orf Found reverse in NC_001143 between 16801 and 17055. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	8.96	3.44	<i>Saccharomyces cerevisiae</i> chromosome IX, complete chromosome sequence. Found forward in NC_001141 between 371963 and 372495.
---	5.47	0.60	<i>Saccharomyces cerevisiae</i> chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 959166 and 960165.
---	5.97	0.86	<i>Saccharomyces cerevisiae</i> chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 960166 and 960596.
---	3.16	0.52	<i>Saccharomyces cerevisiae</i> chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 1051294 and 1051379.
---	2.90	0.50	<i>Saccharomyces cerevisiae</i> chromosome XIII, complete

			chromosome sequence. Found forward in NC_001145 between 356810 and 357809.
<i>COS8</i>	2.43	0.04	Protein with similarity to subtelomerically-encoded proteins
<i>COS6</i>	2.55	0.17	Protein with strong similarity to other subtelomerically-encoded proteins
<i>YGLCDELTA5</i>	2.54	0.27	Ty1 LTR
<i>YERWDELTA18</i>	9.26	3.24	Ty1 LTR
<i>COS4</i>	2.93	0.49	Protein with strong similarity to subtelomerically-encoded proteins
<i>YERCTAU3</i>	16.16	2.15	Ty4 LTR
---	8.92	2.13	<i>Saccharomyces cerevisiae</i> chromosome IV, complete chromosome sequence. Found forward in NC_001136 between 804494 and 805681.
<i>YDLWTAUI</i>	5.66	2.33	Ty4 LTR
<i>COS2</i>	2.65	0.18	Protein with similarity to members of the Cos3\Cos5\Cos1\Cos4\Cos8\Cos6\Cos9 family
<i>COS1</i>	2.82	0.36	Protein with similarity to subtelomerically-encoded proteins
<i>YNLWTAUI</i>	12.19	2.82	Ty4 LTR
<i>YNRCTAU3</i>	6.92	1.33	Ty4 LTR
<i>YMRCTAU3</i>	2.59	0.22	Ty4 LTR
<i>COS3</i>	2.68	0.22	Protein with strong similarity to subtelomerically-encoded proteins
<i>COS3</i>	2.48	0.15	Protein with strong similarity to subtelomerically-encoded proteins
<i>COS5</i>	2.35	0.02	Protein with similarity to members of the Ybr302p\Ycr007p\Cos8p\Cos9p family
---	3.99	0.37	2mic_D_protein 2 micron plasmid D protein
---	2.90	0.30	non-annotated SAGE orf Found reverse in NC_001141 between 355843 and 356004. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	3.23	0.70	non-annotated SAGE orf Found forward in NC_001141 between 385618 and 385767. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	6.94	0.48	non-annotated SAGE orf Found forward in NC_001141 between 144104 and 144268. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	2.86	0.45	non-annotated SAGE orf Found reverse in NC_001140 between 422746 and 422961. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	2.67	0.29	non-annotated SAGE orf Found forward in NC_001139 between 810221 and 810499. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	3.41	0.11	non-annotated SAGE orf Found forward in NC_001139 between 318551 and 318691. See citation

---

---	4.00	0.46	Velculescu, V.E., et al. (1997) Cell 8:243-251 non-annotated SAGE orf Found reverse in NC_001139 between 707915 and 708058. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	13.81	2.16	non-annotated SAGE orf Found forward in NC_001139 between 393563 and 393697. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	6.97	3.27	non-annotated SAGE orf Found forward in NC_001138 between 161226 and 161405. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	2.96	0.33	non-annotated SAGE orf Found reverse in NC_001137 between 407032 and 407214. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	4.01	0.24	non-annotated SAGE orf Found forward in NC_001136 between 733117 and 733251. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	4.43	0.48	non-annotated SAGE orf Found reverse in NC_001136 between 34050 and 34184. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	3.03	0.42	non-annotated SAGE orf Found forward in NC_001136 between 192383 and 192544. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	3.38	0.23	non-annotated SAGE orf Found reverse in NC_001135 between 130174 and 130308. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	10.07	4.12	non-annotated SAGE orf Found reverse in NC_001135 between 172336 and 172488. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	4.65	0.61	non-annotated SAGE orf Found reverse in NC_001134 between 747849 and 748010. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	2.62	0.17	non-annotated SAGE orf Found forward in NC_001134 between 649944 and 650114. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	3.79	0.33	non-annotated SAGE orf Found forward in NC_001148 between 809943 and 810116. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	2.83	0.08	non-annotated SAGE orf Found reverse in NC_001148 between 624294 and 624434. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	2.98	0.45	non-annotated SAGE orf Found forward in NC_001148 between 743828 and 743980. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	3.92	0.38	non-annotated SAGE orf Found forward in NC_001148 between 298197 and 298373. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251

---

---	5.99	0.66	non-annotated SAGE orf Found forward in NC_001147 between 758077 and 758286. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	4.02	0.72	non-annotated SAGE orf Found forward in NC_001147 between 60049 and 60273. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	15.19	1.72	non-annotated SAGE orf Found forward in NC_001147 between 680789 and 680935. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	18.03	7.84	non-annotated SAGE orf Found forward in NC_001146 between 101909 and 102082. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	31.61	5.30	non-annotated SAGE orf Found reverse in NC_001146 between 519600 and 519773. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	3.29	0.17	non-annotated SAGE orf Found reverse in NC_001145 between 623382 and 623516. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	4.71	1.60	non-annotated SAGE orf Found reverse in NC_001145 between 347179 and 347406. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
---	3.52	0.58	non-annotated SAGE orf Found forward in NC_001144 between 390278 and 390421. See citation Velculescu, V.E., et al. (1997) Cell 8:243-251
<i>ASI2</i>	3.72	0.16	Predicted membrane protein
<i>ASI3</i>	4.35	0.48	Putative integral membrane E3 ubiquitin ligase
<i>YOR302W</i>	5.81	0.76	CPA1 leader peptide
<i>IST1</i>	3.72	0.65	Putative translation initiation factor
<i>RIC1</i>	2.64	0.21	Ribosome Control, Ric1p binds to Rgp1p
<i>STS1</i>	4.55	0.36	restores protein transport when overexpressed and rRNA stability to a sec23 mutation
<i>MSC1</i>	8.43	1.12	C-terminal part starting with aa 262 cause growth inhibition when overexpressed
<i>GFD1</i>	3.62	1.39	Great for FULL DEAD box protein activity
<i>NMD4</i>	2.98	0.44	putative Upf1p-interacting protein
<i>TIS11</i>	29.11	6.89	zinc finger containing homolog of mammalian TIS11, glucose repressible gene
<i>SSU1</i>	40.48	7.27	putative sulfite pump
<i>VPS25</i>	3.53	0.28	hypothetical protein
<i>VPS73</i>	3.55	0.63	similarity to glucose transport proteins
<i>VPS60</i>	2.76	0.31	weak similarity to Snf7p
<i>VPS27</i>	4.00	0.48	hydrophilic protein; has cysteine rich putative zinc finger essential for function
<i>RCY1</i>	2.81	0.25	weak similarity to Tor2p
<i>AST2</i>	3.54	0.62	Protein involved in targeting of plasma membrane [H <sup>+</sup> ]ATPase

<i>SNF7</i>	4.08	0.27	involved in derepression of SUC2 in response to glucose limitation
<i>GYP7</i>	9.96	1.83	GTPase-activating protein for yeast Rab family members including
<i>GGA1</i>	12.12	1.93	Golgi-localized, gamma-adaptin homology
<i>MRL1</i>	4.02	0.62	Mannose 6-phosphate Receptor Like
<i>MPD1</i>	4.36	1.14	Disulfide isomerase related protein
<i>BOP2</i>	36.09	19.21	Protein of unknown function, overproduction suppresses a pam1 slv3 double null mutation
<i>SRL3</i>	5.97	0.93	Cytoplasmic protein that, when overexpressed, suppresses the lethality of a rad53 null mutation
<i>ECM4</i>	12.05	3.31	ExtraCellular Mutant
<i>NFU1</i>	3.41	0.23	NifU-like protein B
<i>PTM1</i>	2.79	0.27	Putative membrane protein
<i>RMA1</i>	2.64	0.23	probable foyl-polyglutamate synthetase
<i>SDS22</i>	3.57	0.49	Interacts with and may be a positive regulator of GLC7 which encodes type1 protein phosphatase
<i>STR2</i>	14.66	1.42	similarity to O-succinylhomoserine (thiol)-lyase
<i>CSN12</i>	3.70	0.49	Subunit of the Cop9 signalosome
<i>BET4</i>	3.84	0.96	Geranylgeranyltransferase Type II alpha subunit
<i>SNX4</i>	5.95	0.60	autophagy, transport
<i>PSF2</i>	3.34	0.59	Partner of Sld Five 2
<i>MPM1</i>	3.21	0.25	mitochondrial membrane protein
<i>PRM9</i>	5.21	0.49	Pheromone-regulated protein
<i>PRM5</i>	6.26	0.57	Pheromone-regulated protein
<i>SDP1</i>	8.02	3.37	strong similarity to dual-specificity phosphatase Msg5p
<i>NIT1</i>	10.01	2.62	Nit1 nitrilase
<i>SET5</i>	2.48	0.06	weak similarity to YPL165c
<i>BZZ1</i>	3.21	0.61	SH3 domain, Associated with LAS17p/Bee1p
<i>YSC84</i>	3.59	0.28	SH3 domain in C-terminus
<i>HSE1</i>	7.53	2.09	Has Symptoms of class E vps mutant
<i>LSB1</i>	3.17	0.26	weak similarity to chicken growth factor receptor-binding protein GRB2 homolog
<i>MDR1</i>	2.88	0.22	Mac1-dependent regulator
<i>SDS23</i>	2.77	0.11	homologue of pombe SDS23\; localizes to spindle pole body
<i>PRM8</i>	4.58	0.58	Pheromone-regulated protein
<i>NBP35</i>	3.47	0.28	NBP35 encodes an essential evolutionary conserved protein with homology to bacterial partitioning ATPases
<i>CUE3</i>	5.39	2.08	Protein of unknown function; has a CUE domain that binds ubiquitin
<i>CWC23</i>	3.58	0.75	weak similarity to rat cysteine string protein
<i>YRB30</i>	2.52	0.32	Competes with yeast RanBP1 (Yrb1p) for binding to the GTP-bound form of yeast Ran

<i>YIP5</i>	3.98	0.23	Protein that interacts with Rab GTPases
<i>YIP4</i>	2.58	0.19	Protein that interacts with Rab GTPases
<i>SDT1</i>	5.48	0.62	suppressor of deletion of TFIIS
<i>COG1</i>	5.96	1.19	Conserved Oligomeric Golgi complex 1
<i>GYP8</i>	2.90	0.14	GTPase-activating protein for yeast Rab family members
<i>TMT1</i>	31.90	5.89	Trans-aconitate Methyltransferase 1
<i>SHC1</i>	8.85	1.67	Required for proper maturation of the ascospore
<i>YAT2</i>	14.73	4.68	similarity to carnitine O-acetyltransferase Yat1p
<i>PHM8</i>	5.51	1.41	Protein of unknown function, expression is induced by low phosphate levels and by inactivation of Pho85p
<i>EMI2</i>	4.04	0.34	strong similarity to glucokinase
<i>PEX29</i>	11.58	3.04	weak similarity to YHR150w
<i>SNX41</i>	4.60	0.56	sorting nexins Snx4p, Snx41p, and Snx42p mediate distinct retrieval pathways from endosomes
<i>IVY1</i>	3.57	0.21	Phospholipid-binding protein that interacts with Vpt7p and Vps33p
<i>AMD2</i>	3.17	0.68	putative amidase
<i>NBP2</i>	3.07	0.25	interacts with Nap1, which is involved in histone assembly
<i>DOP1</i>	6.37	3.72	Protein of unknown function, involved in establishing cellular polarity and morphogenesis
<i>MCH1</i>	5.29	0.58	Monocarboxylate Permease Homologue
<i>UGX2</i>	12.06	3.79	protein of unknown function
<i>RRI1</i>	8.05	1.39	subunit of COP9 signalosome (CSN)
<i>RTN2</i>	6.55	2.67	reticulon gene member of the RTNLA (reticulon-like A) subfamily
<i>SYP1</i>	5.25	0.40	Suppressor of Yeast Profilin deletion
<i>GID7</i>	4.78	0.11	Protein of unknown function, involved in proteasome-dependent catabolite inactivation of fructose-1,6-bisphosphatase
<i>LSB5</i>	3.87	0.15	LAs17 Binding protein
<i>BSD2</i>	2.75	0.14	metal homeostasis protein\; putative membrane protein
<i>SDS24</i>	14.92	2.69	strong similarity to hypothetical protein YGL056c
<i>PIN3</i>	2.43	0.09	similarity to chicken growth factor receptor-binding protein GRB2 homolog
<i>ATG21</i>	4.83	0.63	Maturation of pro-AmInopeptidase I (proAPI) defective
<i>ISU1</i>	4.22	0.78	NifU-like protein A
<i>GYP5</i>	14.03	5.56	GTPase-activating protein for Rab family members
<i>ISU2</i>	3.55	0.33	NifU-like protein A
<i>ISN1</i>	3.98	0.25	Inosine 5'monophosphate Specific Nucleotidase
<i>CUE5</i>	3.49	0.29	Protein containing a CUE domain that binds ubiquitin,
<i>EMI5</i>	4.86	0.16	similarity to hypothetical <i>S. pombe</i> protein
<i>MCH4</i>	13.71	2.91	similarity to monocarboxylate transporter proteins
<i>COG5</i>	3.80	0.73	Conserved Oligomeric Golgi complex 5

<i>COG6</i>	3.63	0.48	Conserved Oligomeric Golgi complex 6
<i>NCE103</i>	19.37	9.50	involved in secretion of proteins that lack classical secretory signal sequences
<i>STB1</i>	3.87	1.57	Binds Sin3p in two-hybrid assay and is present in a large protein complex with Sin3p and Stb2p
<i>DIA1</i>	8.37	1.03	Protein of unknown function, involved in invasive and pseudohyphal growth
<i>GID8</i>	5.76	1.13	Protein of unknown function, involved in proteasome-dependent catabolite inactivation of fructose-1,6-bisphosphatase
<i>SHP1</i>	2.56	0.15	isolated as a suppressor of the lethality caused by overexpression of the phosphoprotein phosphatase 1 catalytic subunit encoded by <i>GLC7</i>
<i>AIP1</i>	3.66	0.13	Protein localizes to actin cortical patches
<i>IOC4</i>	3.26	0.38	Iswi One Complex
<i>FMS1</i>	3.91	0.50	Multicopy suppressor of fenpropimorph resistance
<i>ORM2</i>	4.78	0.47	Evolutionarily conserved protein with similarity to Orm1p, required for resistance to agents that induce the unfolded protein response
<i>YLR290C</i>	4.04	0.35	hypothetical protein
<i>YLR257W</i>	4.24	0.27	hypothetical protein
<i>YLR271W</i>	6.50	1.21	hypothetical protein
<i>YLR241W</i>	3.40	0.32	similarity to hypothetical <i>S.pombe</i> protein SPAC2G11.09
<i>SYM1</i>	10.57	3.92	stress-induced yeast MPV17 homolog
<i>YLR252W</i>	8.13	0.71	questionable ORF
<i>YLR225C</i>	5.27	1.05	strong similarity to YDR222w
<i>YLR193C</i>	2.98	0.42	similarity to <i>G.gallus</i> px19 and Msf1p
<i>FMP53</i>	3.71	0.92	The authentic, non-tagged protein was localized to the mitochondria
<i>YLR177W</i>	3.81	0.28	similarity to suppressor protein Psp5p
<i>YLR149C</i>	16.15	3.91	hypothetical protein
<i>YLR152C</i>	4.83	0.33	similarity to YOR3165w and YNL095c
<i>YLR164W</i>	11.83	3.90	strong similarity to Sdh4p
<i>YLR137W</i>	3.52	0.35	hypothetical protein
<i>HRT3</i>	9.50	2.98	hypothetical protein
<i>ALT1</i>	2.36	0.08	putative alanine transaminase
<i>YLL029W</i>	6.89	1.40	similarity to <i>M.jannaschii</i> X-Pro dipeptidase and <i>S.pombe</i> hypothetical protein
<i>YLL023C</i>	2.69	0.05	similarity to hypothetical protein YLR064w
<i>YLL055W</i>	8.89	3.44	similarity to Dal5p
<i>YLL058W</i>	5.14	0.61	similarity to <i>N.crassa</i> O-succinylhomoserine -lyase
<i>STC1</i>	3.03	0.21	Protein of unknown function found in lipid particles
<i>DRE2</i>	2.52	0.23	Protein of unknown function; mutation displays synthetic lethal interaction with the pol3-13 allele of <i>CDC2</i>

<i>PET10</i>	5.14	0.99	Protein of unknown function that co-purifies with lipid particles
<i>FMP46</i>	3.39	0.19	The authentic, non-tagged protein was localized to the mitochondria
<i>YKR018C</i>	2.43	0.22	strong similarity to hypothetical protein YJL082w
<i>YKR023W</i>	6.92	1.74	similarity to <i>S.pombe</i> hypothetical protein SPAC23C4
<i>YKL023W</i>	6.79	1.25	weak similarity to human cyclicin II
<i>YET1</i>	2.72	0.22	Yeast homolog of human BAP31 protein
<i>YKL091C</i>	8.07	0.85	strong similarity to Sec14p
<i>SRX1</i>	8.03	4.13	hypothetical protein
<i>YKL100C</i>	3.37	0.18	similarity to <i>C.elegans</i> hypothetical protein
<i>YKL121W</i>	2.82	0.12	strong similarity to YMR102c
<i>YKL151C</i>	5.61	0.74	similarity to <i>C.elegans</i> hypothetical protein R107.2
<i>YKL206C</i>	7.70	3.06	hypothetical protein
<i>YKL218C</i>	10.36	1.90	Pyridoxal-5'phosphate-dependent enzyme homologous to mouse glial serine racemase
<i>YJR149W</i>	3.88	0.95	similarity to 2-nitropropane dioxygenase
<i>YJR142W</i>	3.88	0.96	similarity to thiamin pyrophosphokinase
<i>YJR111C</i>	4.67	0.32	weak similarity to <i>E.coli</i> colanic acid biosynthesis positive regulator RcsB
<i>ACF4</i>	3.10	0.46	Protein of unknown function, computational analysis of large-scale protein-protein interaction data suggests a possible role in actin cytoskeleton organization
<i>YJR088C</i>	2.43	0.13	weak similarity to <i>S.pombe</i> hypothetical protein SPBC14C8.18c
<i>YJR096W</i>	5.22	0.23	Protein with similarity to aldo-keto reductases
<i>BBC1</i>	4.52	1.23	shows synthetic fitness defect with <i>bni1</i> mutants and associates with the Bee1p-Vrp1p-Myo3/5p complex
<i>YJL017W</i>	11.55	7.06	hypothetical protein
<i>YJL016W</i>	5.01	0.32	weak similarity to hypothetical protein YNL278w and YLR187w
<i>YJL048C</i>	2.42	0.11	similarity to hypothetical protein YBR273c
<i>YJL070C</i>	3.14	0.26	similarity to AMP deaminases
<i>YJL057C</i>	8.56	2.45	probable serine/threonine kinase
<i>YJL084C</i>	7.15	1.30	Cytoplasmic protein of unknown function that interacts with Pcl7p, phosphorylated in vitro
<i>YJL144W</i>	3.66	0.39	hypothetical protein
<i>YJL142C</i>	6.75	0.38	questionable ORF
<i>YJL149W</i>	4.13	0.38	similarity to hypothetical protein YDR131c
<i>YJL213W</i>	4.09	0.59	similarity to <i>Methanobacterium</i> arylalkylphosphatase related protein
<i>FRT2</i>	3.82	0.64	Exhibits physical and genetic interactions with FRT1 and genetic interactions with TCP1
<i>YKL033W-A</i>	2.55	0.28	strong similarity to holacid-halido-hydrolyase
<i>CFD1</i>	2.87	0.19	Highly conserved, putative P-loop ATPase
<i>YIL001W</i>	3.04	0.68	similarity to <i>S.pombe</i> hypothetical protein, weak

			similarity to human ankyrin
<i>YIR003W</i>	3.83	0.20	weak similarity to mammalian neurofilament triplet H proteins
<i>YIR007W</i>	2.38	0.28	hypothetical protein
<i>YIL056W</i>	4.91	0.87	similarity to YER064c
<i>YIL055C</i>	4.00	0.25	hypothetical protein
<i>YIL087C</i>	3.32	0.41	hypothetical protein
<i>YIL077C</i>	2.67	0.12	hypothetical protein
<i>YIL165C</i>	7.12	1.19	putative pseudogene
<i>YIL167W</i>	24.13	7.57	serine dehydratase
<i>YHR209W</i>	12.57	5.31	Putative S-adenosylmethionine-dependent methyltransferase of the seven beta-strand family
<i>FMP34</i>	5.05	0.79	The authentic, non-tagged protein was localized to the mitochondria
<i>YHR162W</i>	3.89	0.48	strong similarity to hypothetical protein YGR243w
<i>YHR122W</i>	3.98	0.49	similarity to hypothetical <i>C. elegans</i> protein F45G2.a
<i>YHR087W</i>	12.03	2.18	hypothetical protein
<i>YHR029C</i>	7.52	1.81	Thymidylate synthase (putative\); weak)
<i>FMP12</i>	59.55	32.93	The authentic, non-tagged protein was localized to the mitochondria
<i>VMR1</i>	5.36	0.74	Protein of unknown function, member of the ATP-binding cassette (ABC) family
<i>YGR266W</i>	3.06	0.38	hypothetical protein
<i>HUA1</i>	3.68	0.62	weak similarity to <i>S.pombe</i> hypothetical protein SPAC17A5
<i>YGR237C</i>	3.22	0.30	weak similarity to YOR019w
<i>SOL4</i>	9.68	0.93	similar to SOL3, 6-phosphogluconolactonase activity
<i>YGR250C</i>	3.47	0.40	weak similarity to human cleavage stimulation factor 64K chain
<i>YGR223C</i>	3.10	0.42	weak similarity to hypothetical protein YFR021w
<i>YGR149W</i>	3.70	0.28	hypothetical protein
<i>RTS3</i>	27.72	6.62	hypothetical protein
<i>YGR127W</i>	5.51	0.51	weak similarity to mouse T10 protein
<i>RPN14</i>	4.38	0.58	weak similarity to Tup1p
<i>YGL059W</i>	12.84	2.11	similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
<i>YGL117W</i>	23.49	2.43	hypothetical protein
<i>YGL114W</i>	4.52	0.22	weak similarity to <i>H.influenzae</i> permease
<i>YGL196W</i>	3.14	0.39	hypothetical protein
<i>YGL226W</i>	2.71	0.26	similarity to <i>N.crassa</i> cytochrome-c oxidase chain V
<i>YGL250W</i>	8.43	4.03	hypothetical protein
<i>YFR055W</i>	2.66	0.18	strong similarity to beta-cystathionases
<i>YFL043C</i>	8.90	3.48	hypothetical protein
<i>ERJ5</i>	2.86	0.09	Endoplasmic reticulum protein that may function as a cochaperone
<i>YFR017C</i>	9.34	1.12	hypothetical protein

<i>YER067W</i>	12.07	0.88	strong similarity to hypothetical protein YIL057c
<i>YER079W</i>	3.32	0.43	hypothetical protein
<i>YER053C</i>	4.55	0.56	sequence similarity to mitochondrial phosphate transporters
<i>YEL020C</i>	2.55	0.33	similarity to <i>O. formigenes</i> oxalyl-CoA decarboxylase
<i>EDC3</i>	3.13	0.34	weak similarity to Spa2p
<i>HSP31</i>	6.05	1.15	Protein crystal structure indicates structural and functional homology to <i>E. coli</i> Hsp31
<i>YDR411C</i>	3.04	0.17	weak similarity to Der1p
<i>YDR391C</i>	3.96	0.36	strong similarity to hypothetical protein YOR013w
<i>YDR333C</i>	3.01	0.09	similarity to hypothetical <i>S. pombe</i> protein
<i>YDR330W</i>	2.31	0.08	similarity to hypothetical <i>S. pombe</i> protein
<i>YDR306C</i>	2.61	0.18	weak similarity to <i>S. pombe</i> hypothetical protein SPAC6F6
<i>YDR089W</i>	3.67	0.23	weak similarity to <i>Streptococcus</i> transposase
<i>TVP15</i>	2.76	0.21	similarity to <i>Dictyostelium</i> development-specific membrane protein
<i>YDR067C</i>	7.28	1.67	similarity to YNL099c
<i>YDR003W</i>	6.86	0.75	strong similarity to hypothetical protein YBR005w
<i>YDL025C</i>	24.22	11.93	ser/thr protein kinase of the DEAD/DEAH box family
<i>YDL010W</i>	3.66	0.19	similarity to hypothetical protein YBR014c and glutaredoxins
<i>YDL091C</i>	10.19	4.53	weak similarity to mouse FAF1 protein
<i>YDL072C</i>	3.65	0.16	weak similarity to hypothetical protein YMR040w
<i>YDL110C</i>	4.32	0.52	hypothetical protein
<i>YDL099W</i>	2.41	0.11	weak similarity to myosin heavy chain proteins
<i>YDL124W</i>	12.71	2.66	similarity to aldose reductases
<i>IWR1</i>	10.74	1.69	interacts with RNA polymerase II
<i>SCM3</i>	2.88	0.33	suppressor of chromosome missegregation
<i>YCL042W</i>	9.90	5.87	questionable ORF
<i>YBR293W</i>	2.58	0.17	Probable multidrug resistance protein
<i>YBR056w-a</i>	14.76	8.16	identified by SAGE
<i>YBR085c-a</i>	9.67	1.64	hypothetical protein
<i>FMP21</i>	4.17	0.44	The authentic, non-tagged protein was localized to the mitochondria
<i>YBR273C</i>	3.81	0.54	similarity to hypothetical protein YJL048c
<i>YBR280C</i>	3.04	0.18	hypothetical protein
<i>YBR241C</i>	3.17	0.26	Probable sugar transport protein
<i>YBR255W</i>	4.91	1.98	hypothetical protein
<i>YBR204C</i>	3.19	0.26	Probable serine-active lipase, peroxisomal
<i>YBR147W</i>	8.94	1.24	strong similarity to hypothetical protein YOL092w
<i>YBR137W</i>	2.84	0.16	hypothetical protein
<i>YBR139W</i>	3.47	0.16	Probable serine-type carboxypeptidase
<i>YBR099C</i>	2.84	0.41	weak similarity to <i>T. brucei</i> mitochondrion hypothetical protein 6
<i>YBR043C</i>	5.79	0.56	similarity to benomyl/methotrexate resistance protein

<i>FMP23</i>	18.57	2.62	The authentic, non-tagged protein was localized to the mitochondria
<i>YBR053C</i>	5.63	0.60	similarity to rat regucalcin
<i>YBR056W</i>	5.11	0.24	Homolog to glucan-1,3--glucosidase
<i>YBL060W</i>	8.25	1.33	hypothetical protein
<i>SCS22</i>	2.29	0.09	weak similarity to SCS2
<i>YBL086C</i>	5.56	0.73	involved in sugar metabolism
<i>YPR196W</i>	3.61	0.17	strong similarity to regulatory protein Mal63p
<i>YPR148C</i>	3.19	0.24	hypothetical protein
<i>YPR158W</i>	3.03	0.37	similarity to YGR142w
<i>YPR085C</i>	3.91	0.50	hypothetical protein
<i>LSP1</i>	2.74	0.16	strong similarity to YGR086c
<i>MUK1</i>	5.76	1.84	weak similarity to Vps9p
<i>YPL110C</i>	2.92	0.21	similarity to C.elegans hypothetical protein, weak similarity to Pho81p
<i>YPL206C</i>	4.00	0.68	weak similarity to glycerophosphoryl diester phosphodiesterases
<i>YPL229W</i>	7.02	3.01	weak similarity to YMR181c
<i>ICY2</i>	22.27	2.14	Protein that interacts with the cytoskeleton and is involved in chromatin organization and nuclear transport
<i>YPL264C</i>	4.23	0.46	strong similarity to YMR253c
<i>YPL260W</i>	2.75	0.10	hypothetical protein
<i>YOR289W</i>	8.74	1.63	similarity to C.elegans hypothetical protein
<i>YOR220W</i>	11.51	2.31	hypothetical protein
<i>YOR223W</i>	3.69	0.22	protein of unknown function
<i>YOR227W</i>	8.00	3.68	similarity to microtubule-interacting protein Mhp1p
<i>DCS2</i>	29.62	16.28	protein containing a HIT (histidine triad) motif
<i>YOR121C</i>	14.63	2.54	questionable ORF
<i>RUP1</i>	3.12	0.53	hypothetical protein
<i>YVCI</i>	2.12	0.05	weak similarity to human calcium influx channel
<i>YOR052C</i>	2.60	0.15	hypothetical protein
<i>YOR059C</i>	3.15	0.24	weak similarity to YGL144c
<i>YOR019W</i>	6.08	2.42	similarity to YDR474c
<i>YOL008W</i>	11.44	9.05	hypothetical protein
<i>YOL032W</i>	5.23	0.39	hypothetical protein
<i>YOL048C</i>	4.30	0.26	similarity to YAL018c and YOL047c
<i>YOL083W</i>	2.83	0.22	similarity to YOL082w
<i>YOL073C</i>	3.38	0.81	hypothetical protein
<i>YOL153C</i>	24.16	6.70	strong similarity to Cps1p
<i>YNR064C</i>	13.31	1.46	similarity to R.capsulatus 1-chloroalkane halidohydrolase
<i>YNR068C</i>	92.63	38.38	similarity to Bul1p
<i>YNR034w-a</i>	8.45	0.39	hypothetical protein
<i>YNL011C</i>	2.71	0.21	similarity to hypothetical A. thaliana protein T14G11.21

<i>YNL092W</i>	10.35	3.08	similarity to hypothetical <i>C. elegans</i> proteins Y48E1C.2 and Y48E1C.c
<i>YNL100W</i>	2.53	0.12	hypothetical protein
<i>YNL134C</i>	16.69	5.16	similarity to <i>C.carbonum</i> toxD gene
<i>YNL129W</i>	3.41	0.38	weak similarity to <i>M.pneumoniae</i> uridine kinase udk
<i>YNL157W</i>	3.23	0.24	weak similarity to <i>S.pombe</i> hypothetical protein SPAC10F6
<i>IES2</i>	3.56	0.31	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions
<i>YNL274C</i>	6.93	1.27	similarity to glycerate- and formate-dehydrogenases
<i>YNL260C</i>	12.19	5.24	hypothetical protein
<i>YNL305C</i>	5.47	0.43	similarity to C-term. of <i>A.nidulans</i> regulatory protein
<i>YNL335W</i>	1307.71	135.30	similarity to <i>M.verrucaria</i> cyanamide hydratase, identical to hypothetical protein YFL061w
<i>YMR258C</i>	3.97	0.53	hypothetical protein
<i>YMR262W</i>	7.80	1.24	similarity to <i>S.pombe</i> scn1 protein
<i>YMR237W</i>	2.98	0.18	similarity to CHS6 protein
<i>SPG5</i>	2.44	0.11	Protein required for survival at high temperature during stationary phase
<i>YMR196W</i>	9.21	2.24	hypothetical protein
<i>YMR210W</i>	4.91	0.52	similarity to <i>P.glauca</i> late embryogenesis abundant protein and YBR177c and YPL095c
<i>YMR184W</i>	3.24	0.05	hypothetical protein
<i>YMR160W</i>	2.44	0.16	weak similarity to fruit fly ecdysone-inducible protein
<i>YMR090W</i>	10.48	3.53	strong similarity to <i>B. subtilis</i> conserved hypothetical protein yhfK
<i>YMR103C</i>	4.68	0.53	hypothetical protein
<i>YMR110C</i>	4.61	0.41	similarity to aldehyde dehydrogenase
<i>TVP18</i>	2.45	0.32	Tlg2-Vesicle Protein of 18 kDa
<i>YMR087W</i>	6.38	1.01	hypothetical protein
<i>YMR052C-A</i>	11.30	2.70	questionable ORF
<i>YMR027W</i>	3.00	0.22	High level expression reduced Ty3 Transposition
<i>NAB6</i>	3.82	0.13	similarity to YPL184c
<i>YML117W-A</i>	4.40	0.24	questionable ORF
<i>YML131W</i>	3.30	0.50	similarity to human leukotriene b4 12-hydroxydehydrogenase
<i>FMP27</i>	3.49	0.87	The authentic, non-tagged protein was localized to the mitochondria
<i>YLR414C</i>	2.87	0.29	weak similarity to YLR413w
<i>YLR387C</i>	3.67	0.18	similarity to YBR267w
<i>YLR345W</i>	6.64	0.51	similarity to Pfk26p and other 6-phosphofructo-2-kinases
<i>YLR356W</i>	8.06	3.45	similarity to SCM4 protein
<i>YLR327C</i>	5.24	1.04	strong similarity to Stf2p