

**Up regulated genes in BER-defective cells following 0.4mM H<sub>2</sub>O<sub>2</sub> exposure for 30 minutes**

<b>Gene name</b>	<b>Average Fold change</b>	<b>S.E.M.</b>	<b>Description</b>
<b>Cell Stress</b>			
<i>GTT2</i>	29.59	4.14	Glutathione transferase
<i>GPX1</i>	4.13	0.81	strong similarity to glutathione peroxidase
<i>GSH1</i>	3.51	0.37	gamma-glutamylcysteine synthetase
<i>GTT1</i>	3.04	0.16	Glutathione transferase
<i>GRE3</i>	2.38	0.13	Aldo-keto reductase
<i>TRR2</i>	2.71	0.35	Thioredoxin reductase
<i>SOD2</i>	6.02	0.46	Manganese-containing superoxide dismutase
<i>CTT1</i>	16.34	0.83	cytoplasmic catalase T
<i>SSA4</i>	5.86	0.92	member of 70 kDa heat shock protein family
<i>HSP12</i>	9.59	3.89	12 kDa heat shock protein
<i>TSA2</i>	13.82	3.35	strong similarity to thiol-specific antioxidant proteins
<i>CTA1</i>	16.49	4.69	catalase A
<i>HSP78</i>	3.34	0.19	Mitochondrial heat shock protein 78 kDa
<i>HSP42</i>	3.87	0.59	Similar to HSP26\; expression is regulated by stress conditions
<i>HSP30</i>	7.09	1.02	Protein induced by heat shock, ethanol treatment, and entry into stationary phase\; located in plasma membrane
<i>GPX2</i>	6.94	0.62	Probable glutathione peroxidase
<i>SSE2</i>	4.42	0.62	HSP70 family member, highly homologous to Sse1p
<i>YBR070C</i>	2.30	0.07	osmotolerance protein
<i>HSP26</i>	6.88	0.73	heat shock protein 26
<i>ZTA1</i>	4.79	0.41	Homolog to quinone oxidoreductase (E. coli)
<i>YBL064C</i>	6.05	0.50	Homolog to thiol-specific antioxidant
<i>ATH1</i>	4.18	0.22	null mutant is viable\; increased tolerance to dehydration, freezing, and toxic levels of ethanol
<i>HAL1</i>	2.50	0.17	Protein induced by NaCl, KCl, or sorbitol; involved in halotolerance tolerance to salt
<i>POS5</i>	2.60	0.19	involved in oxidative stress interacts with gts1(tf)
<i>OXR1</i>	4.47	0.39	OXidation Resistance
<i>ROD1</i>	3.41	0.31	Resistance to o-dinitrobenzene, calcium, and zinc
<i>GRE2</i>	6.52	0.63	induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants
<i>DDR2</i>	8.38	2.09	Multistress response protein
<i>DAK1</i>	2.41	0.08	putative dihydroxyacetone kinase
<b>DNA Repair/ Replication</b>			

<i>RAD4</i>	2.88	0.27	Nucleotide excision repair protein
<i>MAG1</i>	2.14	0.08	3-methyladenine DNA glycosylase
<i>DDI1</i>	2.84	0.17	DNA Damage Inducible
<i>MHR1</i>	2.47	0.15	Involved in mitochondrial homologous DNA recombination
<i>RAD28</i>	2.54	0.18	Protein involved in the same pathway as Rad26p
<i>DUN1</i>	2.18	0.04	protein kinase
<i>HSM3</i>	2.57	0.04	Hsm3p may be a member of the yeast MutS homolog family
<i>PHR1</i>	3.85	0.13	photolyase
<i>NTG2</i>	2.78	0.26	Endonuclease III-like glycosylase 2
<b>Signal Transduction</b>			
<i>IKS1</i>	6.09	0.05	probable serine\threonine kinase
<i>YAK1</i>	4.41	0.62	Serine-threonine protein kinase
<i>TPK1</i>	4.38	0.34	putative catalytic subunit of cAMP-dependent protein kinase
<i>PIG2</i>	2.56	0.21	protein phosphatase regulator, interacts with gsy2
<i>KSS1</i>	2.87	0.57	MAP protein kinase homolog involved in pheromone signal transduction
<i>APG1</i>	2.36	0.11	Protein kinase
<i>PDE1</i>	2.47	0.04	3',5'-Cyclic-nucleotide phosphodiesterase, low affinity, cAMP-mediated signaling
<i>CMK1</i>	3.33	0.40	Calmodulin-dependent protein kinase
<i>RIM15</i>	2.22	0.11	Trehalose-associated protein kinase related to <i>S. pombe cek1+</i> , involved in meiosis
<i>GIP2</i>	4.12	0.51	Glc7-interacting protein\; shares homology with PIG2\; protein phosphatase regulator
<i>GPA2</i>	2.21	0.10	homologous to mammalian G proteins; potential role in regulation of cAMP levels
<i>PPM1</i>	3.16	0.18	carboxy methyl transferase for protein phosphatase 2A catalytic subunit
<i>PPZ2</i>	3.02	0.21	serine-threonine phosphatase Z
<i>KIN1</i>	2.41	0.10	Serine\threonine protein kinase
<i>PPH21</i>	2.52	0.05	serine-threonine protein phosphatase 2A
<i>PTP1</i>	2.52	0.16	phosphotyrosine-specific protein phosphatase
<i>KIN82</i>	3.13	0.01	Putative serine\threonine protein kinase, similar to cyclic nucleotide-dependent protein kinase and protein kinase C
<i>FRM2</i>	14.56	2.02	Protein involved in the integration of lipid signaling pathways with cellular homeostasis
<i>GIP1</i>	28.58	19.20	Glc7-interacting protein, Developmentally-regulated protein phosphatase 1
<i>PTC3</i>	2.55	0.10	protein phosphatase type 2C
<i>SMK1</i>	25.83	1.95	MAP kinase

<i>BRO1</i>	2.80	0.22	BCK1-like resistance to osmotic shock, signal transduction
<i>TPK2</i>	2.82	0.06	cAMP-dependent protein kinase catalytic subunit
<i>GSP2</i>	3.32	0.81	maintenance of nuclear organization; homologous to mammalian Ran, small nuclear GTPase of ras superfamily
<i>PKH2</i>	4.34	1.11	Ser/Thr protein kinase
<i>MDG1</i>	3.66	0.41	multicopy suppressor of <i>bem1</i> mutation, may be involved in G-protein mediated signal transduction
<i>GLC8</i>	3.83	0.24	Regulates activity of protein phosphatase 1, Glc7p, which is involved in proper chromosome segregation
<i>RIM11</i>	2.54	0.11	Serine/threonine protein kinase, phosphorylates the mitotic activator IME1
<i>CMP2</i>	3.18	0.18	Catalytic A subunit of calcineurin, type 2B protein serine/threonine phosphatase
<i>STE11</i>	2.52	0.24	Ser/Thr protein kinase; MEKK homolog
<b>Chromatin Modification</b>			
<i>EAF3</i>	2.09	0.02	Esa1p-Associated Factor Esa1 is involved in chromatin modification
<b>Transcription</b>			
<i>CAF17</i>	5.25	0.65	CCR4 associated factor
<i>MET28</i>	4.77	1.06	Transcriptional activator of sulfur amino acid metabolism
<i>YAP5</i>	2.08	0.02	bZIP protein; transcription factor
<i>CST6</i>	2.70	0.15	Chromosome STability; contains an ATF/CREB-like bZIP domain;transcriptional activator
<i>IMP2</i>	3.36	0.57	transcription factor
<i>TFG2</i>	2.82	0.48	transcription initiation factor TFIIF middle subunit
<i>SIP2</i>	2.79	0.22	Member of family of proteins, that interact with Snf1p and Snf4p, involved in the response to glucose starvation
<i>GTS1</i>	5.02	0.56	specific RNA polymerase II transcription factor
<i>SPT3</i>	2.26	0.08	transcription factor, member of the histone acetyltransferase SAGA complex
<i>CAD1</i>	4.21	0.29	Transcriptional activator involved in resistance to 1,10-phenanthroline
<i>NRG1</i>	5.08	0.92	Suppressor of SNf, involved in regulation of glucose repression
<i>PHO2</i>	3.32	0.29	Homeobox-domain containing protein which is a positive regulator of PHO5 and other genes
<i>MED2</i>	2.31	0.16	RNA Polymerase II transcriptional regulation mediator

<i>UGA3</i>	2.49	0.31	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type
<i>RDS1</i>	2.54	0.21	Transcription regulator
<i>ROX1</i>	3.31	0.53	site-specific DNA binding protein, repressor
<i>AFT2</i>	4.57	0.30	similarity to cell size regulation protein Rcs1p, Activator of Iron Fe Transcription
<i>HAP5</i>	2.40	0.03	Component, along with Hap2p and Hap3p, of CCAAT-binding transcription factor
<i>YRR1</i>	3.67	0.54	transcription factor
<i>TFC7</i>	2.55	0.22	TFIIIC (transcription initiation factor) subunit, 55 kDa
<i>CIN5</i>	3.46	0.14	bZIP protein, can activate transcription from a promoter containing a Yap recognition site
<i>YAP7</i>	2.54	0.22	bZIP protein
<i>MSN1</i>	2.50	0.06	43 kDa protein, transcriptional activator
<i>YAP1</i>	4.34	0.08	jun-like transcription factor
<b>Nucleotide Metabolism</b>			
<i>URA8</i>	2.38	0.10	CTP synthase
<i>CPD1</i>	4.57	1.27	2',3'-cyclic nucleotide 3'-phosphodiesterase, similar to cyclic phosphodiesterases from <i>Arabidopsis</i> and wheat
<i>NMA2</i>	4.78	0.82	nicotinamide adenine dinucleotide metabolism
<i>APA2</i>	2.62	0.35	5',5'-P-1,P-4-tetraphosphate phosphorylase II, ATP adenylyltransferase
<b>Degradation</b>			
<i>PCD1</i>	3.01	0.41	peroxisomal nudix hydrolase active towards coenzyme A and its derivatives
<i>UBI4</i>	3.85	0.38	ubiquitin
<i>UBP11</i>	3.36	0.53	Ubiquitin-specific protease
<i>LAP4</i>	7.13	0.80	vacuolar aminopeptidase ysc1
<i>HUL4</i>	2.91	0.30	ubiquitin-protein ligase E3
<i>YPS6</i>	3.77	0.78	GPI-anchored aspartic protease
<i>YPS5</i>	3.69	0.45	GPI-anchored aspartic protease
<i>UBC8</i>	4.50	0.05	ubiquitin-conjugating enzyme; ubiquitin-protein ligase
<i>DOA4</i>	3.71	0.36	ubiquitin isopeptidase
<i>PBN1</i>	2.35	0.08	Protease B Non-derepressible
<i>ULA1</i>	3.77	0.62	Required for activation of RUB1 (ubiquitin-like protein) together with UBA3.
<i>ASI3</i>	2.45	0.23	ubiquitin-protein ligase
<i>UBP15</i>	2.29	0.02	encodes putative deubiquitinating enzyme
<i>PAI3</i>	3.81	0.23	Cytoplasmic inhibitor of proteinase Pep4p

<b>Mitochondrial Maintenance</b>			
<i>MSF1</i>	2.70	0.43	probably involved in intramitochondrial protein sorting
<i>MAS1</i>	3.08	0.23	mitochondrial processing protease subunit
<i>MMM1</i>	2.17	0.08	mitochondrial outer membrane protein
<i>CCP1</i>	7.90	0.79	Cytochrome-c peroxidase
<i>MRS4</i>	5.75	0.26	mitochondrial carrier protein, highly homologous to Mrs3p
<i>NFU1</i>	2.96	0.29	NifU-like protein B, iron homeostasis, mitochondrial matrix
<i>CYT2</i>	3.43	0.28	cytochrome c1 heme lyase
<i>CBT1</i>	2.39	0.23	Subunit of complex involved in processing of the 3' end of cytochrome b pre-mRNA
<i>CYC1</i>	9.11	2.31	iso-1-cytochrome c
<i>MPM1</i>	4.58	0.37	mitochondrial membrane protein
<i>FIS1</i>	2.19	0.03	Involved in mitochondrial division
<i>FMC1</i>	2.69	0.21	Formation of Mitochondrial Cytochromes 1
<i>OM45</i>	8.21	0.42	45-kDa mitochondrial outer membrane protein
<i>GUT2</i>	3.92	0.76	glycerol-3-phosphate dehydrogenase, mitochondrial
<i>SHY1</i>	3.16	0.30	mitochondrial protein with homology to the mammalian SURF-1 gene
<i>STF2</i>	2.54	0.26	ATPase stabilizing factor, ATP synthesis coupled proton transport
<i>CYC7</i>	4.96	1.08	iso-2-cytochrome c
<i>PET117</i>	2.33	0.17	cytochrome c oxidase assembly factor
<i>RSM28</i>	2.24	0.05	Regulator of COX2 Translation
<i>MRPL28</i>	2.67	0.37	Mitochondrial ribosomal protein MRPL28 (YmL28)
<i>COQ4</i>	2.75	0.30	Involved in ubiquinone biosynthesis
<i>COX20</i>	2.54	0.21	20th gene involved in cytochrome oxidase activity
<i>RSM10</i>	2.53	0.21	mitochondrial ribosome small subunit component
<i>STF1</i>	3.43	0.48	ATPase stabilizing factor
<i>MSS18</i>	2.60	0.09	Protein involved in splicing intron a15beta of COX1
<i>ISA2</i>	2.46	0.35	Iron Sulfur Assembly -- IscA/NifA homolog
<i>MSF1</i>	2.64	0.15	alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
<i>MRP51</i>	2.32	0.08	Component of small subunit of the mitochondrial ribosome
<i>MMT2</i>	2.33	0.14	Protein involved in mitochondrial iron accumulation
<i>ISU2</i>	7.88	0.25	Iron-sulfur cluster nifU-like protein
<i>GLO4</i>	3.91	1.18	Mitochondrial glyoxylase-II
<i>COQ3</i>	2.90	0.12	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
<i>MMT1</i>	2.91	0.60	Protein involved in mitochondrial iron accumulation
<i>CYB2</i>	2.36	0.09	Cytochrome b2 [L--lactate cytochrome-c oxidoreductase]

<i>RPM2</i>	2.69	0.22	subunit of mitochondrial RNase P
<b>Cell Cycle</b>			
<i>APC9</i>	2.57	0.25	subunit of the anaphase promoting complex (APC)
<i>SAP4</i>	3.08	0.27	SAP4 associates with the SIT4 protein phosphatase, G1/S transition of mitotic cell cycle
<i>PCL6</i>	2.52	0.28	PHO85 cyclin
<i>SSN8</i>	2.43	0.19	C-type cyclin associated with the Ssn3p cyclin-dependent kinase
<b>Cell Growth/ Maintenance</b>			
<i>ENT2</i>	2.28	0.06	cytoskeletal adaptor
<i>ACF2</i>	2.35	0.08	Identified as an activity necessary for actin polymerization in permeabilized cells
<i>NYV1</i>	2.35	0.04	vacuolar v-SNARE
<i>KTR2</i>	3.11	0.13	putative mannosyltransferase\; type 2 membrane protein
<i>DID2</i>	2.35	0.11	RAD52 Inhibitor (Fifty Two Inhibitor), protein-vacuolar targeting
<i>DID4</i>	2.27	0.08	Golgi retention
<i>YPT52</i>	2.39	0.04	rab5-like GTPase involved in vacuolar protein sorting and endocytosis
<i>CAP1</i>	2.17	0.03	alpha subunit of capping protein
<i>MYO3</i>	2.47	0.27	myosin I
<i>PIR3</i>	2.97	0.28	Protein containing tandem internal repeats, cell wall organization and biogenesis
<i>ENT3</i>	2.47	0.20	cytoskeletal adaptor
<i>APL1</i>	2.25	0.10	beta-adaptin, large subunit of the clathrin-associated protein complex
<i>EXO70</i>	2.17	0.07	70 kD component of the Exocyst complex\; required for exocytosis
<i>PEP8</i>	3.74	0.41	Plays a role in delivery of proteins to the vacuole
<i>PRM9</i>	4.63	0.43	membrane protein, phermone regulated protein
<i>VPS8</i>	2.11	0.07	Vps8p is a membrane-associated hydrophilic protein
<i>VID28</i>	3.36	0.23	Vacuole import and degradation
<i>YAP1801</i>	2.41	0.05	Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
<i>APG7</i>	4.02	0.13	autophagy
<i>SPS100</i>	3.09	0.55	sporulation-specific wall maturation protein
<i>APM2</i>	2.17	0.04	Similiar to clathrin coat proteins
<i>TWF1</i>	2.54	0.09	Twinfilin A, an actin monomer sequestering protein
<i>PRM8</i>	4.51	0.11	phermone regulated protein
<i>PEX14</i>	2.32	0.03	Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins
<i>AMS1</i>	4.27	0.27	vacuolar alpha mannosidase

<i>AST2</i>	2.38	0.12	Protein involved in targeting of plasma membrane [H <sup>+</sup> ]ATPase
<i>VID30</i>	3.50	0.39	vacuole import and degradation VID, TOR inhibitor
<i>GGA1</i>	6.41	0.03	Golgi-localized, gamma-adaptin homology, Arf-binding
<i>PEX3</i>	2.90	0.30	48-kDa peroxisomal integral membrane protein
<i>VPS60</i>	2.48	0.06	vacuolar protein sorting putative
<i>PEX10</i>	3.46	0.13	C3HC4 zinc-binding integral peroxisomal membrane protein
<i>RAV2</i>	3.25	0.54	Regulator of H <sup>+</sup> -ATPase in Vacuolar membrane
<i>AFR1</i>	3.08	0.14	coordinates regulation of alpha-factor receptor signalling and induction of morphogenesis during conjugation
<i>ENT1</i>	3.38	0.02	cytoskeletal adaptor
<i>CVT20</i>	3.37	0.22	Cytoplasm to vacuole targeting
<i>GYP7</i>	2.34	0.06	vesicle mediated transport
<i>AME1</i>	2.40	0.32	regulator of microtubule stability
<i>SEC17</i>	3.07	0.29	peripheral membrane protein required for vesicular transport between ER and Golgi
<i>AUT7</i>	3.51	0.24	Form a protein complex with Aut2p, to mediate attachment of autophagosomes to microtubules
<i>MRL1</i>	3.54	0.19	Mannose 6-phosphate Receptor Like, vacuolar transport
<i>SDF1</i>	2.60	0.20	SDF1 the first observed null phenotype was Sporulation DeFiciency
<i>CSR2</i>	2.50	0.17	cell wall organization and biogenesis
<i>ICY2</i>	4.18	0.80	Interacting with the cytoskeleton Involved in chromatin organization and nuclear transport
<i>VPS5</i>	2.10	0.07	Sorting nexin I homologue
<i>SCD5</i>	2.60	0.12	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1
<i>VPS17</i>	2.37	0.18	Peripheral membrane protein required for vacuolar protein sorting
<i>CRS5</i>	2.10	0.05	Metallothionein-like protein, heavy metal sensitivity/resistance
<i>SHE4</i>	2.50	0.14	Required for mother cell-specific HO expression
<i>PEP12</i>	4.16	0.17	integral membrane protein, Golgi to vacuole transport
<i>TLG2</i>	2.70	0.06	tSNARE that affects a Late Golgi compartment
<i>PEX15</i>	2.50	0.11	44 kDa phosphorylated integral peroxisomal membrane protein
<i>YOL083W</i>	5.32	0.65	Cytoplasm to Vacuole Targeting
<i>CVT19</i>	3.22	0.22	Cytoplasm to Vacuole Targeting
<i>MSO1</i>	2.68	0.15	small hydrophilic protein, enriched in microsomal membrane fraction, interacts with Sec1p
<i>VPS27</i>	2.84	0.15	hydrophilic protein\; has cysteine rich putative zinc

<i>AUT1</i>	3.84	0.10	finger essential for function, Golgi retention Protein involved in autophagocytosis during starvation
<i>SPO1</i>	2.35	0.07	required for meiotic spindle pole body duplication/separation, meiosis I, meiosis II, and spore formation
<i>END3</i>	3.14	0.12	Required for endocytosis and organization of the cytoskeleton
<i>PEX17</i>	2.76	0.11	23 kDa peroxisome associated protein, binds Pex14p
<i>NAR1</i>	3.63	0.56	Nuclear architecture related protein with homology to human Narf Nuclear prelamin A Recognition Factor
<i>VTI1</i>	3.90	0.39	Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p
<b>Metabolism</b>			
<i>GSY2</i>	6.52	0.89	Glycogen synthase (UDP-glucose--starch glucosyltransferase)
<i>UGT51</i>	2.26	0.05	Udp-glycosyltransferase, sterol metabolism
<i>IDP2</i>	2.20	0.10	Cytosolic form of NADP-dependent isocitrate dehydrogenase
<i>CKII</i>	2.61	0.12	choline kinase
<i>GPT2</i>	5.72	0.28	Encodes a Glycerol-3-phosphate acyltransferase
<i>GLG1</i>	6.54	1.60	self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogenin
<i>OSH6</i>	2.85	0.15	steroid biosynthesis
<i>STR2</i>	3.46	0.14	similarity to O-succinylhomoserine (thiol)-lyase
<i>BNA3</i>	2.33	0.08	Biosynthesis of Nicotinic Acid
<i>FBP26</i>	4.28	0.31	Fructose-2,6-bisphosphatase
<i>BDH1</i>	3.82	0.53	2R,3R -2,3-butanediol dehydrogenase
<i>MEL1</i>	3.31	0.21	MEL1 Required for the catabolism of melibiose and regulated by several GAL genes
<i>UGA2</i>	2.56	0.22	Probable aldehyde dehydrogenase
<i>PFK26</i>	3.27	0.38	6-Phosphofructose-2-kinase
<i>NIT1</i>	7.18	1.53	Nit1 nitrilase
<i>GND2</i>	8.83	1.00	6-phosphogluconate dehydrogenase
<i>XKS1</i>	5.22	0.37	xylulokinase
<i>TMT1</i>	10.98	1.68	Trans-aconitate Methyltransferase 1
<i>CEM1</i>	2.12	0.07	3-oxoacyl-[acyl-carrier protein] synthase
<i>GLC3</i>	6.56	1.10	1,4-glucan-6-(1,4-glucano)-transferase
<i>RIB3</i>	2.37	0.13	3,4-dihydroxy-2-butanone 4-phosphate synthase
<i>DIT1</i>	7.08	1.72	first enzyme in dityrosine synthesis
<i>TPS2</i>	4.62	0.82	Trehalose-6-phosphate phosphatase
<i>TGL2</i>	3.38	0.21	TriGlyceride Lipase
<i>NTH1</i>	4.17	0.46	neutral trehalase (alpha,alpha-trehalase)

<i>GPM2</i>	5.21	0.78	Similar to GPM1 (phosphoglycerate mutase)
<i>FAD1</i>	2.97	0.12	FAD synthetase
<i>NDE2</i>	4.15	0.30	strong similarity to NADH dehydrogenase (ubiquinone)
<i>CRD1</i>	2.66	0.16	Cardiolipin synthase
<i>GDH2</i>	2.38	0.10	NAD-dependent glutamate dehydrogenase
<i>AAD4</i>	33.96	1.43	Hypothetical aryl-alcohol dehydrogenase
<i>UGA2</i>	3.31	0.19	Probable aldehyde dehydrogenase
<i>MAL33</i>	2.87	0.35	Maltose fermentation regulatory protein
<i>RIB5</i>	2.46	0.27	Riboflavin synthase alpha-chain
<i>EHT1</i>	2.75	0.29	alcohol acyl transferase lipid metabolism
<i>YPC1</i>	2.75	0.25	Yeast Phyto-ceramidase sphingolipid metabolism
<i>YBR137W</i>	3.06	0.23	hypothetical protein
<i>YBR139W</i>	2.25	0.14	Probable serine-type carboxypeptidase
<i>ADH5</i>	5.66	0.37	alcohol dehydrogenase isoenzyme V
<i>TKL2</i>	6.25	1.58	transketolase, homologous to tk11
<i>NTH2</i>	2.77	0.11	Neutral trehalase, highly homologous to Nth1p
<i>RIB1</i>	3.78	0.51	First step in the riboflavin biosynthesis pathway
<i>YBL086C</i>	5.42	0.17	involved in sugar metabolism
<i>GDB1</i>	4.59	0.74	similarity to human 4-alpha-glucanotransferase/ amylo-1,6-glucosidase
<i>GPH1</i>	4.69	0.97	Glycogen phosphorylase
<i>YDC1</i>	2.65	0.04	Yeast dihydro-ceramidase sphingolipid metabolism
<i>OYE3</i>	22.16	3.24	NAD(P)H dehydrogenase
<i>PYK2</i>	3.76	0.65	Pyruvate kinase, glucose-repressed isoform
<i>MCT1</i>	2.75	0.40	malonyl-CoA:ACP transferase
<i>GCY1</i>	13.38	2.79	Similar to mammalian aldo\keto reductases
<i>AAD15</i>	2.71	0.30	Hypothetical aryl-alcohol dehydrogenase (AAD)
<i>ZWF1</i>	3.91	0.65	Glucose-6-phosphate dehydrogenase
<i>MLS1</i>	4.86	1.30	carbon-catabolite sensitive malate synthase
<i>TPS3</i>	2.23	0.11	115 kD regulatory subunit of trehalose-6-phosphate synthase\phosphatase complex
<i>GAD1</i>	8.35	1.80	similarity to glutamate decarboxylases
<i>ALD3</i>	9.42	1.06	Aldehyde Dehydrogenase (NAD(P)+)
<i>PGM2</i>	8.49	2.80	Phosphoglucomutase
<i>TSL1</i>	4.31	0.78	123 kD regulatory subunit of trehalose-6-phosphate synthase\phosphatase complex
<b>Amino Acid Metabolism</b>			
<i>SRY1</i>	3.10	0.24	threonine dehydratase
<i>NTA1</i>	2.74	0.19	amidase specific for N-terminal asparagine and glutamine
<i>ARG2</i>	2.11	0.04	Acetylglutamate Synthase
<i>HIS5</i>	3.25	0.38	histidinol-phosphate aminotransferase
<i>SDL1</i>	4.12	1.34	L-serine dehydratase

<i>YIL167W</i>	6.04	0.69	serine dehydratase
<i>STR3</i>	5.11	1.07	methionine biosynthesis cystathionine beta-lyase
<i>SER3</i>	2.62	0.24	strong similarity to phosphoglycerate dehydrogenases
<i>ARG82</i>	2.84	0.61	Regulator of arginine-responsive genes with ARG80 and ARG81
<i>HIS4</i>	2.74	0.22	histidinol dehydrogenase
<i>MET16</i>	2.94	0.47	3 phosphoadenylylsulfate reductase, interacts with YkU80
<i>URA10</i>	5.15	0.13	Orotate phosphoribosyltransferase 2
<i>LYS7</i>	2.32	0.12	Homocitrate
<b>RNA Processing</b>			
<i>PUF2</i>	3.70	0.20	mRNA binding protein
<i>RNY1</i>	6.44	0.64	similarity to ribonucleases
<b>Transport</b>			
<i>SMF3</i>	2.20	0.19	strong similarity to SMF2 protein, Putative metal transporter
<i>ARN2</i>	3.27	0.32	Siderophore transporter for triacetylfusarinine C
<i>ARN1</i>	3.12	0.13	Siderophore transporter for triacetylfusarinine C
<i>YHL035C</i>	2.25	0.13	ABC transporter
<i>CCC2</i>	3.78	0.40	Copper-transporting P-type ATPase with similarity to human Menkes and Wilsons genes
<i>NPL4</i>	2.59	0.13	Nuclear pore or nuclear pore-associated protein required for nuclear membrane integrity and nuclear transport
<i>AGP2</i>	3.15	0.48	Amino acid permease
<i>FLR1</i>	11.25	1.85	Major Facilitator Transporter
<i>COT1</i>	2.79	0.18	Protein involved in cobalt accumulation\; dosage dependent suppressor of cobalt toxicity
<i>MCH4</i>	4.16	0.13	similarity to monocarboxylate transporter proteins
<i>ENB1</i>	2.75	0.57	sSiderophore transporter for enterobactin; AFT1 regulon
<i>ATR1</i>	7.13	1.36	multidrug efflux pump
<b>Unknown</b>			
<i>YLR297W</i>	3.19	0.50	weak similarity to <i>Vibrio vulnificus</i> VvpC protein
<i>YLR311C</i>	18.65	1.37	weak similarity to <i>S.tarentolae</i> cryptogene protein G4
<i>YLR312C</i>	8.77	0.94	hypothetical protein
<i>YLR257W</i>	2.68	0.37	hypothetical protein
<i>YLR270W</i>	2.91	0.13	strong similarity to YOR173w
<i>YLR271W</i>	3.04	0.07	hypothetical protein
<i>YLR251W</i>	4.79	0.53	similarity to peroxisomal rat membrane protein

			PMP22
<i>YLR252W</i>	5.93	0.91	questionable ORF
<i>YLR218C</i>	2.09	0.07	hypothetical protein
<i>YLR193C</i>	2.98	0.30	similarity to G.gallus px19 and Msf1p
<i>YLR173W</i>	2.86	0.41	hypothetical protein
<i>YLR149C</i>	9.43	2.09	hypothetical protein
<i>YLR164W</i>	15.14	4.88	strong similarity to Sdh4p
<i>TIS11</i>	14.30	1.38	zinc finger containing homolog of mammalian TIS11, glucose repressible gene
<i>YLR108C</i>	3.71	0.19	strong similarity to YDR132c
<i>EMP46</i>	3.95	0.47	strong similarity to Emp47p
<i>YLR047C</i>	2.83	0.30	similarity to hypothetical protein YGL160w
<i>LOT6</i>	2.78	0.20	weak similarity to E.coli hypothetical 20.4 kDa protein
<i>SNF7</i>	2.19	0.05	involved in derepression of SUC2 in response to glucose limitation
<i>YLL033W</i>	2.36	0.04	hypothetical protein
<i>YLL023C</i>	2.76	0.27	similarity to hypothetical protein YLR064w
<i>YLL057C</i>	7.88	2.27	similarity to E.coli dioxygenase
<i>YLL056C</i>	9.67	0.78	weak similarity to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-L-glycero-4-hexulose-5-epimerase
<i>YLL055W</i>	10.11	1.07	similarity to Dal5p
<i>FRE6</i>	2.70	0.32	similar to FRE2
<i>DRE2</i>	2.74	0.15	weak similarity to C.elegans hypothetical protein
<i>ECM4</i>	10.43	2.38	ExtraCellular Mutant
<i>YKR046C</i>	6.49	1.35	hypothetical protein
<i>TOS5</i>	3.46	0.41	hypothetical protein
<i>YKL023W</i>	3.93	0.72	weak similarity to human cyclicin II
<i>PTM1</i>	2.25	0.10	Putative membrane protein
<i>YKL071W</i>	65.57	3.80	weak similarity to A.parasiticus nor-1 protein
<i>YKL070W</i>	4.00	1.05	similarity to B.subtilis transcriptional regulatory protein
<i>MNR2</i>	2.59	0.02	overexpression overcomes manganese toxicity
<i>YKL091C</i>	7.89	0.88	strong similarity to Sec14p
<i>YKL088W</i>	2.15	0.09	similarity to C.tropicalis hal3 protein, to C-term. of Sis2p and to hypothetical protein YOR054c
<i>YKL086W</i>	82.07	15.00	hypothetical protein
<i>YKL107W</i>	88.66	33.74	weak similarity to S.antibioticus probable oxidoreductase
<i>YKL100C</i>	2.91	0.20	similarity to C.elegans hypothetical protein
<i>YJU3</i>	2.33	0.06	weak similarity to E.coli hypothetical protein
<i>YKL133C</i>	2.82	0.32	probable purine nucleotide-binding protein
<i>SSH4</i>	7.56	4.62	suppressor of SHR3\; confers leflunomide resistance when overexpressed
<i>YKL121W</i>	2.46	0.23	strong similarity to YMR102c

<i>YKL151C</i>	4.63	0.38	similarity to <i>C.elegans</i> hypothetical protein R107.2
<i>YKL162C</i>	3.17	0.31	hypothetical protein
<i>SDS22</i>	3.25	0.19	Interacts with and may be a positive regulator of GLC7 which encodes type1 protein phosphatase
<i>YKL187C</i>	7.87	2.38	strong similarity to hypothetical protein YLR413w
<i>NJR005C</i>	33.42	2.74	non-annotated SAGE orf
<i>NJR008W</i>	2.49	0.09	non-annotated SAGE orf
<i>NJR009W</i>	3.47	0.28	non-annotated SAGE orf
<i>NJR015C</i>	2.32	0.23	non-annotated SAGE orf
<i>NJL023C</i>	7.10	2.66	non-annotated SAGE orf
<i>YJR142W</i>	2.46	0.23	similarity to thiamin pyrophosphokinase
<i>YJR110W</i>	2.14	0.06	similarity to human myotubularin
<i>YJR096W</i>	6.27	0.54	similarity to <i>Corynebacterium</i> 2,5-diketo-D-gluconic acid reductase and aldehyde reductases
<i>YJR020W</i>	2.31	0.04	questionable ORF
<i>YJR008W</i>	6.06	0.96	similarity to <i>S.pombe</i> hypothetical protein
<i>YJL048C</i>	3.21	0.16	similarity to hypothetical protein YBR273c
<i>SNX4</i>	4.15	0.11	weak similarity to Mvp1p
<i>YJL070C</i>	3.09	0.42	similarity to AMP deaminases
<i>IML2</i>	2.31	0.14	strong similarity to hypothetical protein YKR018c
<i>YJL144W</i>	3.22	0.50	hypothetical protein
<i>YJL142C</i>	3.83	0.42	questionable ORF
<i>YJL131C</i>	2.67	0.15	weak similarity to nonepidermal <i>Xenopus</i> keratin, type I
<i>YJL161W</i>	9.63	2.74	hypothetical protein
<i>YJL199C</i>	3.12	0.29	hypothetical protein
<i>YAL061W</i>	5.55	1.84	similarity to alcohol/sorbitol dehydrogenase
<i>gNR09_4</i>	2.52	0.08	<i>Saccharomyces cerevisiae</i> chromosome XIV, Found forward in NC_001146 between 685191 and 686190
<i>gKR07_1</i>	2.72	0.26	<i>Saccharomyces cerevisiae</i> chromosome XI, Found forward in NC_001143 between 643133 and 644132
<i>YHLCOMEGA1</i>	2.75	0.40	YHLCOMEGA1 Ty5 LTR
<i>YGRCDDELTA25</i>	6.71	2.18	YGRCDDELTA25 Ty1 LTR
<i>YFLWDELTA1</i>	3.98	0.75	YFLWDELTA1 Ty1 LTR
<i>NIR004C</i>	3.82	0.31	non-annotated SAGE orf
<i>NIR005C</i>	3.26	0.36	non-annotated SAGE orf
<i>DRE3</i>	2.70	0.29	strong similarity to Nbp35p and human nucleotide-binding protein
<i>YIR003W</i>	2.55	0.17	weak similarity to mammalian neurofilament triplet H proteins
<i>YIL007C</i>	2.76	0.27	similarity to <i>C.elegans</i> hypothetical protein
<i>YIL055C</i>	4.81	0.24	hypothetical protein
<i>YIL087C</i>	3.24	0.43	hypothetical protein
<i>YIL077C</i>	2.28	0.17	hypothetical protein
<i>YIL113W</i>	3.77	0.52	strong similarity to dual-specificity phosphatase Msg5p

<i>FYV10</i>	4.04	0.39	hypothetical protein
<i>YIL165C</i>	8.40	1.62	putative pseudogene
<i>YHR209W</i>	6.49	1.08	similarity to hypothetical protein YER175c
<i>NHR002C</i>	7.09	1.31	non-annotated SAGE orf
<i>NHR009C</i>	7.15	2.41	non-annotated SAGE orf
<i>YHR198C</i>	2.92	0.20	strong similarity to hypothetical protein YHR199c
<i>YHR199C</i>	4.35	0.29	strong similarity to hypothetical protein YHR198c
<i>NVJ1</i>	2.61	0.12	Vac8p binding protein; nucleus-vacuole junction
<i>YHR159W</i>	3.07	0.76	hypothetical protein
<i>YHR138C</i>	2.88	0.22	hypothetical protein
<i>YHR140W</i>	2.59	0.23	hypothetical protein
<i>YHR111W</i>	3.39	0.28	moeB, thiF, UBA1
<i>YHR087W</i>	5.81	1.73	hypothetical protein
<i>YHR097C_ex2</i>	3.32	0.36	strong similarity to hypothetical protein YDR348c
<i>YHR097C_ex1</i>	2.86	0.14	strong similarity to hypothetical protein YDR348c
<i>YHR105W</i>	2.47	0.32	weak similarity to Mvp1p
<i>YHR080C</i>	2.14	0.01	similarity to hypothetical protein YDR326c, YFL042c and YLR072w
<i>YHR048W</i>	17.15	7.79	similarity to multidrug resistance proteins
<i>YHR029C</i>	3.47	0.59	Thymidylate synthase (putative\; weak)
<i>YSC84</i>	4.61	0.19	SH3 domain in C-terminus
<i>YHL021C</i>	4.67	0.52	weak similarity to Pseudomonas gamma- butyrobetaine hydroxylase
<i>YHL017W</i>	2.11	0.03	Probable transmembrane protein PTM1
<i>YHL010C</i>	9.61	4.82	similarity to C.elegans hypothetical protein
<i>NGL018W</i>	2.10	0.05	non-annotated SAGE orf
<i>NGR001W</i>	5.61	1.31	non-annotated SAGE orf
<i>NGR042W</i>	3.00	0.36	non-annotated SAGE orf
<i>NGR053C</i>	2.15	0.10	non-annotated SAGE orf
<i>NGL007W</i>	5.53	0.69	non-annotated SAGE orf
<i>YGR268C</i>	2.42	0.34	weak similarity to S.pombe hypothetical protein SPAC17A5
<i>YGR235C</i>	2.35	0.22	hypothetical protein
<i>YGR237C</i>	3.32	0.12	weak similarity to YOR019w
<i>SOL4</i>	11.33	2.96	similar to SOL3
<i>YGR250C</i>	2.34	0.10	weak similarity to human cleavage stimulation factor 64K chain
<i>RTA1</i>	3.63	0.74	involved in 7-aminocholesterol resistance
<i>YGR223C</i>	2.99	0.44	weak similarity to hypothetical protein YFR021w
<i>YGR201C</i>	2.80	0.18	strong similarity to translation elongation factor eEF1 alpha chain Cam1p
<i>YGR205W</i>	2.91	0.56	similarity to S.pombe hypothetical protein D89234
<i>YGR149W</i>	2.82	0.33	hypothetical protein
<i>YGR127W</i>	3.36	0.22	weak similarity to mouse T10 protein
<i>YGR130C</i>	3.22	0.19	weak similarity to myosin heavy chain proteins
<i>VPS62</i>	2.44	0.10	strong similarity to hypothetical protein YPR157w

<i>YGR066C</i>	3.14	0.17	similarity to hypothetical protein YBR105c
<i>YGR043C</i>	13.01	1.16	strong similarity to transaldolase
<i>YGR011W</i>	4.96	0.89	questionable ORF
<i>YGL059W</i>	4.07	0.51	similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
<i>YGL045W</i>	2.64	0.26	hypothetical protein
<i>VPS73</i>	2.58	0.24	similarity to glucose transport proteins
<i>TOS8</i>	2.30	0.12	similarity to copper homeostasis protein Cup9p
<i>NBP35</i>	3.90	0.30	NBP35 encodes an essential evolutionary conserved protein with homology to bacterial partitioning ATPases
<i>YGL121C</i>	8.02	0.64	hypothetical protein
<i>YGL117W</i>	3.59	0.76	hypothetical protein
<i>YGL114W</i>	4.37	0.17	weak similarity to H.influenzae permease
<i>MMM2</i>	2.79	0.12	hypothetical protein
<i>YGL226W</i>	2.89	0.04	similarity to N.crassa cytochrome-c oxidase chain V
<i>YGL250W</i>	3.20	0.31	hypothetical protein
<i>NFL008W</i>	2.39	0.26	non-annotated SAGE orf
<i>NFR001W</i>	2.64	0.18	non-annotated SAGE orf
<i>YFL043C</i>	4.16	0.26	hypothetical protein
<i>YFL042C</i>	3.69	0.17	similarity to hypothetical protein YLR072w
<i>YFR003C</i>	3.42	0.22	hypothetical protein
<i>YFR008W</i>	2.52	0.10	weak similarity to human centromere protein E
<i>YFR017C</i>	6.49	1.46	hypothetical protein
<i>YFL030W</i>	3.72	0.34	similarity to several transaminases
<i>YFL057C</i>	30.88	4.15	strong similarity to aryl-alcohol dehydrogenases
<i>NEL017W</i>	2.69	0.13	non-annotated SAGE orf
<i>YER067c-a</i>	4.02	0.33	questionable ORF
<i>SPII</i>	3.45	0.74	Stationary Phase Induced; strongly expressed during stationary phase
<i>YER134C</i>	2.44	0.22	weak similarity to S.pombe SPBC13G1 and C.elegans F26F2.d hypothetical proteins
<i>YER067W</i>	14.94	3.08	strong similarity to hypothetical protein YIL057c
<i>YER079W</i>	2.72	0.11	hypothetical protein
<i>YER053C</i>	4.10	0.63	strong similarity to mitochondrial phosphate carrier protein
<i>YEL020C</i>	2.20	0.16	similarity to O.formigenes oxalyl-CoA decarboxylase
<i>YEL041W</i>	2.87	0.18	strong similarity to Utr1p
<i>YEL057C</i>	2.12	0.03	hypothetical protein
<i>NDR156C</i>	2.70	0.17	non-annotated SAGE orf
<i>YDR516C</i>	2.72	0.21	strong similarity to glucokinase
<i>YDR533C</i>	4.67	0.75	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c
<i>YDR479C</i>	4.75	0.13	weak similarity to YHR150w
<i>ARO80</i>	3.33	0.96	hypothetical protein

<i>YDR425W</i>	3.18	0.22	similarity to hypothetical protein YDL113c
<i>ARO10</i>	2.97	0.24	similarity to Pdc6p, Thi3p and to pyruvate decarboxylases
<i>YDR387C</i>	2.18	0.03	similarity to Itr1p and Itr2p and E.coli araE
<i>YDR391C</i>	3.32	0.56	strong similarity to hypothetical protein YOR013w
<i>YDR330W</i>	3.10	0.33	similarity to hypothetical S. pombe protein
<i>RTT103</i>	2.96	0.24	Regulator of Ty1 Transposition
<i>YDR306C</i>	2.40	0.11	weak similarity to S.pombe hypothetical protein SPAC6F6
<i>YDR229W</i>	2.46	0.04	hypothetical protein
<i>STB3</i>	2.93	0.05	Binds Sin3p in two-hybrid assay
<i>YDR132C</i>	13.33	3.35	strong similarity to hypothetical protein YLR108c
<i>YDR067C</i>	2.28	0.10	similarity to YNL099c
<i>YDR070C</i>	20.13	5.45	hypothetical protein
<i>YDR066C</i>	3.10	0.50	similarity to hypothetical protein YER139c
<i>YDR031W</i>	2.74	0.13	hypothetical protein
<i>YDR003W</i>	5.41	0.42	strong similarity to hypothetical protein YBR005w
<i>MAF1</i>	2.90	0.21	required for sorting of Mod5p
<i>YDR018C</i>	4.84	0.41	strong similarity to hypothetical protein YBR042c
<i>YDL025C</i>	4.38	0.45	ser/thr protein kinase of the DEAD/DEAH box family
<i>YDL027C</i>	2.46	0.21	hypothetical protein
<i>YDL057W</i>	2.72	0.26	hypothetical protein
<i>YDL091C</i>	4.62	0.74	weak similarity to mouse FAF1 protein
<i>YDL110C</i>	5.02	0.41	hypothetical protein
<i>YDL129W</i>	2.62	0.14	hypothetical protein
<i>YDL124W</i>	4.94	0.70	similarity to aldose reductases
<i>IWR1</i>	4.12	0.43	hypothetical protein
<i>YDL146W</i>	3.58	0.16	weak similarity to Orc3p
<i>YDL204W</i>	15.11	3.33	similarity to hypothetical protein YDR233c
<i>UGX2</i>	7.51	0.64	protein of unknown function
<i>YDL218W</i>	74.10	11.24	weak similarity to hypothetical protein YNR061c
<i>ADY3</i>	3.42	0.20	hypothetical protein
<i>YDL238C</i>	3.71	0.07	similarity to E.coli hypothetical protein and to chlorohydrolases
<i>HBT1</i>	4.46	0.80	weak similarity to mucin, hub1 target
<i>NCL004W</i>	3.02	0.34	non-annotated SAGE orf
<i>YCR102C</i>	8.82	2.91	Alcohol dehydrogenase
<i>SYP1</i>	2.78	0.10	Suppressor of Yeast Profilin deletion
<i>YCL039W</i>	2.76	0.29	regulatory protein
<i>YCL049C</i>	2.22	0.09	hypothetical protein
<i>NBR036W</i>	22.12	15.97	non-annotated SAGE orf
<i>NBR063C</i>	2.76	0.11	non-annotated SAGE orf
<i>NBR047W</i>	2.50	0.22	non-annotated SAGE orf
<i>NBR048W</i>	2.51	0.34	non-annotated SAGE orf
<i>YBR293W</i>	2.23	0.05	Probable multidrug resistance protein

<i>YBR085c-a</i>	3.05	0.30	hypothetical protein
<i>YBR269C</i>	4.17	0.39	hypothetical protein
<i>YBR273C</i>	3.38	0.08	similarity to hypothetical protein YJL048c
<i>YBR280C</i>	4.63	1.06	hypothetical protein
<i>YBR255W</i>	3.95	1.13	hypothetical protein
<i>SDS24</i>	5.80	1.46	strong similarity to hypothetical protein YGL056c
<i>YBR204C</i>	3.35	0.43	Probable serine-active lipase, peroxisomal
<i>FTH1</i>	2.33	0.13	probable membrane protein, FTS3 Homolog 1
<i>IML3</i>	2.21	0.19	Increase Minichromosome Loss
<i>YBR047W</i>	10.89	0.35	hypothetical protein
<i>YBR053C</i>	2.50	0.16	similarity to rat regucalcin
<i>YBR056W</i>	2.71	0.39	Homolog to glucan-1,3--glucosidase 2
<i>YBL049W</i>	3.37	0.25	hypothetical protein
<i>YBL048W</i>	4.15	0.44	hypothetical protein
<i>ECM13</i>	11.52	3.51	ExtraCellular Mutant
<i>YBL091C-A</i>	3.96	0.26	weak similarity to SCS2
<i>NPR015C</i>	3.54	0.53	non-annotated SAGE orf
<i>ARR2</i>	3.84	0.68	Required for arsenate but not for arsenite resistance
<i>ARR3</i>	5.78	1.82	involved in arsenite transport
<i>YPR127W</i>	7.37	0.76	similarity to C-term. of <i>N.tabacum</i> auxin-induced protein
<i>YPR081C</i>	3.32	0.14	strong similarity to glycyl-tRNA synthetases
<i>YPR085C</i>	2.79	0.48	hypothetical protein
<i>YPR093C</i>	5.32	0.38	weak similarity to zinc-finger proteins
<i>YPR061C</i>	2.29	0.17	weak similarity to <i>Synechococcus</i> sp. DnaJ protein
<i>YPR077C</i>	4.02	1.24	questionable ORF
<i>YPR045C</i>	3.22	0.25	similarity to <i>C.elegans</i> hypothetical protein
<i>YPR015C</i>	6.90	1.26	similarity to transcription factors
<i>YPL017C</i>	6.12	3.59	strong similarity to Lpd1p and other dihydrolipoamide dehydrogenases
<i>YPL070W</i>	3.30	0.08	weak similarity to Vps9p
<i>MAI1</i>	3.32	0.32	Maturation of pro-AmInopeptidase I proAPI defective
<i>YPL103C</i>	2.46	0.23	similarity to hypothetical <i>M. tuberculosis</i> protein
<i>YPL166W</i>	3.23	0.34	weak similarity to paramyosins
<i>RRD2</i>	4.07	0.27	Resistant to Rapamycin Deletion 2
<i>UIP4</i>	4.44	0.61	weak similarity to <i>Xenopus</i> protein xlgv7
<i>YPL206C</i>	2.32	0.16	weak similarity to glycerophosphoryl diester phosphodiesterases
<i>YPL191C</i>	2.60	0.27	strong similarity to YGL082w
<i>YPL230W</i>	14.06	7.36	Up in StarVation
<i>YPL222W</i>	9.77	3.15	similarity to <i>C.perfringens</i> hypothetical protein
<i>GYP5</i>	3.34	0.37	similarity to mouse Tbc1 protein, GAP for Ypt protein
<i>YPL247C</i>	3.45	0.44	similarity to human HAN11 protein and petunia an11 protein

<i>NOR052W</i>	3.31	0.16	non-annotated SAGE orf
<i>FRE5</i>	8.18	1.57	similar to FRE2
<i>NOR012W</i>	2.51	0.30	non-annotated SAGE orf
<i>FRE3</i>	4.34	0.79	similar to FRE2
<i>YOR352W</i>	2.28	0.24	hypothetical protein
<i>YOR289W</i>	9.55	0.60	similarity to C.elegans hypothetical protein
<i>YOR292C</i>	2.80	0.13	similarity to human and mouse glomerulosclerosis protein Mpv17
<i>RIM20</i>	2.27	0.05	similarity to A.nidulans palA protein, Regulator of IME2
<i>YOR215C</i>	3.19	0.34	similarity to M.xanthus hypothetical protein
<i>YOR220W</i>	3.93	0.45	hypothetical protein
<i>YOR223W</i>	3.08	0.48	protein of unknown function
<i>YOR227W</i>	2.77	0.13	similarity to microtubule-interacting protein Mhp1p
<i>YOR173W</i>	15.54	3.26	strong similarity to YLR270w
<i>YOR152C</i>	4.42	0.86	hypothetical protein
<i>YOR155C</i>	3.07	0.04	similarity to 5'-flanking region of the Pichia MOX gene
<i>YOR138C</i>	2.44	0.09	hypothetical protein
<i>YOR114W</i>	2.50	0.16	hypothetical protein
<i>YOR052C</i>	2.80	0.67	hypothetical protein
<i>YOR042W</i>	2.68	0.23	weak similarity to YDR273w
<i>YOR019W</i>	3.17	0.91	similarity to YDR474c
<i>YOR022C</i>	3.08	0.22	weak similarity to D.melanogaster probable Ca <sup>2+</sup> transporter rdgB
<i>YOL032W</i>	4.11	0.77	hypothetical protein
<i>YOL029C</i>	2.97	0.24	hypothetical protein
<i>YOL048C</i>	5.59	0.81	similarity to YAL018c and YOL047c
<i>YOL071W</i>	3.26	0.32	similarity to hypothetical S. pombe protein
<i>YOL087C</i>	2.38	0.13	similarity to S.pombe hypothetical protein
<i>YOL117W</i>	3.75	0.14	weak similarity to human sodium channel alpha chain HBA
<i>YOL150C</i>	3.56	0.45	questionable ORF
<i>NNL034W</i>	2.71	0.47	non-annotated SAGE orf
<i>YOL163W</i>	4.53	1.10	similarity to P.putida phthalate transporter
<i>YOL162W</i>	3.01	0.32	strong similarity to hypothetical protein YIL166c
<i>YOL153C</i>	16.23	2.62	strong similarity to Cps1p
<i>YNR034w-a</i>	14.53	3.57	hypothetical protein
<i>SOL1</i>	4.46	0.15	shows similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol2p and Sol3p
<i>YNL092W</i>	5.43	1.37	similarity to hypothetical C. elegans proteins Y48E1C.2 and Y48E1C.c
<i>YNL115C</i>	3.04	0.25	weak similarity to S.pombe hypothetical protein SPAC23C11
<i>YNL100W</i>	2.94	0.03	hypothetical protein

<i>YNL134C</i>	7.47	2.03	similarity to C.carbonum toxD gene
<i>YNL144C</i>	2.74	0.09	similarity to YHR131c
<i>YNL200C</i>	3.36	0.15	strong similarity to human TGR-CL10C
<i>YNL195C</i>	8.46	1.37	hypothetical protein
<i>YNL194C</i>	51.15	29.06	strong similarity to YDL222c and similarity to Sur7p
<i>IES2</i>	2.46	0.19	similarity to hypothetical S. pombe protein
<i>YNL253W</i>	2.16	0.05	hypothetical protein
<i>YTP1</i>	5.61	0.07	Yeast putative Transmembrane Protein
<i>YNL274C</i>	6.91	0.71	similarity to glycerate- and formate-dehydrogenases
<i>IST1</i>	2.73	0.15	Similar to Nuf1p spindle pole body component
<i>YNL260C</i>	4.76	0.87	hypothetical protein
<i>YNL305C</i>	4.15	0.46	similarity to C-term. of A.nidulans regulatory protein (qutR)
<i>SNZ2</i>	2.11	0.05	Snooze: stationary phase-induced gene family
<i>NMR047C</i>	2.33	0.16	non-annotated SAGE orf
<i>YMR313C</i>	2.46	0.15	similarity to YKR089c and YOR081c
<i>YMR315W</i>	2.43	0.16	similarity to hypothetical S. pombe protein
<i>YMR278W</i>	2.55	0.09	similarity to phosphomannomutases
<i>YMR258C</i>	3.57	0.34	hypothetical protein
<i>YMR262W</i>	4.12	0.44	similarity to S.pombe scn1 protein
<i>YMR265C</i>	2.27	0.09	hypothetical protein
<i>YMR244C-A</i>	3.17	0.25	questionable ORF
<i>YMR251W</i>	4.33	0.17	strong similarity to YKR076w and YGR154c
<i>YMR253C</i>	3.30	0.80	strong similarity to YPL264c
<i>YMR196W</i>	4.41	0.66	hypothetical protein
<i>YMR210W</i>	3.42	0.22	similarity to P.gluca late embryogenesis abundant protein and YBR177c and YPL095c
<i>SIP18</i>	11.82	7.57	Salt-Induced Protein
<i>YMR181C</i>	3.27	0.46	similarity to YPL229w
<i>YMR160W</i>	2.75	0.28	weak similarity to fruit fly ecdysone-inducible protein
<i>YMR135C</i>	2.87	0.39	hypothetical protein
<i>YMR140W</i>	2.46	0.06	hypothetical protein
<i>YMR090W</i>	8.85	1.82	strong similarity to B. subtilis conserved hypothetical protein yhfK
<i>YMR097C</i>	2.36	0.17	weak similarity to M.genitalium hypothetical protein homolog MG442
<i>YMR103C</i>	3.66	0.54	hypothetical protein
<i>YMR110C</i>	2.35	0.16	similarity to aldehyde dehydrogenase
<i>YMR085W</i>	19.12	2.90	putative pseudogene
<i>YMR087W</i>	3.20	0.28	hypothetical protein
<i>STB2</i>	3.73	0.61	Binds Sin3p in two-hybrid assay and is part of large protein complex with Sin3p and Stb1p
<i>YMR029C</i>	2.24	0.04	weak similarity to human nuclear autoantigen
<i>YMR041C</i>	4.75	0.45	weak similarity to Pseudomonas L-fucose

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			dehydrogenase
<i>YML002W</i>	2.19	0.08	hypothetical protein
<i>YML030W</i>	2.38	0.16	hypothetical protein
<i>YML087C</i>	9.40	2.16	strong similarity to YML125c, similarity to cytochrome-b5- and nitrate reductases
<i>YML117W</i>	2.77	0.27	similarity to YPL184c
<i>YML131W</i>	4.63	0.69	similarity to human leukotriene b4 12-hydroxydehydrogenase
<i>YLR460C</i>	8.46	2.90	similarity to C.carbonum toxD protein
<i>YLR408C</i>	2.38	0.09	hypothetical protein
<i>YLR392C</i>	2.59	0.38	hypothetical protein
<i>YLR345W</i>	4.23	0.39	similarity to Pfk26p and other 6-phosphofructo-2-kinases
<i>YLR352W</i>	2.35	0.14	hypothetical protein
<i>YLR356W</i>	3.26	0.35	similarity to SCM4 protein
<i>MSC1</i>	11.80	2.72	C-terminal part starting with aa 262 cause growth inhibition when overexpressed
<i>YLR327C</i>	13.80	3.96	strong similarity to Stf2p
<i>TFS1</i>	4.87	1.05	suppressor of cdc25, putative lipid binding protein

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