

**Up regulated genes in NER-defective cells following 0.3mM 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>HSP104</i>	2.50	0.13	heat shock protein 104
<i>GTT2</i>	47.01	7.53	Glutathione transferase
<i>GPX1</i>	4.98	1.23	strong similarity to glutathione peroxidase
<i>GTT1</i>	4.69	0.46	Glutathione transferase
<i>GRE3</i>	3.09	0.07	Aldo-keto reductase
<i>TRR2</i>	2.89	0.28	Thioredoxin reductase
<i>SOD2</i>	7.00	0.68	Manganese-containing superoxide dismutase
<i>CTT1</i>	6.52	1.73	cytoplasmic catalase T
<i>HSP12</i>	15.96	3.83	12 kDa heat shock protein
<i>SSA4</i>	5.26	0.22	member of 70 kDa heat shock protein family
<i>TTR1</i>	2.31	0.10	Glutaredoxin (thioltransferase) (glutathione reductase)
<i>TSA2</i>	30.00	5.42	strong similarity to thiol-specific antioxidant proteins
<i>CTA1</i>	10.30	4.04	catalase A
<i>HSP42</i>	3.62	0.38	Similar to HSP26\; expression is regulated by stress conditions
<i>TRX3</i>	2.54	0.09	Thioredoxin type II
<i>HSP30</i>	4.64	2.12	Protein induced by heat shock, ethanol, and entry into stationary phase
<i>SSE2</i>	3.72	0.40	HSP70 family member, highly homologous to Sse1p
<i>GPX2</i>	5.74	1.06	Probable glutathione peroxidase
<i>HSP26</i>	7.07	0.69	YBR072W heat shock protein 26
<i>ZTA1</i>	5.10	0.50	Homolog to quinone oxidoreductase (E. coli)
<i>YBL064C</i>	8.00	0.75	Homolog to thiol-specific antioxidant
<i>ATH1</i>	4.77	0.38	null mutant is viable\; increased tolerance to dehydration, freezing, and toxic levels of ethanol
<i>GLR1</i>	2.53	0.17	Glutathione oxidoreductase
<i>POS5</i>	2.35	0.15	involved in oxidative stress, interacts with gts1
<i>OXR1</i>	4.04	0.73	OXidation Resistance
<i>GRE2</i>	8.45	2.69	induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants
<i>DDR2</i>	12.94	2.98	Multistress responsive protein
<b>DNA Repair/ Replication</b>			
<i>SRL3</i>	3.08	0.58	Suppressor of rad53 lethality nucleobase, nucleoside, nucleotide and nucleic acid metabolism
<i>RNR3</i>	6.00	1.39	Ribonucleotide reductase large subunit
<i>RAD2</i>	2.72	0.08	homolog of XPG protein, copurifies with TFIIH, mRNA is induced by DNA damage and meiosis
<i>MMS2</i>	2.05	0.03	Member of error-free postreplication DNA repair

			pathway, ubiquitin conjugating enzyme
<i>RAD4</i>	2.97	0.43	Nucleotide excision repair protein
<i>MAG1</i>	2.19	0.09	3-methyladenine DNA glycosylase
<i>DDI1</i>	2.82	0.14	DNA Damage Inducible
<i>MHR1</i>	2.53	0.25	Involved in mitochondrial homologous DNA recombination
<i>RAD28</i>	2.75	0.10	Protein involved in the same pathway as Rad26p, has beta-transducin (WD-40) repeats
<i>PHR1</i>	3.62	0.60	photolyase
<i>DDR48</i>	2.39	0.18	DNA-damage responsive protein
<b>Signal Transduction</b>			
<i>SSK1</i>	2.45	0.24	Two-component signal transducer, regulates osmosensing MAP kinase cascade(suppressor of sensor kinase)
<i>YPK1</i>	2.17	0.03	76.5 kDa Serine\threonine protein kinase with similarity to protein kinase C
<i>IKS1</i>	5.58	0.43	probable serine\threonine kinase
<i>YAK1</i>	3.55	0.29	Serine-threonine protein kinase
<i>TPK1</i>	4.64	0.52	putative catalytic subunit of cAMP-dependent protein kinase
<i>BCY1</i>	2.40	0.14	regulatory subunit of cAMP-dependent protein kinase
<i>APG1</i>	2.30	0.08	Protein kinase, required for autophagy
<i>PDE1</i>	3.01	0.30	3 ,5 -Cyclic-nucleotide phosphodiesterase, low affinity, cAMP-mediated signaling
<i>CMK1</i>	3.44	0.18	Calmodulin-dependent protein kinase
<i>RIM15</i>	2.48	0.28	RIM15 is glucose-repressed; RIM15 is required for IME2 expression, protein kinase involved in meiosis
<i>GIP2</i>	4.49	0.16	Glc7-interacting protein\ protein phosphatase regulator
<i>PKH1</i>	2.40	0.21	Ser\Thr protein kinase
<i>PPM1</i>	3.74	0.09	carboxy methyl transferase for protein phosphatase 2A catalytic subunit
<i>PPZ2</i>	3.82	0.46	serine-threonine phosphatase Z
<i>KIN1</i>	2.46	0.23	Serine\threonine protein kinase
<i>AFR1</i>	4.21	0.14	coordinates regulation of alpha-factor receptor signalling and induction of morphogenesis during conjugation
<i>PPH21</i>	2.28	0.08	serine-threonine protein phosphatase 2A
<i>PTP1</i>	2.55	0.15	phosphotyrosine-specific protein phosphatase
<i>FRM2</i>	17.17	1.53	Protein involved in the integration of lipid signaling pathways with cellular homeostatis
<i>GIP1</i>	19.12	2.66	Developmentally-regulated protein phosphatase 1 Glc7 interacting protein, required for spore formation.
<i>PTC3</i>	2.43	0.31	protein phosphatase type 2C
<i>SMK1</i>	17.96	6.72	MAP kinase

<i>RRD2</i>	4.87	0.32	Resistant to Rapamycin Deletion 2, protein phosphatase type 2A, regulator, osmotic response
<i>TPK2</i>	2.64	0.26	cAMP-dependent protein kinase catalytic subunit
<i>GSP2</i>	3.71	0.35	GTP binding protein maintenance of nuclear organization a small nuclear GTPase of the ras superfamily
<i>PKH2</i>	3.96	0.55	Ser\Thr protein kinase
<i>GLC8</i>	2.80	0.30	Regulates activity of protein phosphatase 1, Glc7p, which is involved in proper chromosome segregation
<i>RIM11</i>	2.99	0.26	Serine\threonine protein kinase, phosphorylates the mitotic activator IME1
<i>CMP2</i>	2.60	0.21	Catalytic A subunit of calcineurin, type 2B protein serine\threonine phosphatase
<b>Chromatin Structure</b>			
<i>MGA2</i>	2.93	0.12	may be involved in the remodeling chromatin structure
<i>CST6</i>	2.32	0.14	weak similarity to human cAMP response element-binding protein
<i>CST9</i>	3.13	0.18	weak similarity to chicken RING zinc finger protein
<b>Transcription</b>			
<i>CAF17</i>	5.37	0.98	CCR4 associated factor
<i>OAF1</i>	2.63	0.16	peroxisome proliferating transcription factor
<i>YAP5</i>	2.59	0.01	bZIP protein\; transcription factor
<i>IMP2</i>	3.05	0.36	transcription factor
<i>TFG2</i>	2.43	0.21	transcription initiation factor TFIIIF middle subunit
<i>GTS1</i>	4.61	0.33	specific RNA polymerase II transcription factor
<i>SIP2</i>	2.92	0.27	Member of family of proteins that interact with Snf1p Snf4p, involved in the response to glucose starvation
<i>NPR2</i>	2.74	0.40	Putative post-transcriptional regulator of nitrogen permeases
<i>CAD1</i>	3.58	0.08	Transcriptional activator involved in resistance to 1,10-phenanthroline
<i>PHO2</i>	3.16	0.38	Homeobox-domain containing protein which is a positive regulator of PHO5 and other genes
<i>PHO85</i>	2.37	0.13	negative transcriptional regulator, protein kinase homolog
<i>AFT2</i>	3.57	0.32	Activator of Iron Fe Transcription
<i>HAP5</i>	2.85	0.24	Component, along with Hap2p and Hap3p, of CCAAT-binding transcription factor
<i>YRR1</i>	3.98	0.33	transcription factor
<i>CIN5</i>	2.84	0.70	bZIP protein, can activate transcription from a promoter containing a Yap recognition site
<i>YAP7</i>	2.53	0.23	bZIP protein
<i>YAP1</i>	3.59	0.34	jun-like transcription factor

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<b>Nucleotide Metabolism</b>			
<i>URA10</i>	4.44	0.85	Orotate phosphoribosyltransferase 2
<b>Degradation</b>			
<i>UBI4</i>	5.15	0.69	ubiquitin
<i>UBP11</i>	2.90	0.18	Ubiquitin-specific protease
<i>TUL1</i>	2.26	0.16	Transmembrane Ubiquitin Ligase
<i>LAP4</i>	11.52	1.97	vacuolar aminopeptidase ysc1
<i>HUL4</i>	2.38	0.24	ubiquitin-protein ligase E3
<i>YPS6</i>	5.34	0.98	GPI-anchored aspartic protease
<i>HUL5</i>	3.27	0.07	ubiquitin-protein ligase E3
<i>YPS5</i>	7.70	1.13	GPI-anchored aspartic protease
<i>UBC8</i>	4.42	0.34	ubiquitin-conjugating enzyme\; ubiquitin-protein ligase
<i>UBP9</i>	2.30	0.14	ubiquitin carboxyl-terminal hydrolase
<i>PRB1</i>	2.98	0.46	vacuolar protease B
<i>DOA4</i>	2.97	0.49	ubiquitin isopeptidase
<i>UBC5</i>	2.84	0.24	ubiquitin-conjugating enzyme
<i>PBN1</i>	2.40	0.20	Protease B Non-derepressible
<i>ULA1</i>	3.33	0.37	Required for activation of RUB1 (ubiquitin-like protein) together with UBA3
<i>LAP3</i>	2.29	0.11	Aminopeptidase of cysteine protease family
<i>UBP15</i>	2.67	0.06	encodes putative deubiquitinating enzyme
<i>PAI3</i>	3.79	0.39	Cytoplasmic inhibitor of proteinase Pep4p
<b>Mitochondrial Maintenance</b>			
<i>CCP1</i>	5.10	0.15	Cytochrome-c peroxidase
<i>MRS4</i>	4.57	0.39	mitochondrial carrier protein, highly homologous to Mrs3p
<i>CYT2</i>	3.13	0.07	cytochrome c1 heme lyase
<i>MCR1</i>	3.06	0.28	NADH-cytochrome b5 reductase
<i>MRP8</i>	2.89	0.14	mitochondrial ribosomal protein
<i>CBT1</i>	2.30	0.17	Subunit of complex involved in processing of the 3 end of cytochrome b pre-mRNA
<i>CYC1</i>	8.03	0.92	iso-1-cytochrome c
<i>MPM1</i>	5.20	0.53	mitochondrial membrane protein
<i>FIS1</i>	2.81	0.12	involved in mitochondrial division
<i>OM45</i>	8.15	1.53	45-kDa mitochondrial outer membrane protein
<i>GUT2</i>	4.81	0.52	glycerol-3-phosphate dehydrogenase, mitochondrial
<i>SHY1</i>	2.68	0.13	mitochondrial protein with homology to the mammalian SURF-1 gene
<i>STF2</i>	4.07	0.42	ATP synthesis coupled proton transport
<i>MRF1</i>	2.73	0.50	Mitochondrial polypeptide chain release factor
<i>YMR31</i>	2.54	0.11	mitochondrial ribosomal protein (precursor)

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<i>COX15</i>	2.50	0.25	cytochrome oxidase assembly factor
<i>CYC7</i>	4.77	0.48	iso-2-cytochrome c
<i>RSM28</i>	2.18	0.06	Regulator of COX2 Translation
<i>MRPL28</i>	2.30	0.17	Mitochondrial ribosomal protein MRPL28 (YmL28)
<i>MSW1</i>	2.18	0.16	mitochondrial tryptophanyl-tRNA synthetase
<i>HSP78</i>	3.71	0.62	Mitochondrial heat shock protein 78 kDa
<i>COX20</i>	2.27	0.10	involved in cytochrome oxidase activity
<i>COQ4</i>	2.82	0.20	Involved in ubiquinone biosynthesis
<i>STF1</i>	4.25	0.59	ATPase stabilizing factor
<i>INH1</i>	2.91	0.23	ATPase inhibitor
<i>GDH2</i>	3.41	0.26	NAD-dependent glutamate dehydrogenase
<i>MRF1</i>	2.42	0.17	May be transcriptional regulator of genes involved in assembly of mitochondrial respiratory proteins
<i>MSS18</i>	2.68	0.09	Protein involved in splicing intron a15beta of COX1
<i>MSF1</i>	2.79	0.06	alpha subunit of yeast mitochondrial phenylalanyl-tRNA synthetase
<i>MMT2</i>	2.63	0.13	Protein involved in mitochondrial iron accumulation
<i>ISU2</i>	4.96	0.33	NifU-like protein A, iron homeostasis, mitochondrial matrix
<i>GLO4</i>	3.45	0.17	Mitochondrial glyoxylase-II
<i>COQ3</i>	3.32	0.29	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
<i>NDE1</i>	2.49	0.26	mitochondrial cytosolically directed NADH dehydrogenase
<b>Cell Cycle</b>			
<i>APC9</i>	2.55	0.30	subunit of the anaphase promoting complex (APC)
<i>SAP4</i>	3.46	0.28	protein serine/threonine phosphatase, involved in g1/s transition
<i>PCL6</i>	2.27	0.15	PHO85 cyclin
<i>GRH1</i>	2.29	0.08	involved in mitotic spindle checkpoint
<b>Cell growth/ Maintenance</b>			
<i>ENT2</i>	2.31	0.04	cytoskeletal adaptor
<i>MYO3</i>	2.28	0.05	myosin I
<i>APL1</i>	2.52	0.31	beta-adaptin, large subunit of the clathrin-associated protein complex
<i>PEP8</i>	4.22	0.39	Vacuolar protein similar to mouse gene H<beta>58
<i>PRM9</i>	3.68	0.63	membrane protein, phermone regulated
<i>VPS8</i>	3.09	0.14	nvolved in vacuolar protein sorting;
<i>PRM5</i>	2.73	0.27	hydrophobic transmembrane domain phermone regulated
<i>YAP1801</i>	2.90	0.16	Yeast Assembly Polypeptide, member of AP180 protein family, binds Pan1p and clathrin
<i>APG7</i>	4.15	0.27	autophagy
<i>SPS100</i>	2.39	0.05	sporulation-specific wall maturation protein

<i>APM2</i>	2.41	0.03	Similar to clathrin coat proteins
<i>TWF1</i>	2.87	0.20	Twinfilin A, an actin monomer sequestering protein
<i>PRM8</i>	4.04	0.47	membrane protein, pheromone regulated
<i>PEX14</i>	2.56	0.07	Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins
<i>GGA1</i>	6.11	0.78	Golgi-localized, gamma-adaptin homology, Arf-binding
<i>PEX3</i>	2.72	0.23	48-kDa peroxisomal integral membrane protein
<i>CVT20</i>	3.31	0.59	Cytoplasm to vacuole targeting
<i>PEX10</i>	2.99	0.36	C3HC4 zinc-binding integral peroxisomal membrane protein
<i>AUT7</i>	3.28	0.33	Form a protein complex with Aut2p, to mediate attachment of autophagosomes to microtubules
<i>VPS30</i>	2.25	0.11	Required for sorting and delivery of soluble hydrolases to the vacuole.
<i>ICY2</i>	3.39	0.79	Interacting with the cytoskeleton Involved in chromatin organization and nuclear transport
<i>SCD5</i>	2.94	0.23	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1
<i>VPS17</i>	2.63	0.13	Peripheral membrane protein required for vacuolar protein sorting
<i>PEP12</i>	3.54	1.02	integral membrane protein\; c-terminal TMD\; located in endosome
<i>TLG2</i>	2.77	0.17	tSNARE that affects a Late Golgi compartment
<i>PEX15</i>	2.08	0.06	44 kDa phosphorylated integral peroxisomal membrane protein
<i>CVT19</i>	2.95	0.13	Cytoplasm to Vacuole Targeting
<i>AUT1</i>	3.31	0.35	Protein involved in autophagocytosis during starvation
<i>END3</i>	3.41	0.18	Required for endocytosis and organization of the cytoskeleton
<i>YTP1</i>	4.04	0.62	Yeast putative Transmembrane Protein
<i>MSB3</i>	2.60	0.37	Multicopy Suppressor of Bud Emergence
<i>VTI1</i>	3.63	0.51	Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p
<b>Metabolism</b>			
<i>ECM38</i>	3.46	0.65	glutathione biosynthesis
<i>GSY2</i>	6.59	0.30	Glycogen synthase
<i>UGT51</i>	2.26	0.10	Udp-glycosyltransferase , sterol metabolism
<i>MAS1</i>	2.47	0.08	mitochondrial processing protease subunit
<i>CKII</i>	2.70	0.12	choline kinase
<i>GPT2</i>	4.42	0.60	Encodes a Glycerol-3-phosphate acyltransferase
<i>GLG1</i>	5.20	0.34	self-glucosylating initiator of glycogen synthesis\; similar to mammalian glycogenin
<i>OSH6</i>	2.94	0.21	Oxysterol Binding Protein, steroid biosynthesis
<i>TGL1</i>	2.24	0.17	triglyceride lipase-cholesterol esterase

<i>MRPL38</i>	2.12	0.04	mitochondrial ribosomal protein L14
<i>STR2</i>	3.09	0.20	similarity to O-succinylhomoserine (thiol)-lyase
<i>OPI3</i>	2.89	0.44	Methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipid N-methyltransferase)
<i>GSH1</i>	3.53	0.19	gamma-glutamylcysteine synthetase
<i>NIT2</i>	2.15	0.07	Nit2 nitrilase
<i>FBP26</i>	4.57	0.73	Fructose-2,6-bisphosphatase
<i>FSP2</i>	3.02	0.06	homology to maltase(alpha-D-glucosidase)
<i>GDH3</i>	3.31	0.59	NADP-linked glutamate dehydrogenase
<i>YAL061W</i>	4.89	0.79	similarity to alcohol/sorbitol dehydrogenase
<i>BDH1</i>	4.56	0.60	similarity to alcohol/sorbitol dehydrogenase
<i>MEL1</i>	4.69	0.57	MEL1 Required for the catabolism of melibiose and regulated by several GAL genes
<i>UGA2</i>	3.37	0.21	Probable aldehyde dehydrogenase
<i>PFK26</i>	3.70	0.65	6-Phosphofructose-2-kinase
<i>SGA1</i>	11.21	3.92	intracellular glucoamylase
<i>NIT1</i>	5.96	1.81	Nit1 nitrilase
<i>GUT1</i>	2.51	0.32	glycerol kinase (converts glycerol to glycerol-3-phosphate)
<i>GND2</i>	7.95	1.03	6-phosphogluconate dehydrogenase
<i>XKS1</i>	5.44	0.76	xylulokinase
<i>UGA1</i>	2.23	0.12	gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase)
<i>AMS1</i>	4.76	0.13	vacuolar alpha mannosidase
<i>HXK1</i>	3.30	0.69	Hexokinase I (PI) (also called Hexokinase A)
<i>GSY1</i>	3.02	0.09	Glycogen synthase (UDP-glucose--starch glucosyltransferase)
<i>HOR2</i>	3.11	0.38	DL-glycerol-3-phosphatase
<i>PHM8</i>	3.48	0.74	involved in phosphate metabolism
<i>GLC3</i>	6.85	0.26	1,4-glucon-6-(1,4-glucono)-transferase
<i>APA2</i>	2.47	0.22	5,5 -P-1,P-4-tetraphosphate phosphorylase II
<i>LPP1</i>	2.13	0.04	Lipid phosphate phosphatase
<i>RIB3</i>	2.83	0.11	3,4-dihydroxy-2-butanone 4-phosphate synthase
<i>ARO10</i>	3.43	0.56	similarity to Pdc6p, Thi3p and to pyruvate decarboxylases
<i>IPK1</i>	2.09	0.04	inositol polyphosphate kinase
<i>DPL1</i>	2.56	0.21	dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase)
<i>TPS2</i>	3.94	0.25	Trehalose-6-phosphate phosphatase
<i>NTH1</i>	4.67	0.60	neutral trehalase (alpha,alpha-trehalase)
<i>TGL2</i>	3.21	0.43	TriGlyceride Lipase
<i>GPM2</i>	5.04	1.14	Similar to GPM1 (phosphoglycerate mutase)
<i>FAD1</i>	3.49	0.55	FAD synthetase
<i>NDE2</i>	15.40	3.85	strong similarity to NADH dehydrogenase (ubiquinone)
<i>CRD1</i>	3.05	0.17	Cardiolipin synthase

<i>UGA2</i>	3.58	0.08	involved in utilization of GABA as nitrogen source, glutamate catabolism, oxidative stress response
<i>MAL33</i>	3.58	0.32	Maltose fermentation regulatory protein
<i>YPC1</i>	3.76	0.68	sphingolipid metabolism
<i>TPS1</i>	2.95	0.27	56 kD synthase subunit of trehalose-6-phosphate synthase\phosphatase complex
<i>ADH5</i>	3.53	0.57	alcohol dehydrogenase isoenzyme V
<i>TKL2</i>	14.25	8.79	transketolase, homologous to tk11
<i>NTH2</i>	2.87	0.40	Neutral trehalase, highly homologous to Nth1p
<i>RIB1</i>	2.91	0.30	First step in the riboflavin biosynthesis pathway
<i>GDB1</i>	6.61	1.79	Glycogen debranching enzyme
<i>GPH1</i>	7.08	1.46	Glycogen phosphorylase
<i>YDC1</i>	3.12	0.13	sphingolipid metabolism
<i>RNY1</i>	8.15	0.56	RiboNuclease from Yeast
<i>OYE3</i>	26.24	0.53	NAD(P)H dehydrogenase
<i>YPL206C</i>	2.40	0.17	weak similarity to glycerophosphoryl diester phosphodiesterases
<i>THI6</i>	2.37	0.13	thiamin biosynthetic bifunctional enzyme
<i>FRE5</i>	9.69	2.55	similar to FRE2, iron homeostasis
<i>FRE3</i>	3.53	0.45	similar to FRE2, iron homeostasis
<i>FRE1</i>	2.24	0.12	Ferric (and cupric) reductase
<i>PYK2</i>	3.15	0.41	Pyruvate kinase, glucose-repressed isoform
<i>GCY1</i>	11.89	2.17	Similar to mammalian aldo\keto reductases
<i>IDH2</i>	2.33	0.08	NAD <sup>+</sup> -dependent isocitrate dehydrogenase
<i>AAD15</i>	2.72	0.36	Hypothetical aryl-alcohol dehydrogenase (AAD)
<i>ZWF1</i>	3.34	0.53	Glucose-6-phosphate dehydrogenase
<i>ARE2</i>	3.03	0.57	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase)
<i>SNZ2</i>	2.43	0.12	Snooze: stationary phase-induced gene family, vitamin B6 metabolism
<i>TPS3</i>	2.61	0.02	115 kD regulatory subunit of trehalose-6-phosphate synthase\phosphatase complex
<i>GAD1</i>	9.48	1.06	similarity to glutamate decarboxylases
<i>ALD3</i>	9.60	0.67	Aldehyde Dehydrogenase (NAD(P) <sup>+</sup> )
<i>ALD2</i>	2.70	0.09	aldehyde dehydrogenase, (NAD(P) <sup>+</sup> ), likely cytosolic
<i>PGM2</i>	10.63	2.62	Phosphoglucomutase
<i>FMS1</i>	2.59	0.47	Multicopy suppressor of fenpropimorph resistance (fen2 mutant), pantothenate biosynthesis
<i>GLO1</i>	2.26	0.06	lactoylglutathione lyase (glyoxalase I)
<i>TSL1</i>	6.21	0.94	123 kD regulatory subunit of trehalose-6-phosphate synthase\phosphatase complex
<b>Amino Acid Metabolism</b>			
<i>SRY1</i>	3.06	0.17	threonine dehydratase
<i>MET3</i>	2.78	0.08	ATP sulfurylase

<i>HIS5</i>	3.40	0.35	histidinol-phosphate aminotransferase
<i>YIL167W</i>	5.23	0.66	serine dehydratase
<i>ARO9</i>	3.88	0.20	aromatic amino acid aminotransferase II
<i>LYS5</i>	2.30	0.12	aminoadipate-semialdehyde dehydrogenase small subunit (alpha-aminoadipate reductase)
<i>STR3</i>	3.51	0.68	cystathionine beta-lyase, methionine biosynthesis
<i>DIT1</i>	5.92	1.28	first enzyme in dityrosine synthesis
<i>HIS4</i>	3.29	0.09	histidinol dehydrogenase
<i>MET16</i>	2.86	0.38	3 phosphoadenylylsulfate reductase, interacts with yku80
<b>RNA Processing</b>			
<i>PUF2</i>	2.96	0.45	mRNA binding protein
<b>Transport</b>			
<i>SMF3</i>	2.24	0.08	strong similarity to SMF2 protein, involved in iron transport
<i>PXA2</i>	3.83	0.34	peroxisomal ABC transporter 2
<i>ARN2</i>	4.33	1.30	Siderophore transporter for triacetylfusarinine C
<i>ARN1</i>	3.23	0.53	Siderophore transporter for triacetylfusarinine C
<i>YHL035C</i>	2.65	0.23	ABC transporter
<i>MAL11</i>	2.44	0.15	alpha-glucoside transporter
<i>PDR15</i>	2.48	0.23	probable multidrug resistance transporter
<i>CCC2</i>	2.81	0.24	Copper-transporting P-type ATPase with similarity to human Menkes and Wilsons genes
<i>YCF1</i>	2.37	0.11	Metal resistance protein cadmium ion transporter
<i>PCA1</i>	2.52	0.13	Putative P-type Cu(2+)-transporting ATPase
<i>NPL4</i>	2.63	0.23	Nuclear pore or pore-associated protein required for nuclear membrane integrity and nuclear transport
<i>AGP2</i>	3.36	0.65	Amino acid permease
<i>FLR1</i>	10.87	0.48	Major Facilitator Transporter
<i>MRL1</i>	3.23	0.22	vacuolar transport
<i>COT1</i>	2.53	0.27	Protein involved in cobalt accumulation, cobalt and zinc ion transport
<i>SMF1</i>	2.46	0.28	localized to both the plasma membrane and mitochondrial membrane, manganese ion transport
<i>MCH4</i>	3.93	0.55	similarity to monocarboxylate transporter proteins
<i>ATR1</i>	5.72	0.28	multidrug transport
<b>Unknown</b>			
<i>YLR297W</i>	3.12	0.82	weak similarity to <i>Vibrio vulnificus</i> VvpC protein
<i>YLR311C</i>	15.67	2.69	similarity to <i>S.tarentolae</i> cryptogene protein G4
<i>YLR312C</i>	6.69	1.01	hypothetical protein
<i>YLR270W</i>	4.13	0.20	strong similarity to YOR173w
<i>YLR271W</i>	2.82	0.45	hypothetical protein

<i>LIP2</i>	2.20	0.08	weak similarity to H.influenzae lipoate biosynthesis protein B
<i>YLR251W</i>	4.31	0.58	similarity to peroxisomal rat membrane protein PMP22
<i>YLR252W</i>	5.91	1.09	questionable ORF
<i>YLR173W</i>	2.63	0.08	hypothetical protein
<i>RFX1</i>	2.13	0.05	DNA binding protein, homologous to mammalian RFX1-4 proteins with novel DNA binding domain
<i>YLR177W</i>	3.01	0.26	similarity to suppressor protein Psp5p
<i>TFS1</i>	8.77	1.03	suppressor of <i>cdc25</i> , putative lipid binding protein
<i>YLR149C</i>	14.77	1.29	hypothetical protein
<i>YLR164W</i>	8.24	1.76	strong similarity to Sdh4p
<i>YLR122C</i>	8.08	3.40	hypothetical protein
<i>TIS11</i>	10.84	2.54	zinc finger containing homolog of mammalian TIS11, glucose repressible gene
<i>YLR097C</i>	2.26	0.14	hypothetical protein
<i>YLR108C</i>	3.30	0.64	strong similarity to YDR132c
<i>YLR077W</i>	2.43	0.10	weak similarity to Xenopus RCC1 protein
<i>EMP46</i>	4.14	0.82	strong similarity to Emp47p
<i>XDJ1</i>	2.32	0.22	Homolog of E. coli DnaJ, closely related to Ydj1p
<i>YLR047C</i>	2.94	0.31	similarity to hypothetical protein YGL160w
<i>LOT6</i>	3.25	0.30	weak similarity to E.coli hypothetical 20.4 kDa protein
<i>YLL023C</i>	3.08	0.16	similarity to hypothetical protein YLR064w
<i>YLL057C</i>	12.51	3.66	similarity to E.coli dioxygenase
<i>YLL056C</i>	8.08	1.01	similar to Y.pseudotuberculosis CDP-3,6-dideoxy-D-glycero-L-glycero-4-hexulose-5-epimerase
<i>YLL055W</i>	10.73	1.46	similarity to Dal5p
<i>YKR104W</i>	2.90	0.51	similarity to multidrug resistance proteins
<i>ECM4</i>	19.25	4.58	ExtraCellular Mutant
<i>YKR046C</i>	8.31	1.83	hypothetical protein
<i>YKR049C</i>	6.43	1.05	hypothetical protein
<i>TOS5</i>	4.39	0.48	hypothetical protein
<i>YKL023W</i>	4.24	0.71	weak similarity to human cyclin II
<i>YKL071W</i>	56.99	4.44	weak similarity to A.parasiticus nor-1 protein
<i>MNR2</i>	2.27	0.09	overexpression overcomes manganese toxicity
<i>YKL091C</i>	8.13	0.52	strong similarity to Sec14p
<i>YKL086W</i>	123.97	16.41	hypothetical protein
<i>YKL107W</i>	65.02	31.57	weak similarity to S.antibioticus probable oxidoreductase
<i>YKL100C</i>	2.81	0.14	similarity to C.elegans hypothetical protein
<i>YKL098W</i>	2.14	0.09	hypothetical protein
<i>YJU3</i>	2.36	0.09	weak similarity to E.coli hypothetical protein
<i>YKL133C</i>	2.97	0.59	probable purine nucleotide-binding protein
<i>YKL121W</i>	2.54	0.07	strong similarity to YMR102c
<i>YKL151C</i>	5.74	1.00	similarity to C.elegans hypothetical protein R107.2
<i>YKL206C</i>	2.55	0.20	hypothetical protein
<i>YKL195W</i>	3.03	0.23	similarity to rabbit histidine-rich calcium-binding

			protein
<i>SDS22</i>	3.50	0.21	Interacts with and may be a positive regulator of GLC7 which encodes type1 protein phosphatase
<i>YKL187C</i>	11.61	4.32	strong similarity to hypothetical protein YLR413w
<i>NJR005C</i>	36.89	11.59	non-annotated SAGE orf
<i>NJR003W</i>	2.55	0.21	non-annotated SAGE orf
<i>NJL023C</i>	27.44	24.34	non-annotated SAGE orf
<i>YJR142W</i>	2.97	0.12	similarity to thiamin pyrophosphokinase
<i>ENT3</i>	2.61	0.18	similarity to human KIAA0171 protein
<i>YJR096W</i>	6.80	0.31	similarity to <i>Corynebacterium</i> 2,5-diketo-D-gluconic acid reductase and aldehyde reductases
<i>PTK2</i>	2.51	0.13	Putative serine/threonine protein kinase
<i>BNA2</i>	7.74	2.29	similarity to mammalian indoleamine 2,3-dioxygenase
<i>YJR039W</i>	3.83	0.41	hypothetical protein
<i>YJR008W</i>	6.85	2.89	similarity to <i>S.pombe</i> hypothetical protein
<i>YJL017W</i>	3.03	0.38	hypothetical protein
<i>YJL016W</i>	3.16	0.40	weak similarity to hypothetical protein YNL278w and YLR187w
<i>YJL070C</i>	3.28	0.21	similarity to AMP deaminases
<i>BNA3</i>	3.26	0.32	similarity to kynurenine aminotransferase and glutamine-phenylpyruvate transaminase
<i>YJL084C</i>	2.08	0.03	similarity to hypothetical protein YKR021w
<i>YJL119C</i>	4.98	1.69	questionable ORF
<i>YJL142C</i>	3.42	0.57	questionable ORF
<i>YJL131C</i>	2.33	0.04	similarity to nonepidermal <i>Xenopus</i> keratin, type I
<i>YJL163C</i>	3.43	0.41	hypothetical protein
<i>YJL161W</i>	12.64	1.64	hypothetical protein
<i>YJL149W</i>	2.53	0.32	similarity to hypothetical protein YDR131c
<i>YJL185C</i>	2.88	0.32	hypothetical protein
<i>YJL199C</i>	3.38	0.58	hypothetical protein
<i>VTH2</i>	2.50	0.11	strong similarity to Pep1p
<i>YAL028W</i>	2.52	0.09	similarity to hypothetical protein YOR324c
<i>gIR04_6</i>	2.43	0.27	<i>Saccharomyces cerevisiae</i> chromosome IX, Found forward in NC_001141 between 371963 and 372495
<i>YHLCOMEGA1</i>	2.66	0.21	YHLCOMEGA1 Ty5 LTR
<i>YERCTAU3</i>	3.16	0.48	YERCTAU3 Ty4 LTR
<i>TY1B_DR2_ex2_1</i>	2.43	0.09	<i>Saccharomyces cerevisiae</i> chromosome IV, Found forward in NC_001136 between 804494 and 805681
<i>YNRCDELTA9</i>	2.13	0.03	YNRCDELTA9 Ty1 LTR
<i>YMRCTAU3</i>	2.22	0.04	YMRCTAU3 Ty4 LTR
<i>NIR004C</i>	3.70	0.79	non-annotated SAGE orf
<i>NIR005C</i>	2.66	0.12	non-annotated SAGE orf
<i>NIR010W</i>	2.82	0.54	non-annotated SAGE orf
<i>DRE3</i>	2.52	0.13	strong similarity to Nbp35p and human nucleotide-binding protein
<i>YIR003W</i>	2.72	0.14	weak similarity to mammalian neurofilament triplet H

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			proteins
<i>YIR007W</i>	2.40	0.12	hypothetical protein
<i>VID28</i>	3.26	0.31	hypothetical protein
<i>YIL067C</i>	2.25	0.02	hypothetical protein
<i>YIL055C</i>	4.41	0.60	hypothetical protein
<i>YIL087C</i>	3.90	0.18	hypothetical protein
<i>YIL077C</i>	2.46	0.13	hypothetical protein
<i>YIL113W</i>	4.53	0.22	similarity to dual-specificity phosphatase Msg5p
<i>FYV10</i>	3.94	0.56	hypothetical protein
<i>YIL165C</i>	7.37	1.18	putative pseudogene
<i>ECM37</i>	2.42	0.10	ExtraCellular Mutant
<i>YIL166C</i>	2.41	0.11	similarity to allantoate permease Dal5p
<i>YHR209W</i>	8.19	0.44	similarity to hypothetical protein YER175c
<i>NHR017W</i>	2.56	0.26	non-annotated SAGE orf
<i>NHR002C</i>	8.40	0.93	non-annotated SAGE orf
<i>YHR198C</i>	2.94	0.35	strong similarity to hypothetical protein YHR199c
<i>YHR199C</i>	5.45	0.49	strong similarity to hypothetical protein YHR198c
<i>YHR192W</i>	2.27	0.00	hypothetical protein
<i>NVJ1</i>	2.86	0.14	hypothetical protein
<i>YHR138C</i>	3.33	0.59	hypothetical protein
<i>YHR111W</i>	3.40	0.37	moeB, thiF, UBA1
<i>YHR112C</i>	2.29	0.02	Cystathionine gamma-synthase
<i>YHR087W</i>	9.22	0.94	hypothetical protein
<i>YHR097C_ex2</i>	2.72	0.24	strong similarity to hypothetical protein YDR348c
<i>BIG1</i>	2.51	0.26	Bad in glucose or big cells
<i>YHR080C</i>	2.57	0.16	similarity to hypothetical protein YDR326c, YFL042c and YLR072w
<i>YHR048W</i>	9.94	2.75	similarity to multidrug resistance proteins
<i>YHR029C</i>	3.69	0.43	Thymidylate synthase (putative\; weak)
<i>YSC84</i>	6.17	0.54	SH3 domain in C-terminus
<i>YHL021C</i>	6.28	0.55	weak similarity to Pseudomonas gamma-butyrobetaine hydroxylase
<i>HSE1</i>	2.64	0.16	SH3 domain
<i>NGR001W</i>	4.94	0.78	non-annotated SAGE orf
<i>NGR042W</i>	2.62	0.23	non-annotated SAGE orf
<i>NGL040C</i>	2.73	0.60	non-annotated SAGE orf
<i>NGR052C</i>	2.57	0.25	non-annotated SAGE orf
<i>NGR053C</i>	2.88	0.26	non-annotated SAGE orf
<i>NGL007W</i>	4.15	0.52	non-annotated SAGE orf
<i>YGR237C</i>	3.29	0.29	weak similarity to YOR019w
<i>SOL4</i>	16.76	2.06	similar to SOL3
<i>YGR223C</i>	2.79	0.30	weak similarity to hypothetical protein YFR021w
<i>YGR201C</i>	3.17	0.11	strong similarity to translation elongation factor eEF1 alpha chain Cam1p
<i>YGR205W</i>	2.89	0.19	similarity to S.pombe hypothetical protein D89234
<i>YGR146C</i>	2.64	0.09	hypothetical protein

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<i>YGR149W</i>	2.99	0.11	hypothetical protein
<i>YGR127W</i>	3.70	0.25	weak similarity to mouse T10 protein
<i>YGR130C</i>	3.23	0.53	weak similarity to myosin heavy chain proteins
<i>VPS62</i>	2.69	0.22	strong similarity to hypothetical protein YPR157w
<i>MDR1</i>	2.78	0.16	Mac1-dependent regulator
<i>YGR053C</i>	2.76	0.34	hypothetical protein
<i>YGR043C</i>	13.59	0.97	strong similarity to transaldolase
<i>NMA2</i>	4.57	0.48	strong similarity to hypothetical protein YLR328w
<i>YGR011W</i>	4.98	0.82	questionable ORF
<i>YGL059W</i>	3.26	0.77	similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
<i>YGL047W</i>	2.28	0.03	similarity to hypothetical <i>S. pombe</i> protein
<i>YGL045W</i>	2.65	0.14	hypothetical protein
<i>VPS73</i>	4.17	0.04	similarity to glucose transport proteins
<i>YGL121C</i>	7.74	0.61	hypothetical protein
<i>YGL114W</i>	4.35	0.43	weak similarity to <i>H. influenzae</i> permease
<i>YGL161C</i>	2.46	0.08	hypothetical protein
<i>YGL157W</i>	2.40	0.21	similarity to <i>V. vinifera</i> dihydroflavonol 4-reductase
<i>MMM2</i>	2.55	0.17	hypothetical protein
<i>YGL198W</i>	2.07	0.02	weak similarity to Yip1p
<i>VID30</i>	3.87	0.26	TOR inhibitor
<i>YGL226W</i>	3.09	0.46	similarity to <i>N. crassa</i> cytochrome-c oxidase chain V
<i>YGL250W</i>	3.50	1.08	YGL250W hypothetical protein
<i>NFL009W</i>	2.50	0.34	non-annotated SAGE orf
<i>NFR001W</i>	2.87	0.20	non-annotated SAGE orf
<i>YFL043C</i>	5.59	0.52	hypothetical protein
<i>YFL042C</i>	4.25	0.34	similarity to hypothetical protein YLR072w
<i>YFR003C</i>	3.73	0.09	hypothetical protein
<i>YFR017C</i>	7.19	0.75	hypothetical protein
<i>YFR022W</i>	2.50	0.19	similarity to Rod1p
<i>YFL030W</i>	4.54	0.57	similarity to several transaminases
<i>YFL057C</i>	34.24	4.52	strong similarity to aryl-alcohol dehydrogenases
<i>NEL017W</i>	3.94	0.22	non-annotated SAGE orf
<i>YER067c-a</i>	4.96	0.89	questionable ORF
<i>TMT1</i>	10.42	2.40	similarity to hypothetical protein YHR209w
<i>YER039C-A</i>	2.22	0.11	hypothetical protein
<i>SPII</i>	3.64	0.36	Stationary Phase Induced
<i>YER119C</i>	2.83	0.35	weak similarity to <i>E. herbicola</i> tyrosine permease
<i>SHC1</i>	2.58	0.20	sporulation-specific homolog of <i>csd4</i>
<i>YER067W</i>	24.11	5.85	strong similarity to hypothetical protein YIL057c
<i>YER053C</i>	3.92	0.73	strong similarity to mitochondrial phosphate carrier protein
<i>YEL020C</i>	2.34	0.15	similarity to <i>O. formigenes</i> oxalyl-CoA decarboxylase
<i>YEL041W</i>	3.33	0.59	strong similarity to Utr1p
<i>NDR156C</i>	2.78	0.06	non-annotated SAGE orf
<i>SNA2</i>	2.24	0.11	hypothetical protein identified by SAGE

<i>YDR516C</i>	3.35	0.16	strong similarity to glucokinase
<i>YDR533C</i>	4.14	0.55	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c
<i>PLM2</i>	4.05	0.89	similarity to hypothetical protein YLR183c, plasmid maintenance
<i>YDR479C</i>	4.46	0.30	weak similarity to YHR150w
<i>VPS60</i>	2.71	0.27	weak similarity to Snf7p
<i>ARO80</i>	2.82	0.31	hypothetical protein
<i>YDR425W</i>	2.72	0.26	similarity to hypothetical protein YDL113c
<i>YDR387C</i>	2.69	0.32	similarity to Itr1p and Itr2p and E.coli araE
<i>YDR391C</i>	3.65	0.17	strong similarity to hypothetical protein YOR013w
<i>YDR330W</i>	2.78	0.16	similarity to hypothetical <i>S. pombe</i> protein
<i>RTT103</i>	2.89	0.45	Regulator of Ty1 Transposition
<i>YDR306C</i>	2.41	0.19	weak similarity to <i>S.pombe</i> hypothetical protein SPAC6F6
<i>YDR287W</i>	2.52	0.16	similarity to inositolmonophosphatases
<i>YDR221W</i>	2.21	0.03	weak similarity to the beta subunit of an ER luminal alpha-glucosidase from mouse
<i>STB3</i>	2.61	0.26	Binds Sin3p in two-hybrid assay
<i>YDR132C</i>	8.79	2.29	strong similarity to hypothetical protein YLR108c
<i>YDR070C</i>	11.89	2.46	hypothetical protein
<i>YDR061W</i>	2.58	0.03	similarity to E.coli modF and photorepair protein phrA
<i>YDR031W</i>	2.65	0.19	hypothetical protein
<i>YDR003W</i>	4.37	0.37	strong similarity to hypothetical protein YBR005w
<i>YDR018C</i>	13.91	8.57	strong similarity to hypothetical protein YBR042c
<i>YDL057W</i>	2.38	0.23	hypothetical protein
<i>YDL091C</i>	2.71	0.32	weak similarity to mouse FAF1 protein
<i>YDL089W</i>	2.52	0.10	hypothetical protein
<i>YDL110C</i>	5.48	0.30	hypothetical protein
<i>YDL124W</i>	5.28	0.18	similarity to aldose reductases
<i>IWR1</i>	3.97	0.36	hypothetical protein
<i>YDL146W</i>	3.77	0.21	weak similarity to Orc3p
<i>UGX2</i>	8.81	0.98	protein of unknown function
<i>ENT1</i>	2.88	0.47	strong similarity to hypothetical protein YLR206w and to human KIAA0171 protein
<i>YDL218W</i>	62.69	0.67	weak similarity to hypothetical protein YNR061c
<i>YDL206W</i>	2.46	0.11	weak similarity to transporter proteins
<i>YDL204W</i>	19.33	1.53	similarity to hypothetical protein YDR233c
<i>AAD4</i>	33.23	3.18	Hypothetical aryl-alcohol dehydrogenase
<i>ADY3</i>	4.47	0.48	hypothetical protein
<i>HBT1</i>	5.49	1.23	weak similarity to mucin
<i>YDL222C</i>	2.95	0.12	strong similarity to hypothetical protein YNL194c and similarity to YML052w
<i>YCR102C</i>	5.33	0.48	Alcohol dehydrogenase
<i>YCL039W</i>	2.42	0.05	regulatory protein
<i>YCL049C</i>	2.77	0.44	hypothetical protein

<i>NBR034W</i>	2.55	0.29	non-annotated SAGE orf
<i>NBR063C</i>	2.87	0.30	non-annotated SAGE orf
<i>NBR047W</i>	2.70	0.21	non-annotated SAGE orf
<i>NBR048W</i>	2.42	0.13	non-annotated SAGE orf
<i>YBR285W</i>	3.44	0.58	hypothetical protein
<i>YBR293W</i>	2.51	0.12	Probable multidrug resistance protein
<i>YBR085c-a</i>	3.30	0.15	hypothetical protein
<i>YBR262C</i>	2.16	0.11	questionable ORF
<i>YBR269C</i>	4.67	0.23	hypothetical protein
<i>YBR273C</i>	3.32	0.31	similarity to hypothetical protein YJL048c
<i>YBR280C</i>	2.95	0.41	hypothetical protein
<i>YBR255W</i>	3.35	0.75	hypothetical protein
<i>SDS24</i>	5.76	0.80	strong similarity to hypothetical protein YGL056c
<i>YBR204C</i>	2.87	0.37	Probable serine-active lipase, peroxisomal
<i>YBR137W</i>	3.25	0.13	hypothetical protein
<i>YBR139W</i>	2.44	0.07	Probable serine-type carboxypeptidase
<i>YBR062C</i>	2.42	0.16	similarity to rat neurodegeneration associated protein 1
<i>YBR070C</i>	2.56	0.18	osmotolerance protein
<i>YBR047W</i>	8.47	1.23	hypothetical protein
<i>YBR053C</i>	3.13	0.19	similarity to rat regucalcin
<i>YBR056W</i>	3.23	0.59	Homolog to glucan-1,3--glucosidase 2
<i>YBL048W</i>	3.51	0.45	hypothetical protein
<i>ECM13</i>	6.61	3.03	ExtraCellular Mutant
<i>YBL091C-A</i>	3.68	0.33	weak similarity to SCS2
<i>YBL086C</i>	3.78	1.18	involved in sugar metabolism
<i>ECM21</i>	2.28	0.07	ExtraCellular Mutant
<i>NPR015C</i>	3.31	0.64	non-annotated SAGE orf
<i>ARR2</i>	3.45	0.33	Required for arsenate but not for arsenite resistance
<i>ARR3</i>	5.64	1.47	involved in arsenite transport
<i>YPR172W</i>	2.61	0.26	strong similarity to YLR456w
<i>YPR127W</i>	4.49	1.22	similarity to C-term. of <i>N.tabacum</i> auxin-induced protein
<i>YPR081C</i>	3.64	0.30	strong similarity to glycyl-tRNA synthetases
<i>YPR085C</i>	2.61	0.37	hypothetical protein
<i>YPR093C</i>	3.26	0.42	weak similarity to zinc-finger proteins
<i>OPY2</i>	2.80	0.30	imparts Far- phenotype
<i>YPR077C</i>	5.67	2.58	questionable ORF
<i>YPR015C</i>	4.88	0.97	similarity to transcription factors
<i>EAF3</i>	2.16	0.09	similarity to human hypothetical protein
<i>YPL017C</i>	11.00	1.42	strong similarity to Lpd1p and other dihydrolipoamide dehydrogenases
<i>YPL070W</i>	3.10	0.15	weak similarity to Vps9p
<i>UIP4</i>	4.39	0.31	weak similarity to <i>Xenopus</i> protein xlgv7
<i>YPL191C</i>	3.13	0.50	strong similarity to YGL082w
<i>YPL230W</i>	10.95	4.84	Up in StarVation
<i>YPL229W</i>	2.30	0.18	weak similarity to YMR181c

<i>YPL222W</i>	5.76	1.10	similarity to <i>C.perfringens</i> hypothetical protein
<i>GYP5</i>	3.72	0.41	similarity to mouse Tbc1 protein
<i>YPL247C</i>	2.83	0.26	similarity to human HAN11 protein and petunia an11 protein
<i>NOR052W</i>	3.08	0.07	non-annotated SAGE orf
<i>NOR080W</i>	8.92	2.22	non-annotated SAGE orf
<i>YOR352W</i>	2.56	0.25	hypothetical protein
<i>YOR289W</i>	9.85	0.92	similarity to <i>C.elegans</i> hypothetical protein
<i>YOR292C</i>	3.07	0.36	similarity to human and mouse glomerulosclerosis protein Mpv17
<i>YOR215C</i>	3.23	0.49	similarity to <i>M.xanthus</i> hypothetical protein
<i>YOR220W</i>	2.86	0.22	hypothetical protein
<i>YOR223W</i>	3.11	0.47	protein of unknown function
<i>YOR227W</i>	4.32	0.57	similarity to microtubule-interacting protein Mhp1p
<i>YOR173W</i>	17.88	1.22	strong similarity to YLR270w
<i>YOR152C</i>	3.59	0.41	hypothetical protein
<i>YOR161C</i>	3.31	0.19	similarity to <i>C.elegans</i> cosmid F35C8
<i>YOR121C</i>	3.82	0.13	questionable ORF
<i>YOR138C</i>	2.95	0.10	hypothetical protein
<i>YOR114W</i>	2.73	0.40	hypothetical protein
<i>YOR052C</i>	2.31	0.03	hypothetical protein
<i>YOR042W</i>	2.84	0.32	weak similarity to YDR273w
<i>ROD1</i>	2.92	0.49	Resistance to o-dinitrobenzene, calcium, and zinc
<i>YOL032W</i>	3.22	0.57	hypothetical protein
<i>YOL029C</i>	2.94	0.23	hypothetical protein
<i>YOL048C</i>	4.26	0.38	similarity to YAL018c and YOL047c
<i>YOL083W</i>	6.20	0.85	similarity to YOL082w
<i>YOL071W</i>	4.02	0.21	similarity to hypothetical <i>S. pombe</i> protein
<i>AMI3</i>	2.58	0.20	similarity to <i>C.elegans</i> hypothetical protein M02F4.4
<i>YOL101C</i>	5.83	1.64	similarity to YOL002c and YDR492w
<i>YOL117W</i>	2.88	0.15	weak similarity to human sodium channel alpha chain HBA
<i>NNL034W</i>	3.92	0.54	non-annotated SAGE orf
<i>YOL163W</i>	3.55	1.11	similarity to <i>P.putida</i> phthalate transporter
<i>YOL153C</i>	14.65	2.19	strong similarity to Cps1p
<i>YNR034w-a</i>	21.96	5.58	hypothetical protein
<i>YNR047W</i>	2.49	0.19	similarity to ser/thr protein kinases
<i>MSO1</i>	2.44	0.11	small hydrophilic protein, enriched in microsomal membrane fraction, interacts with Sec1p
<i>SOL1</i>	5.05	0.67	similaer to glucose-6-phosphate dehydrogenase non-catalytic domains
<i>VPS27</i>	2.89	0.22	hydrophilic protein\; has cysteine rich putative zinc finger esential for function
<i>YNL092W</i>	14.77	7.45	similarity to hypothetical <i>C. elegans</i> proteins Y48E1C.2 and Y48E1C.c
<i>YNL115C</i>	4.06	0.12	weak similarity to <i>S.pombe</i> hypothetical protein

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			SPAC23C11
<i>YNL100W</i>	3.20	0.55	hypothetical protein
<i>YNL134C</i>	9.52	2.46	similarity to <i>C.carbonum</i> toxD gene
<i>YNL156C</i>	2.26	0.14	similarity to YHR133c
<i>YNL165W</i>	2.24	0.09	similarity to YOR385w and YMR316w
<i>YNL200C</i>	3.54	0.24	strong similarity to human TGR-CL10C
<i>YNL195C</i>	6.26	1.45	hypothetical protein
<i>YNL194C</i>	33.16	14.18	strong similarity to YDL222c and similarity to Sur7p
<i>YNL253W</i>	2.42	0.34	hypothetical protein
<i>YNL274C</i>	6.97	1.18	similarity to glycerate- and formate-dehydrogenases
<i>RIM21</i>	2.68	0.14	Regulator of IME2
<i>YNL305C</i>	3.29	0.17	similarity to C-term. of <i>A.nidulans</i> regulatory protein (qutR)
<i>YMR293C</i>	2.17	0.06	similarity to amidases
<i>YMR258C</i>	3.82	0.51	hypothetical protein
<i>YMR262W</i>	5.35	0.60	similarity to <i>S.pombe</i> scn1 protein
<i>YMR265C</i>	2.47	0.38	hypothetical protein
<i>YMR244C-A</i>	2.91	0.20	questionable ORF
<i>YMR253C</i>	2.33	0.08	strong similarity to YPL264c
<i>YMR196W</i>	8.27	1.27	hypothetical protein
<i>YMR210W</i>	3.04	0.21	similarity to <i>P.glauca</i> late embryogenesis abundant protein and YBR177c and YPL095c
<i>SIP18</i>	13.83	8.57	protein of unknown function
<i>YMR181C</i>	3.71	0.37	similarity to YPL229w
<i>YMR157C</i>	2.15	0.07	hypothetical protein
<i>YMR135C</i>	3.04	0.50	hypothetical protein
<i>YMR090W</i>	15.74	1.01	strong similarity to <i>B. subtilis</i> conserved hypothetical protein yhfK
<i>YMR107W</i>	16.50	6.39	hypothetical protein
<i>YMR110C</i>	2.50	0.14	similarity to aldehyde dehydrogenase
<i>YMR087W</i>	3.27	0.47	hypothetical protein
<i>STB2</i>	4.03	0.27	Binds Sin3p in two-hybrid assay and is part of large protein complex with Sin3p and Stb1p
<i>YMR041C</i>	5.04	0.66	weak similarity to <i>Pseudomonas</i> L-fucose dehydrogenase
<i>SEL1</i>	2.50	0.08	hypothetical protein
<i>YML030W</i>	2.35	0.14	hypothetical protein
<i>YML117W</i>	2.32	0.16	similarity to YPL184c
<i>YML131W</i>	5.35	0.46	similarity to human leukotriene b4 12-hydroxydehydrogenase
<i>NLR027W</i>	3.03	0.39	non-annotated SAGE orf
<i>YLR460C</i>	5.16	0.43	similarity to <i>C.carbonum</i> toxD protein
<i>YLR345W</i>	4.19	0.20	similarity to Pfk26p and other 6-phosphofructo-2-kinases
<i>YLR352W</i>	2.29	0.06	hypothetical protein
<i>YLR356W</i>	2.66	0.11	similarity to SCM4 protein

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<i>YLR326W</i>	2.42	0.06	hypothetical protein
<i>YLR327C</i>	23.80	6.17	strong similarity to Stf2p
<i>MSC1</i>	19.88	5.25	C-terminal part starting with aa 262 cause growth inhibition when overexpressed

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