

Down regulated genes in BER-defective cells following 0.4mM H₂O₂ exposure for 30 minutes

Gene name	Average Fold Change	S.E.M.	Description
DNA Repair/ Replication			
<i>RNR1</i>	-3.25	0.35	ribonucleotide reductase
<i>MCM3</i>	-2.36	0.07	Member of complex that acts at ARS s to initiate replication
Signal Transduction			
<i>ALK1</i>	-3.80	0.30	Protein serine/threonine kinase activity
<i>RAS1</i>	-2.69	0.22	ras proto-oncogene homolog, G-protein signaling, adenylate cyclase activating pathway
Chromatin Structure			
<i>HTB1</i>	-3.09	0.24	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
<i>SCC2</i>	-3.17	0.05	Sister chromatid cohesion protein
<i>SIR2</i>	-2.54	0.20	regulator of silent mating loci
<i>CST13</i>	-2.20	0.06	chromosome stability
<i>HTA2</i>	-3.83	0.30	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)
<i>HTB2</i>	-10.26	0.42	Histone H2B (HTB1 and HTB2 code for nearly identical proteins)
<i>NHP6A</i>	-2.60	0.05	11-kDa nonhistone chromosomal protein
<i>HST3</i>	-5.88	0.82	Homolog of SIR2
<i>HHF2</i>	-2.54	0.22	Histone H4 (HHF1 and HHF2 code for identical proteins)
Transcription			
<i>ASH1</i>	-2.29	0.12	Zinc-finger inhibitor of HO transcription which is asymmetrically localized to the daughter cell nucleus
<i>RPA12</i>	-4.93	0.20	A12.2 subunit of RNA polymerase I
<i>RPA34</i>	-4.68	0.17	RNA polymerase I subunit, not shared (A34.5)
<i>FKH1</i>	-3.16	0.22	transcription factor fork head protein
<i>RPC10</i>	-2.74	0.04	subunit of RNA polymerase II
<i>RPA14</i>	-2.68	0.09	RNA polymerase I subunit A14
<i>SWI5</i>	-3.16	0.30	transcriptional activator
<i>RPC11</i>	-2.31	0.18	TFIIS-like small Pol III subunit C11
<i>RPO26</i>	-2.60	0.15	subunit common to RNA polymerases I, II, and

			III
<i>RPC82</i>	-2.24	0.06	82-kDa subunit of RNA polymerase III (C)
<i>RPA135</i>	-3.17	0.25	RNA polymerase I subunit A135
<i>SWI1</i>	-2.47	0.16	Zinc-finger transcription factor
<i>MOT1</i>	-3.02	0.26	involved in TBP TATA-binding protein regulation
<i>RPA43</i>	-2.29	0.16	DNA-dependent RNA polymerase I subunit A43
<i>RPA190</i>	-2.67	0.15	RNA polymerase I subunit 190 (alpha)
<i>RPB8</i>	-4.02	0.33	16-kDa RNA polymerase subunit (common to polymerases I, II and III)
<i>RPO31</i>	-3.58	0.12	RNA polymerase III large subunit
<i>RPC19</i>	-2.81	0.13	subunit common to RNA polymerases I (A) and III (C)
<i>RPC31</i>	-3.58	0.14	31-kDa subunit of RNA polymerase III (C); HMG1 like protein
<i>RAP1</i>	-2.38	0.18	DNA-binding protein involved in either activation or repression of transcription, depending on binding site context
<i>RPA49</i>	-4.61	0.48	49-kDa alpha subunit of RNA polymerase A
<i>RRN11</i>	-7.21	1.31	Component of rDNA transcription factor CF
<i>DAT1</i>	-4.48	0.86	RNA polymerase I transcription factor datin, an oligo(dA).oligo(dT)-binding protein, repression of transcription from Pol II promoter
Nucleotide Metabolism			
<i>DCD1</i>	-2.69	0.12	dCMP deaminase
<i>FUR1</i>	-3.79	0.46	UPRTase
<i>FCY2</i>	-3.38	0.32	purine-cytosine permease
<i>GUK1</i>	-2.28	0.10	guanylate kinase
<i>HPT1</i>	-6.36	0.58	Hypoxanthine Phosphoribosyltransferase
<i>DUT1</i>	-2.90	0.22	dUTP pyrophosphatase (dUTPase)
<i>FUI1</i>	-2.55	0.35	uridine permease
<i>URA7</i>	-6.76	0.06	CTP synthase, highly homologous to URA8 CTP synthase
<i>IMD4</i>	-6.90	0.08	strong similarity to IMP dehydrogenases
Degradation			
<i>MKC7</i>	-3.53	0.19	aspartyl protease related to Yap3p
<i>UBP10</i>	-2.95	0.04	a deubiquitinating enzyme
<i>CIC1</i>	-5.24	0.87	Core interacting component 1 protease substrate recruitment factor
Mitochondrial Maintenance			
<i>MAE1</i>	-7.11	0.59	mitochondrial malic enzyme

<i>NUC1</i>	-2.61	0.11	mitochondrial nuclease
<i>QO185_ex4</i>	-2.44	0.12	cytochrome-c oxidase subunit I
<i>AAC3</i>	-3.11	0.64	mitochondrial ADP/ATP translocator
<i>SUN4</i>	-3.47	0.24	Protein involved in the aging process, mitochondrion organization and biogenesis
<i>CYB5</i>	-9.57	1.64	cytochrome b5
<i>YHM2</i>	-6.07	0.74	DNA-binding protein, mtDNA stabilizing protein, mitochondrial inner membrane protein low homology to RIM2
Cell Cycle			
<i>NNF1</i>	-8.08	2.18	involved in nuclear function, interacts with mec3, mitosis
<i>SAP185</i>	-3.26	0.50	SIT4 associated proteinprotein serine/threonine phosphatase G1/S transition of mitotic cell cycle
<i>FAR1</i>	-5.59	0.64	Factor arrest protein, cyclin-dependent protein kinase inhibitor
<i>CDC6</i>	-3.96	0.46	Protein involved in initiation of DNA replication
<i>LTE1</i>	-2.34	0.15	putative GTP-exchange protein
<i>SIM1</i>	-2.74	0.45	involved in cell cycle regulation and aging
<i>CLB1</i>	-3.37	0.44	G(sub)2-specific B-type cyclin
<i>CLB6</i>	-7.46	1.06	B-type cyclin
<i>SCM4</i>	-5.53	0.92	Protein that suppresses ts allele of CDC4 when overexpressed
<i>CDC20</i>	-2.45	0.09	Required for onset of anaphase
<i>CIN8</i>	-2.51	0.15	Kinesin-related protein involved in establishment and maintenance of mitotic spindle
<i>PCL9</i>	-2.96	0.28	PHO85 cyclin
<i>CLB2</i>	-4.29	0.37	G(sub)2-specific B-type cyclin
<i>CLN2</i>	-4.75	0.14	G(sub)1 cyclin
<i>NDD1</i>	-2.42	0.14	G2/M-specific transcription in mitotic cell cycle
<i>CDC33</i>	-2.37	0.13	mRNA cap binding protein eIF-4E
<i>PCL1</i>	-84.89	30.24	G(sub)1 cyclin that associates with PHO85
<i>EGT2</i>	-2.95	0.47	Cell-cycle regulation protein, may be involved in the correct timing of cell separation after cytokinesis
<i>CLN1</i>	-7.05	0.96	G(sub)1 cyclin
<i>CDC5</i>	-3.66	0.25	protein kinase which functions at the G(sub)2/V boundary
Cell Growth/ Maintenance			
<i>RAX2</i>	-3.94	0.38	Involved in the maintenance of bipolar pattern
<i>PIR1</i>	-3.15	0.37	Protein containing tandem internal repeats, structural constituent of cell wall
<i>BUD4</i>	-3.25	0.52	Co-assembles with Bud3p at bud sites

<i>ECM1</i>	-3.98	0.15	putative transmembrane domain protein involved in cell wall biogenesis
<i>SPC97</i>	-2.12	0.06	spindle pole body component, associates in a complex with Spc98p and Tub4p
<i>GIC1</i>	-3.02	0.64	small GTPase regulatory/interacting protein
<i>MSB2</i>	-3.19	0.23	putative integral membrane protein, establishment of cell polarity sensu <i>Saccharomyces</i>
<i>SCW11</i>	-2.86	0.07	glucanase gene family member
<i>VRG4</i>	-2.83	0.07	May regulate Golgi function and glycosylation in Golgi
<i>KAP123</i>	-2.72	0.23	Karyopherin beta 4
<i>UTR2</i>	-10.53	1.44	cell wall organization and biogenesis
<i>GIN4</i>	-2.49	0.13	putative serine/threonine kinase, Growth inhibitory gene
<i>HKR1</i>	-2.30	0.09	cell surface protein that may regulate cell wall beta-glucan synthesis and bud site selection
<i>ATC1</i>	-5.09	0.51	Aip Three Complex; interacts with AIP3, localized to the nucleus
<i>PRM7</i>	-6.12	1.45	pheromone regulated protein
<i>HO</i>	-12.95	0.75	Homothallic switching endonuclease
<i>BUD23</i>	-2.53	0.20	Protein carboxyl methylase
<i>BUD3</i>	-3.63	0.51	Cell cycle regulated protein required for axial bud formation; co-assembles with Bud4p at bud sites
<i>VIK1</i>	-2.69	0.20	Cik1p homolog, microtubule motor
<i>MSB1</i>	-2.50	0.23	Protein that may play a role in polarity establishment and bud formation
<i>YIP3</i>	-2.70	0.05	Interacts with YPT proteins, ER to Golgi transport
<i>SCW10</i>	-2.73	0.05	member of the glucanase gene family
<i>HOF1</i>	-3.04	0.22	SH3 domain containing-protein required for cytokinesis
Metabolism			
<i>DPH2</i>	-2.38	0.06	diphthamide synthesis protein
<i>ILV3</i>	-4.78	0.32	dihydroxyacid dehydratase
<i>FAA3</i>	-3.75	0.42	Acyl CoA synthase
<i>ERG7</i>	-2.28	0.07	2,3-oxidosqualene-lanosterol cyclase
<i>ERG11</i>	-2.80	0.15	cytochrome P450 lanosterol 14a-demethylase
<i>BIO2</i>	-4.78	0.13	Biotin synthase
<i>ERG1</i>	-4.74	0.46	Squalene monooxygenase
<i>ATF2</i>	-5.07	0.87	Alcohol acetyltransferase
<i>ERG25</i>	-2.98	0.09	C-4 sterol methyl oxidase
<i>ADE6</i>	-2.43	0.07	5-phosphoribosylformyl glycinamide synthetase
<i>SEC53</i>	-2.30	0.09	phosphomannomutase
<i>SAH1</i>	-2.65	0.33	putative S-adenosyl-L-homocysteine hydrolase

<i>MNN1</i>	-4.21	0.23	Alpha-1,3-mannosyltransferase
<i>GDA1</i>	-2.30	0.07	Guanosine diphosphatase of Golgi membrane
<i>DLD3</i>	-4.48	0.32	D-lactate dehydrogenase
<i>ASP1</i>	-2.24	0.09	Asparaginase I, intracellular isozyme
<i>SUR2</i>	-2.80	0.16	Syringomycin response protein 2, sphingolipid metabolism
<i>LYS4</i>	-4.87	0.67	homoaconitase
<i>HEM13</i>	-3.05	0.41	Coproporphyrinogen III oxidase
<i>GLT1</i>	-6.93	0.64	Glutamate synthase (NADPH)
<i>FEN1</i>	-5.36	0.78	Probable subunit of 1,3-beta-glucan synthase\; homolog of ELO1
<i>CIT2</i>	-6.03	0.28	non-mitochondrial citrate synthase
<i>TSC10</i>	-2.69	0.08	sphingolipid biosynthesis
<i>ENP1</i>	-2.91	0.62	protein amino acid glycosylation
<i>PHO3</i>	-4.43	0.38	Acid phosphatase, constitutive
<i>CHS2</i>	-2.85	0.17	chitin synthase 2
<i>CDS1</i>	-2.46	0.12	CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidyltransferase, CDP-diglyceride synthetase
<i>HMT1</i>	-3.50	0.37	nuclear protein arginine methyltransferase (mono- and asymmetrically dimethylating enzyme)
<i>TKL1</i>	-2.69	0.13	Transketolase 1
<i>ALD6</i>	-5.44	0.49	cytosolic aldehyde dehydrogenase
<i>SUR1</i>	-2.55	0.12	Involved in maintenance of phospholipid levels
<i>ALG5</i>	-2.55	0.25	UDP-glucose:dolichyl-phosphate glucosyltransferase
<i>HES1</i>	-3.94	1.29	Protein implicated in ergosterol biosynthesis
<i>MVD1</i>	-2.16	0.08	mevalonate pyrophosphate decarboxylase
<i>RK11</i>	-4.66	0.45	Ribose-5-phosphate ketol-isomerase
<i>AAH1</i>	-4.68	0.29	Adenosine deaminase\adenine aminohydrolase
<i>ARG80</i>	-2.50	0.13	Regulator of arginine-responsive genes with ARG81 and ARG82
<i>PLB2</i>	-3.08	0.46	Phospholipase B 2
<i>APT1</i>	-2.54	0.03	Adenine phosphoribosyltransferase
<i>SUR4</i>	-2.70	0.10	required for conversion of 24-carbon fatty acids to 26-carbon species
<i>ILV5</i>	-3.07	0.26	acetohydroxyacid reductoisomerase
Translation			
<i>TEF4</i>	-3.10	0.19	Translation elongation factor EF-1gamma
<i>EFB1</i>	-2.91	0.48	Translation elongation factor EF-1beta, GDP\GTP exchange factor for Tef1p\Tef2p
<i>TIF4631</i>	-2.93	0.23	mRNA cap-binding protein (eIF-4F), 150K subunit , highly homologous to Tif4632p

<i>HYP2</i>	-2.27	0.12	Translation initiation factor eIF-5A
<i>NEW1</i>	-3.50	0.24	similarity to translation elongation factor eEF3
<i>CAF20</i>	-2.20	0.08	Binds to eIF4E, represses cap-dependent translation initiation by interfering with interaction of eIF4E and eIF4G
<i>NIP1</i>	-2.52	0.03	~100 kDa cytoplasmic protein, translation initiation factor
Ribosomal Proteins			
<i>RPS28B</i>	-4.66	0.20	Ribosomal protein S28B (S33B) (YS27)
<i>RPS28B</i>	-3.58	0.13	Ribosomal protein S28B (S33B) (YS27)
<i>UTP13</i>	-3.56	0.25	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>SIK1</i>	-2.77	0.21	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>DIP2</i>	-4.28	0.29	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>RPS0B</i>	-3.56	0.15	Ribosomal protein S0B
<i>RLP24</i>	-3.85	0.33	similarity to ribosomal protein L24.e.B
<i>RPS27A</i>	-4.46	0.25	40S ribosomal protein S27A (rp61) (YS20)
<i>UTP18</i>	-3.05	0.19	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>RPL17B</i>	-2.50	0.09	Ribosomal protein L17B (L20B) (YL17)
<i>RPS14B</i>	-3.62	0.31	Ribosomal protein S14B (rp59B)
<i>UTP9</i>	-4.18	0.46	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>IMP3</i>	-3.66	0.13	ribosomal protein (weak similarity)
<i>RPL14B</i>	-2.73	0.25	Ribosomal protein L14B
<i>RPS0A</i>	-3.04	0.32	Ribosomal protein S0A
<i>UTP8</i>	-2.59	0.29	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>CGR1</i>	-5.63	0.67	ribosome biogenesis
<i>RPL22B</i>	-4.80	0.51	Ribosomal protein L22B (L1c) (rp4) (YL31)
<i>RPS26B</i>	-2.49	0.05	Ribosomal protein S26B
<i>SNU13</i>	-3.62	0.26	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>RPL27B</i>	-2.74	0.29	Ribosomal protein L27B
<i>UTP6</i>	-3.16	0.55	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>UTP4</i>	-2.91	0.10	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>MAK21</i>	-2.80	0.29	essential for 60s ribosome biogenesis
<i>RPS16B</i>	-2.32	0.11	Ribosomal protein S16B (rp61R)
<i>RPL13A</i>	-2.67	0.33	Ribosomal protein L13A
<i>NOPI4</i>	-2.74	0.29	part of small ribosomal subunit SSU

<i>PWP2</i>	-3.61	0.46	processosome contains U3 snoRNA part of small ribosomal subunit SSU
<i>UTP20</i>	-5.17	0.35	processosome contains U3 snoRNA part of small ribosomal subunit SSU
<i>RRP9</i>	-3.78	0.47	processosome contains U3 snoRNA part of small ribosomal subunit SSU
<i>RPS9A</i>	-3.42	0.44	processosome contains U3 snoRNA Ribosomal protein S9A (S13) (rp21) (YS11)
<i>NIP7</i>	-6.93	0.64	Nip7p is required for 60S ribosome subunit biogenesis
<i>RPL7B</i>	-8.77	0.89	Ribosomal protein L7B (L6B) (rp11) (YL8)
<i>NOP58</i>	-3.17	0.30	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>RPS10A</i>	-2.59	0.24	Ribosomal protein S10A
<i>RRS1</i>	-6.51	0.68	Regulator for ribosome synthesis
<i>RPL33B</i>	-3.03	0.22	Ribosomal protein L33B (L37B) (rp47) (YL37)
<i>NOC2</i>	-2.44	0.25	Nucleolar Complex 2; involved in nuclear export of pre-ribosomes
<i>BUD21</i>	-3.45	0.55	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>RLP7</i>	-2.82	0.26	Significant sequence similarity to RPL7B
<i>RPL9B</i>	-3.23	0.39	Ribosomal protein L9B (L8B) (rp24) (YL11)
<i>RPS7B</i>	-4.10	0.47	Ribosomal protein S7B (rp30)
<i>RPS7B</i>	-3.69	0.34	Ribosomal protein S7B (rp30)
<i>RPL18B</i>	-3.52	0.37	Ribosomal protein L18B (rp28B)
<i>RPS10B</i>	-5.61	0.57	Ribosomal protein S10B
<i>RPL36A</i>	-3.91	0.29	Ribosomal protein L36A (L39) (YL39)
<i>UTP15</i>	-3.12	0.23	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>UTP14</i>	-4.68	0.37	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>RPL31B</i>	-2.63	0.18	Ribosomal protein L31B (L34B) (YL28)
<i>UTP21</i>	-2.36	0.12	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>RPL38</i>	-2.17	0.06	Ribosomal protein L38
RNA Processing			
<i>IFH1</i>	-2.37	0.10	has a weak RNA-dependent ATPase activity which is not specific for rRNA
<i>CBF5</i>	-2.67	0.12	major low affinity 55 kDa Centromere/microtubule binding protein, rRNA modification
<i>SOF1</i>	-4.00	0.31	56 kDa nucleolar snRNP protein, shows homology to beta subunits of G-proteins and splicing factor Prp4

<i>DRS1</i>	-3.10	0.22	putative ATP dependent RNA helicase
<i>SRP40</i>	-5.93	0.45	nucleolar protein that is immunologically and structurally related to rat Nopp140
<i>DBP7</i>	-3.65	0.18	putative RNA helicase
<i>MRT4</i>	-3.72	0.19	mRNA turnover 4
<i>DHR2</i>	-2.98	0.28	probable ATP-dependent RNA helicase
<i>EBP2</i>	-3.80	0.24	Nucleolar protein, rRNA processing
<i>MTR4</i>	-3.36	0.15	DEAD-box family helicase required for mRNA export from nucleus
<i>DBP8</i>	-3.42	0.22	DEAD-box protein
<i>GAR1</i>	-4.31	0.38	small nucleolar RNP proteins
<i>NSR1</i>	-6.76	1.01	nuclear localization sequence binding protein, ribosomal small subunit assembly and maintenance
<i>DBP3</i>	-6.12	1.33	ATP-dependent RNA helicase CA3 of the DEAD/DEAH box family
<i>PAB1</i>	-2.39	0.11	Poly(A) binding protein, cytoplasmic and nuclear
<i>FIR1</i>	-2.40	0.16	Putative participant in 3' mRNA processing
<i>TRM1</i>	-3.15	0.26	N ² ,N ² -dimethylguanosine-specific tRNA methyltransferase
<i>RLI1</i>	-4.17	0.43	strong similarity to human RNase L inhibitor and M.jannaschii ABC transporter protein
<i>NOPI</i>	-5.63	0.60	nucleolar protein, homologous to mammalian fibrillarin
<i>DBP10</i>	-2.91	0.11	DEAD box protein 10
<i>NHP2</i>	-3.68	0.16	HMG-like nuclear protein, rRNA processing
<i>TRM8</i>	-2.65	0.04	Transfer RNA methyltransferase
<i>SPB1</i>	-6.23	0.49	Methyltransferase
<i>SNR56</i>	-2.49	0.29	SNR56 snRNA
<i>SNR59</i>	-2.69	0.31	SNR59 snRNA
<i>DED1</i>	-2.66	0.12	ATP-dependent RNA helicase of DEAD box family\; suppressor of a pre-mRNA splicing mutation, prp8-1
<i>RRP12</i>	-5.37	0.82	Required for normal pre-rRNA processing
<i>RCL1</i>	-3.09	0.42	putative RNA 3'-terminal phosphate cyclase
<i>REX4</i>	-3.01	0.08	RNA EXonuclease; member of 3' → 5' exonuclease family
<i>RNH35</i>	-2.46	0.32	RNase H(35), a 35 kDa ribonuclease H
<i>NOP2</i>	-2.92	0.32	90-kDa protein, located in nucleolus, RNA methyltransferase
<i>DBP2</i>	-2.35	0.03	ATP-dependent RNA helicase of DEAD box family
<i>NOP15</i>	-2.47	0.14	weak similarity to fruit fly RNA-binding protein, Nucleolar protein 15
<i>NOP13</i>	-2.66	0.21	similarity to S.pombe Rnp24p, Nucleolar Protein 13

<i>POP3</i>	-2.30	0.13	involved in processing of tRNAs and rRNAs
<i>HAS1</i>	-3.73	0.47	Putative RNA-dependent helicase
<i>RNT1</i>	-2.69	0.20	Ribonuclease III
<i>RRP5</i>	-2.58	0.24	Protein required for processing of pre-rRNA
<i>DUS1</i>	-3.04	0.19	tRNA dihydrouridine synthase
Transport			
<i>PTR2</i>	-3.82	0.78	Peptide transporter
<i>PHO90</i>	-2.37	0.22	Low-affinity phosphate transporter
<i>HXT1</i>	-3.81	0.20	High-affinity hexose (glucose) transporter
<i>HNMI</i>	-2.90	0.16	Transporter (permease) for choline and nitrogen mustard\; share homology with UGA4
<i>KRE30</i>	-3.36	0.22	strong similarity to members of the ABC transporter family
<i>GNP1</i>	-2.19	0.11	high-affinity glutamine permease
<i>BFR2</i>	-3.28	0.22	involved in protein transport step at the Brefeldin A blocks
<i>ENA5</i>	-2.28	0.10	P-type ATPase involved in Na ⁺ efflux
<i>CTP1</i>	-3.22	0.25	citrate transporter in mitochondrial inner membrane
<i>PHO88</i>	-2.72	0.06	May be a membrane protein involved in inorganic phosphate transport
<i>DIP5</i>	-3.31	0.60	dicarboxylic amino acid permease
Unknown			
<i>YLR339C</i>	-2.22	0.18	questionable ORF
<i>YLR190W</i>	-2.22	0.04	hypothetical protein
<i>YLR194C</i>	-2.55	0.21	hypothetical protein
<i>PWPI</i>	-3.00	0.14	Protein with periodic tryptophan residues that resembles members of beta-transducin superfamily
<i>YLR198C</i>	-2.46	0.16	questionable ORF
<i>EMG1</i>	-2.93	0.14	strong similarity to S.pombe hypothetical protein C18G6.07C
<i>EMP70</i>	-2.17	0.15	integral membrane protein\; p24a protein
<i>BUD28</i>	-2.45	0.25	questionable ORF
<i>YLR063W</i>	-2.68	0.29	ser/thr protein kinase
<i>FYV7</i>	-2.62	0.22	Function required for Yeast Viability on toxin exposure
<i>YLR073C</i>	-2.66	0.21	hypothetical protein
<i>YLL012W</i>	-2.91	0.52	similarity to triacylglycerol lipases
<i>NKR009W</i>	-4.63	0.47	non-annotated SAGE orf
<i>YKR079C</i>	-2.53	0.23	similarity to S.pombe hypothetical protein SPAC1D4.10
<i>RPF2</i>	-4.27	0.51	hypothetical protein
<i>YKR060W</i>	-2.30	0.09	hypothetical protein

<i>PRY2</i>	-2.70	0.24	Similar to plant PR-1 class of pathogen related proteins
<i>YKL014C</i>	-2.47	0.19	hypothetical protein
<i>DANI</i>	-3.56	0.44	Protein induced during anaerobic growth
<i>YJR097W</i>	-4.02	0.15	weak similarity to Caj1p
<i>YJR070C</i>	-6.09	0.41	similarity to <i>C.elegans</i> hypothetical protein C14A4.1
<i>YJR071W</i>	-7.93	2.36	questionable ORF
<i>YJR041C</i>	-2.79	0.32	hypothetical protein
<i>YJL051W</i>	-2.69	0.55	hypothetical protein
<i>YJL122W</i>	-6.41	0.76	weak similarity to dog-fish transition protein S2
<i>YJL200C</i>	-3.96	0.28	strong similarity to aconitate hydratase
<i>MAK16</i>	-4.65	0.75	putative nuclear protein
<i>gHR04_11</i>	-16.47	10.50	<i>Saccharomyces cerevisiae</i> chromosome VIII, Found forward in NC_001140 between 310647 and 311646
<i>gHR04_12</i>	-10.85	5.29	<i>Saccharomyces cerevisiae</i> chromosome VIII, Found forward in NC_001140 between 311647 and 312646
<i>gHR04_13</i>	-3.03	0.38	<i>Saccharomyces cerevisiae</i> chromosome VIII, Found forward in NC_001140 between 312647 and 313497
<i>gGR11_6</i>	-2.20	0.09	<i>Saccharomyces cerevisiae</i> chromosome VII, Found forward in NC_001139 between 929127 and 930126
<i>gGL03_3</i>	-5.77	2.46	<i>Saccharomyces cerevisiae</i> chromosome VII, Found forward in NC_001139 between 134050 and 135049
<i>gGL03_4</i>	-7.92	4.40	<i>Saccharomyces cerevisiae</i> chromosome VII, Found forward in NC_001139 between 135050 and 136049
<i>gGL03_5</i>	-3.70	1.05	<i>Saccharomyces cerevisiae</i> chromosome VII, Found forward in NC_001139 between 136050 and 137049
<i>gGR08_3</i>	-10.62	6.61	<i>Saccharomyces cerevisiae</i> chromosome VII, Found forward in NC_001139 between 662764 and 663763
<i>gGR08_5</i>	-3.41	0.63	<i>Saccharomyces cerevisiae</i> chromosome VII, Found forward in NC_001139 between 664764 and 665565
<i>gGL03_2</i>	-5.75	2.71	<i>Saccharomyces cerevisiae</i> chromosome VII, Found forward in NC_001139 between 133050 and 134049
<i>gDL04_1</i>	-4.04	0.41	<i>Saccharomyces cerevisiae</i> chromosome IV, Found forward in NC_001136 between 258132 and 259131

<i>gDL04_3</i>	-3.92	0.61	Saccharomyces cerevisiae chromosome IV, Found forward in NC_001136 between 260132 and 261131
<i>gDL04_4</i>	-3.22	0.42	Saccharomyces cerevisiae chromosome IV, Found forward in NC_001136 between 261132 and 262131
<i>gDL04_5</i>	-2.65	0.29	Saccharomyces cerevisiae chromosome IV, Found forward in NC_001136 between 262132 and 262724
<i>gBL05_9</i>	-3.05	0.59	Saccharomyces cerevisiae chromosome II, Found forward in NC_001134 between 229363 and 230362
<i>gBL05_10</i>	-4.51	0.88	Saccharomyces cerevisiae chromosome II, Found forward in NC_001134 between 230363 and 231362
<i>gBL05_11</i>	-22.80	9.43	Saccharomyces cerevisiae chromosome II, Found forward in NC_001134 between 231363 and 232362
<i>gBL05_12</i>	-8.03	1.21	Saccharomyces cerevisiae chromosome II, Found forward in NC_001134 between 232363 and 233362
<i>gBL05_13</i>	-5.48	0.91	Saccharomyces cerevisiae chromosome II, Found forward in NC_001134 between 233363 and 234362
<i>gBL05_14</i>	-4.23	0.51	Saccharomyces cerevisiae chromosome II, Found forward in NC_001134 between 234363 and 234580
<i>gBR08_9</i>	-2.32	0.11	Saccharomyces cerevisiae chromosome II, Found forward in NC_001134 between 526809 and 526984
<i>gOR09_1</i>	-5.12	1.52	Saccharomyces cerevisiae chromosome XV, Found forward in NC_001147 between 960693 and 961692
<i>gOR09_1</i>	-21.95	9.75	Saccharomyces cerevisiae chromosome XV, Found forward in NC_001147 between 960693 and 961692
<i>gOR09_2</i>	-3.99	0.83	Saccharomyces cerevisiae chromosome XV, Found forward in NC_001147 between 961693 and 962692
<i>gOR09_3</i>	-7.59	1.74	Saccharomyces cerevisiae chromosome XV, Found forward in NC_001147 between 962693 and 963692
<i>gOR09_4</i>	-6.03	0.87	Saccharomyces cerevisiae chromosome XV, Found forward in NC_001147 between 963693 and 964692
<i>gOR09_5</i>	-3.78	0.53	Saccharomyces cerevisiae chromosome XV,

<i>gPL03_1</i>	-4.20	0.84	Found forward in NC_001147 between 964693 and 965472 Saccharomyces cerevisiae chromosome XVI, Found forward in NC_001148 between 109147 and 110146
<i>gPL03_2</i>	-19.78	15.27	Saccharomyces cerevisiae chromosome XVI, Found forward in NC_001148 between 110147 and 111146
<i>gNL04_3</i>	-2.88	0.45	Saccharomyces cerevisiae chromosome XIV, Found forward in NC_001146 between 164130 and 165129
<i>gLR09_1</i>	-3.95	0.58	Saccharomyces cerevisiae chromosome XII, Found forward in NC_001144 between 809817 and 810816
<i>gLR09_2</i>	-2.83	0.49	Saccharomyces cerevisiae chromosome XII, Found forward in NC_001144 between 810817 and 811816
<i>gLR09_3</i>	-6.71	3.67	Saccharomyces cerevisiae chromosome XII, Found forward in NC_001144 between 811817 and 812816
<i>gLR09_4</i>	-5.63	2.82	Saccharomyces cerevisiae chromosome XII, Found forward in NC_001144 between 812817 and 813816
<i>gKL03_2</i>	-10.21	4.29	Saccharomyces cerevisiae chromosome XI, Found forward in NC_001143 between 101643 and 102642
<i>gKL03_3</i>	-9.14	4.19	Saccharomyces cerevisiae chromosome XI, Found forward in NC_001143 between 102643 and 103642
<i>gKL03_4</i>	-8.28	3.09	Saccharomyces cerevisiae chromosome XI, Found forward in NC_001143 between 103643 and 104642
<i>gKL03_5</i>	-3.54	0.45	Saccharomyces cerevisiae chromosome XI, Found forward in NC_001143 between 104643 and 105642
<i>gJR12_5</i>	-9.49	5.63	Saccharomyces cerevisiae chromosome X, Found forward in NC_001142 between 600249 and 601248
<i>gJR12_6</i>	-3.99	0.74	Saccharomyces cerevisiae chromosome X, Found forward in NC_001142 between 601249 and 602248
<i>YRF1-6</i>	-4.97	1.70	strong similarity to subtelomeric encoded proteins
<i>YRF1-5</i>	-3.39	0.57	strong similarity to subtelomeric encoded proteins
<i>YIP3</i>	-2.23	0.07	protein of unknown function
<i>YIL091C</i>	-3.54	0.36	weak similarity to spt5p
<i>YIL141W</i>	-6.65	1.54	questionable ORF

<i>YIL158W</i>	-7.64	1.31	similarity to hypothetical protein YKR100c
<i>NHL005C</i>	-2.82	0.25	non-annotated SAGE orf
<i>NHR015C</i>	-2.34	0.16	non-annotated SAGE orf
<i>NJL013C</i>	-3.72	1.05	non-annotated SAGE orf
<i>TRA1</i>	-3.19	0.15	TRA1 is the homolog of the human protein TRRAP, histone acetylation
<i>SSF1</i>	-3.26	0.50	homologous to Ssf2p
<i>YHR085W</i>	-2.54	0.28	weak similarity to fruit fly brahma transcriptional activator
<i>YHL026C</i>	-2.45	0.19	hypothetical protein
<i>NGR068W</i>	-3.53	0.58	non-annotated SAGE orf
<i>NGR122W</i>	-3.29	0.29	non-annotated SAGE orf
<i>NGR126C</i>	-3.27	0.47	non-annotated SAGE orf
<i>NGR094W</i>	-2.50	0.06	non-annotated SAGE orf
<i>NGR123C</i>	-2.65	0.27	non-annotated SAGE orf
<i>NGR124C</i>	-2.58	0.27	non-annotated SAGE orf
<i>NGL023W</i>	-3.19	0.22	non-annotated SAGE orf
<i>NGL010C</i>	-2.97	0.88	non-annotated SAGE orf
<i>PXR1</i>	-2.93	0.48	weak similarity to Cbf5p
<i>YGR283C</i>	-3.28	0.20	similarity to hypothetical protein YMR310c
<i>YGR272C</i>	-3.22	0.16	similarity to hypothetical S.pombe protein SPAC12G12.02
<i>YGR210C</i>	-2.73	0.12	similarity to M.jannaschii GTP-binding protein and to M.capricolum hypothetical protein SGC3
<i>TOS2</i>	-13.12	1.71	similarity to hypothetical protein YHR149c
<i>HGH1</i>	-3.01	0.29	HMG1\2 homolog
<i>CRH1</i>	-2.52	0.01	similarity to Aspergillus fumigatus rAsp
<i>FYV13</i>	-11.87	4.01	Function required for Yeast Viability on toxin exposure
<i>YGR079W</i>	-2.63	0.13	hypothetical protein
<i>YGR090W</i>	-3.56	0.13	hypothetical protein
<i>DEG1</i>	-2.41	0.26	Depressed growth-rate protein
<i>FYV11</i>	-3.17	0.42	similarity to repeat structures in a Plasmodium falciparum protein (MESA)
<i>NEL022C</i>	-3.24	0.70	non-annotated SAGE orf
<i>NEL022C</i>	-3.32	0.44	non-annotated SAGE orf
<i>NEL021C</i>	-3.78	0.05	non-annotated SAGE orf
<i>NEL020C</i>	-2.48	0.11	non-annotated SAGE orf
<i>YER156C</i>	-5.66	0.94	similarity to hypothetical C. elegans protein C27H6.5
<i>YEL048C</i>	-2.52	0.10	hypothetical protein
<i>NDR014C</i>	-3.26	0.11	non-annotated SAGE orf
<i>HLR1</i>	-2.63	0.14	similarity to Lre1p
<i>PUF6</i>	-3.01	0.18	similarity to hypothetical human and C.elegans proteins
<i>YDR509W</i>	-3.59	0.63	questionable ORF

<i>YHP1</i>	-4.21	0.47	strong similarity to Yox1p
<i>SSF2</i>	-2.87	0.21	high copy suppressor of G beta subunit temperature sensitive mutation
<i>YDR179C</i>	-2.95	0.34	hypothetical protein
<i>YDR119W</i>	-2.08	0.03	similarity to B.subtilis tetracyclin resistance
<i>ARX1</i>	-4.83	0.51	weak similarity to proliferation-associated protein
<i>RRP8</i>	-3.40	0.47	similarity to hypothetical S.pombe protein
<i>YDR020C</i>	-2.66	0.25	weak similarity to uridine kinases and phosphoribulokinases
<i>YDL038C</i>	-4.17	0.76	similarity to mucin proteins
<i>YDL037C</i>	-6.78	1.20	strong similarity to glucan 1,4-alpha-glucosidase
<i>YDL063C</i>	-3.60	0.17	weak similarity to human estrogen-responsive finger protein
<i>TSR1</i>	-2.54	0.13	similarity to C.elegans hypothetical protein
<i>YDL152W</i>	-3.77	0.74	questionable ORF
<i>NRP1</i>	-3.21	0.08	Asparagine-rich protein
<i>YDL211C</i>	-3.50	0.34	similarity to hypothetical protein YNL176c
<i>NCR020C</i>	-7.26	3.09	non-annotated SAGE orf
<i>NCR016C</i>	-2.73	0.37	non-annotated SAGE orf
<i>YCR072C</i>	-3.49	0.39	regulatory protein
<i>YCR043C</i>	-3.35	0.26	hypothetical protein
<i>GFD2</i>	-4.67	0.56	similarity to hypothetical protein YDR514c
<i>YCL012W</i>	-2.42	0.06	part of budding protein Bud3p due to frameshift in DNA sequence
<i>YCL063W</i>	-2.69	0.15	weak similarity to yeast translation regulator Gcd6p
<i>NBL006C</i>	-4.39	0.27	non-annotated SAGE orf
<i>NBR008W</i>	-2.37	0.04	non-annotated SAGE orf
<i>NBL022C</i>	-3.68	0.67	non-annotated SAGE orf
<i>NBL022C</i>	-3.03	0.47	non-annotated SAGE orf
<i>NBL014C</i>	-3.99	0.19	non-annotated SAGE orf
<i>YBR267W</i>	-3.90	0.41	Probable Zn-finger protein (C2H2 type)
<i>YBR056w-a</i>	-5.11	0.71	identified by SAGE
<i>YBR238C</i>	-3.08	0.15	strong similarity to general chromatin factor Spt16p
<i>TOS1</i>	-2.30	0.05	similarity to hypothetical protein YJL171c
<i>YSY6</i>	-2.24	0.09	Protein that participates in secretory pathway
<i>YBR004C</i>	-2.25	0.10	similarity to S.pombe hypothetical protein SPAC18B11.05
<i>YBL028C</i>	-4.68	0.30	involved in mating-type regulation
<i>YBL054W</i>	-2.94	0.09	Homolog to myb transforming proteins
<i>HEK2</i>	-2.29	0.08	weak similarity to hnRNP complex protein homolog YBR233w
<i>YBL071C</i>	-2.24	0.11	hypothetical protein
<i>YBL081W</i>	-2.75	0.06	hypothetical protein
<i>NPR023C</i>	-4.60	1.04	non-annotated SAGE orf

<i>YPR142C</i>	-2.64	0.35	questionable ORF
<i>YPR143W</i>	-2.53	0.13	hypothetical protein
<i>NOG1</i>	-7.99	1.12	similarity to <i>M.jannaschii</i> GTP-binding protein, GTP1/OBG-family, similarity to other GTP-binding proteins
<i>YPL141C</i>	-4.50	0.52	strong similarity to protein kinase Kin4p
<i>SVS1</i>	-2.67	0.24	Serine and threonine rich protein.
<i>YPL183C</i>	-2.69	0.14	similarity to Taf90p
<i>NOR010W</i>	-4.14	0.48	non-annotated SAGE orf
<i>NOR056W</i>	-2.55	0.29	non-annotated SAGE orf
<i>NOR077W</i>	-8.23	0.44	non-annotated SAGE orf
<i>NOR079W</i>	-6.90	0.70	non-annotated SAGE orf
<i>NOR079W</i>	-8.31	0.64	non-annotated SAGE orf
<i>NOR058C</i>	-5.39	1.52	non-annotated SAGE orf
<i>NOL037C</i>	-4.95	0.85	non-annotated SAGE orf
<i>YOR390W</i>	-2.17	0.12	nearly identical to YPL279c
<i>YOR342C</i>	-4.85	0.53	weak similarity to YAI037w
<i>YOR356W</i>	-2.95	0.16	strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreductase
<i>VTI1</i>	-3.50	0.21	hypothetical protein
<i>TEA1</i>	-2.57	0.23	Mutants are defective in Ty1 Enhancer-mediated Activation
<i>YOR305W</i>	-2.36	0.10	hypothetical protein
<i>MCH5</i>	-2.43	0.17	similarity to human X-linked PEST-containing transporter
<i>YOR309C</i>	-3.95	0.33	questionable ORF
<i>YOR315W</i>	-15.18	2.48	hypothetical protein
<i>YOR287C</i>	-8.13	3.46	weak similarity to PITSLRE protein kinase isoforms
<i>YOR252W</i>	-2.28	0.21	hypothetical protein
<i>YOR146W</i>	-3.37	0.30	questionable ORF
<i>YOR108W</i>	-3.27	0.23	putative isoform of Leu4p
<i>YOR066W</i>	-2.22	0.09	hypothetical protein
<i>YOR073W</i>	-3.51	0.03	hypothetical protein
<i>YOL014W</i>	-6.29	1.26	hypothetical protein
<i>YOL007C</i>	-4.06	0.25	Appears to be a structural component of the chitin synthase 3 complex
<i>YOR004W</i>	-4.21	0.34	weak similarity to hypothetical protein YDR339c
<i>TOS7</i>	-2.77	0.31	similarity to Rim9p and YFR012w
<i>NOP12</i>	-3.16	0.59	Nucleolar Protein; isolated as a mutant exhibiting synthetic lethality with a <i>nop2</i> ts allele.
<i>BRX1</i>	-2.41	0.09	Essential nucleolar protein required for biogenesis of the 60S ribosomal subunit
<i>YOL124C</i>	-3.97	0.43	weak similarity to <i>M.jannaschii</i> hypothetical protein
<i>NNL045W</i>	-3.56	0.12	non-annotated SAGE orf

<i>NNL051C</i>	-2.57	0.38	non-annotated SAGE orf
<i>NNL031C</i>	-2.62	0.29	non-annotated SAGE orf
<i>DSE4</i>	-2.67	0.04	similarity to beta-glucan-elicitor receptor - Glycine max
<i>NOG2</i>	-5.05	0.36	Nuclear/Nucleolar GTP-binding protein 2
<i>YNR009W</i>	-4.57	1.19	hypothetical protein
<i>AQR1</i>	-3.58	0.60	similarity to resistance proteins
<i>NIS1</i>	-2.63	0.22	hypothetical protein
<i>KRE33</i>	-2.70	0.12	similarity to <i>A.ambisexualis</i> antheridiol steroid receptor
<i>YNL119W</i>	-2.46	0.13	weak similarity to <i>M.jannaschii</i> hypothetical protein MJ1257
<i>YNL149C</i>	-2.07	0.02	weak similarity to <i>S.pombe</i> hypothetical protein
<i>YNL182C</i>	-2.59	0.31	weak similarity to <i>S.pombe</i> hypothetical protein
<i>YNL313C</i>	-2.65	0.15	similarity to <i>C.elegans</i> hypothetical protein
<i>TOS6</i>	-10.54	1.81	hypothetical protein
<i>NMR057W</i>	-6.04	0.44	non-annotated SAGE orf
<i>NMR057W</i>	-10.80	2.95	non-annotated SAGE orf
<i>NMR057W</i>	-59.55	8.98	non-annotated SAGE orf
<i>NMR059W</i>	-2.65	0.40	non-annotated SAGE orf
<i>NMR070C</i>	-3.56	0.18	non-annotated SAGE orf
<i>GAS3</i>	-2.65	0.31	similarity to GAS1 protein
<i>YMR003W</i>	-3.46	0.69	hypothetical protein
<i>BUD22</i>	-2.99	0.10	weak similarity to <i>S.pombe</i> hypothetical protein SPAC4F10
<i>YML018C</i>	-2.78	0.35	similarity to YDR438w
<i>YOX1</i>	-8.33	0.80	Homeobox-domain containing protein
<i>SUR7</i>	-2.71	0.38	putative integral membrane protein
<i>YML119W</i>	-2.49	0.12	hypothetical protein
<i>NLR019W</i>	-10.48	5.17	non-annotated SAGE orf
<i>NLR001C</i>	-9.91	1.08	non-annotated SAGE orf
<i>NLR128C</i>	-9.69	2.20	non-annotated SAGE orf
<i>YLR264c-a</i>	-2.85	0.10	identified by SAGE
<i>YLR435W</i>	-3.47	0.28	hypothetical protein
<i>YLR437C</i>	-2.23	0.14	hypothetical protein
<i>YLR407W</i>	-2.62	0.17	hypothetical protein
