

Down regulated genes in BER/NER-defective cells following 0.75mM H₂O₂ exposure for 30 minutes

Gene name	Average Fold Change	S.E.M.	Description
DNA Repair/ Replication			
<i>MET18</i>	-3.13	0.04	Involved in nucleotide excision repair and regulation of TFIIH
<i>MSH1</i>	-2.67	0.23	mutS homolog involved in mitochondrial DNA repair
<i>MSH3</i>	-3.01	0.35	mutS homolog, forms a complex with Msh2p to repair insertion-deletion mispairs
<i>POL30</i>	-2.81	0.14	proliferating cell nuclear antigen (PCNA); accessory factor for DNA polymerase delta
<i>RAD9</i>	-2.49	0.15	cell cycle arrest protein
<i>RNR1</i>	-4.86	0.65	ribonucleotide reductase
<i>TBF1</i>	-2.66	0.14	TTAGGG repeat binding factor, interacts with Rad53 affinity precipitation
<i>TID3</i>	-2.50	0.40	Dmc1p interacting protein, and MSH5, and SMC2, recombination
Signal Transduction			
<i>BEM3</i>	-2.46	0.22	has GTPase-activating protein activity toward the essential bud-site assembly GTPase Cdc42
<i>GIN4</i>	-2.62	0.20	putative serine/threonine kinase
<i>KCC4</i>	-5.29	0.43	Ser/Thr protein kinase
<i>LRG1</i>	-3.97	0.09	Protein similar to LIM-domain proteins and to rho GTPase-activating family of proteins
<i>LTE1</i>	-2.84	0.22	putative GTP-exchange protein
<i>RAS1</i>	-2.58	0.07	ras proto-oncogene homolog
<i>SKS1</i>	-2.64	0.04	serine/threonine protein kinase homologous to Ran1p
<i>SSK2</i>	-2.11	0.02	A MAP kinase kinase kinase; activator of Pbs2p
<i>STD1</i>	-2.80	0.41	homologous to MTH1; interacts with the SNF1 protein kinase and TBP in two-hybrid and in in vitro binding studies
<i>SYG1</i>	-2.14	0.03	plasma membrane protein
<i>TOR1</i>	-2.40	0.20	phosphatidylinositol kinase homolog
Chromatin Maintenance			
<i>CST13</i>	-2.74	0.14	Chromosome STability

<i>ELG1</i>	-2.96	0.06	Enhanced Level of Genomic instability
<i>EPL1</i>	-3.31	0.56	Probable chromatin protein because of homology to Drosophila Enhancer of Polycomb
<i>HHO1</i>	-2.23	0.18	histone H1
<i>HHT1</i>	-2.38	0.01	Histone H3
<i>HST3</i>	-3.37	0.17	Homolog of SIR2
<i>HST4</i>	-2.34	0.20	Homolog of SIR2
<i>HOS3</i>	-3.40	0.65	Protein with similarity to Hda1p, Rpd3p, Hos2p, and Hos1p, histone deacetylase
<i>NHP6A</i>	-2.84	0.37	11-kDa nonhistone chromosomal protein
<i>SCC2</i>	-2.92	0.33	Sister chromatid cohesion protein
<i>STH1</i>	-3.07	0.46	helicase related protein, snf2 homolog
Transcription			
<i>BAS1</i>	-2.61	0.21	Transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes
<i>CAF120</i>	-7.76	1.93	similarity to YLR187w
<i>MCM2</i>	-2.39	0.22	Minichromosome maintenance protein, transcription factor
<i>MIG1</i>	-2.14	0.02	Transcription factor involved in glucose repression
<i>MOT1</i>	-4.14	0.40	involved in TATA-binding protein regulation
<i>RPO21</i>	-2.85	0.03	RNA polymerase II large subunit
<i>RPO31</i>	-3.23	0.09	RNA polymerase III large subunit
<i>RRN11</i>	-8.69	2.14	Component of rDNA transcription factor CF, required for rDNA transcription by RNA polymerase I
<i>RRN6</i>	-2.33	0.15	member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn7p and TATA-binding protein
<i>RRN7</i>	-3.73	1.33	member of yeast Pol I core factor (CF) also composed of Rrn11p, Rrn6p and TATA-binding protein
<i>RSC3</i>	-2.67	0.18	similarity to transcriptional regulator proteins
<i>SAC3</i>	-2.62	0.12	Leucine permease transcriptional regulator
<i>SWI1</i>	-2.85	0.16	Zinc-finger transcription factor
<i>SWI5</i>	-2.48	0.29	transcriptional activator
<i>TFC4</i>	-2.84	0.22	transcription factor tau (TFIIIC) subunit 131
<i>THP2</i>	-3.26	0.91	affects transcription elongation
<i>YOX1</i>	-3.08	0.73	Homeobox-domain containing protein
Nucleotide Metabolism			
<i>CDS1</i>	-3.20	0.61	CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidyltransferase, CDP-

<i>DCD1</i>	-2.51	0.08	diglyceride synthetase
<i>HPT1</i>	-2.45	0.20	dCMP deaminase Hypoxanthine Phosphoribosyltransferase
Degradation			
<i>MKC7</i>	-2.29	0.18	aspartyl protease related to Yap3p
<i>UBP10</i>	-2.39	0.10	a deubiquitinating enzyme
<i>UBP13</i>	-2.38	0.08	ubiquitin carboxyl-terminal hydrolase
<i>YPS1</i>	-2.09	0.03	GPI-anchored aspartic protease
Mitochondrial Maintenance			
<i>AAT1</i>	-2.82	0.43	aspartate aminotransferase, mitochondrial
<i>ATP12</i>	-2.64	0.52	essential for assembly of a functional F1-ATPase
<i>BCS1</i>	-2.24	0.15	Mitochondrial protein of the CDC48/PAS1/SEC18 ATPase family
<i>COQ2</i>	-2.40	0.05	para hydroxybenzoate: polyprenyl transferase, ubiquinone metabolism
<i>COX10</i>	-2.61	0.21	Putative farnesyl transferase required for heme A synthesis
<i>CYB5</i>	-2.63	0.16	cytochrome b5
<i>MAM33</i>	-2.29	0.07	mitochondrial acidic matrix protein
<i>MDV1</i>	-2.47	0.10	Involved in mitochondrial division
<i>MEF1</i>	-2.22	0.01	mitochondrial elongation factor G-like protein
<i>MIP1</i>	-3.10	0.02	catalytic subunit of mitochondrial DNA polymerase
<i>MRS1</i>	-2.61	0.31	mitochondrial RNA splicing
<i>MSS116</i>	-3.54	0.52	Mitochondrial RNA helicase of the DEAD box family
<i>MSU1</i>	-2.38	0.21	Protein essential for mitochondrial biogenesis
<i>MTO1</i>	-2.67	0.01	strong similarity to gidA E.coli protein, Mitochondrial Translation Optimization
<i>PET309</i>	-3.29	0.41	Involved in expression of mitochondrial COX1 by regulating translation of COX1 mRNA
<i>PUT1</i>	-2.69	0.02	proline oxidase
<i>PUT2</i>	-2.76	0.12	delta-1-pyrroline-5-carboxylate dehydrogenase
<i>RPO41</i>	-2.60	0.21	mitochondrial RNA polymerase II
<i>SMF2</i>	-2.31	0.02	localized to mitochondrial membrane
<i>TOM20</i>	-2.22	0.16	20 kDa mitochondrial outer membrane protein import receptor
<i>TOM5</i>	-2.53	0.09	Translocase of the Outer Mitochondrial membrane
<i>YHM2</i>	-2.77	0.35	DNA-binding protein, mtDNA stabilizing protein

Cell Cycle			
<i>BBP1</i>	-2.55	0.45	Involved in mitotic cell cycle and meiosis
<i>CDC14</i>	-2.48	0.13	soluble tyrosine-specific protein phosphatase
<i>CDC39</i>	-4.66	1.04	nuclear protein that negatively regulates basal transcription
<i>CDC47</i>	-3.45	0.19	MCM3 protein homolog (<i>S. cerevisiae</i>)
<i>CDC5</i>	-3.11	0.11	protein kinase which functions at the G(sub)2/M boundary
<i>CDC6</i>	-2.89	0.39	Protein involved in initiation of DNA replication
<i>CIN8</i>	-2.37	0.15	Kinesin-related protein involved in establishment and maintenance of mitotic spindle
<i>CLB1</i>	-3.10	0.52	G(sub)2-specific B-type cyclin
<i>CLB3</i>	-2.64	0.10	G(sub)2-specific B-type cyclin
<i>CLB6</i>	-5.93	0.50	B-type cyclin
<i>CLN1</i>	-4.53	0.10	G(sub)1 cyclin
<i>EGT2</i>	-3.15	0.18	Cell-cycle regulation protein, may be involved in the correct timing of cell separation after cytokinesis
<i>ESP1</i>	-2.05	0.03	Esp1 promotes sister chromatid separation by mediating dissociation from the chromatin of the cohesin Scc1
<i>FAR1</i>	-4.81	0.38	Factor arrest protein
<i>MCD1</i>	-2.42	0.22	similar to <i>S. pombe</i> RAD21; may function in chromosome morphogenesis from S phase through mitosis
<i>MCD4</i>	-2.43	0.14	Morphogenesis Checkpoint Dependent, Required for GPI anchor synthesis
<i>PCL1</i>	-8.62	1.58	G(sub)1 cyclin that associates with PHO85
Cell Growth/ Maintenance			
<i>APL3</i>	-3.51	0.40	clathrin Associated Protein complex Large subunit
<i>ATC1</i>	-2.28	0.04	Aip Three Complex; interacts with AIP3, localized to the nucleus
<i>BNI1</i>	-2.48	0.10	contains formin homology domains; homologous to BNR1 (BNI1 related protein)
<i>BNR1</i>	-2.25	0.11	Bni1p-related protein, helps regulate reorganization of the actin cytoskeleton, potential target of Rho4p
<i>BST1</i>	-2.73	0.26	Negatively regulates COPII vesicle formation
<i>CYK3</i>	-2.65	0.13	involved in CYtoKinesis
<i>ERD1</i>	-2.85	0.11	Protein required for retention of luminal ER proteins

<i>HKR1</i>	-3.17	0.10	cell surface protein that may regulate cell wall beta-glucan synthesis and bud site selection
<i>HO</i>	-5.81	2.21	Homothallic switching endonuclease
<i>KAR1</i>	-2.93	0.68	involved in spindle pole body duplication and karyogamy, interacts with Cdc31p
<i>KAR3</i>	-2.59	0.36	kinesin-like nuclear fusion protein
<i>KIP1</i>	-2.53	0.12	kinesin related protein
<i>KRE11</i>	-2.58	0.45	Involved in biosynthetic pathway for cell wall beta-glucans
<i>MNN11</i>	-2.54	0.04	related to Mnn10p, and that is in a complex containing other MNN gene products.
<i>MSB2</i>	-3.19	0.28	putative integral membrane protein
<i>RAX2</i>	-4.14	0.09	Involved in the maintenance of bipolar pattern
<i>SCW11</i>	-2.76	0.12	glucanase gene family member
<i>SMY2</i>	-2.42	0.03	Kinesin-related protein suppressing myosin defects (MYO2)
<i>STU1</i>	-2.53	0.19	suppressor of cold-sensitive tub2 mutation\; shown to be a component of the mitotic spindle
<i>STV1</i>	-2.55	0.06	vacuolar proton pumping ATPase, 110-kDa subunit\; not in vacuole membrane
<i>UTR2</i>	-5.98	0.89	weak similarity to Bacillus 1,3-1,4-beta-glucanase
<i>VIK1</i>	-4.78	2.11	Cik1p homolog
<i>WSC4</i>	-3.31	0.73	integral membrane protein containing novel cysteine motif. Similarity to SLG1 (WSC1), WSC2 and WSC3
Metabolism			
<i>CHS2</i>	-2.82	0.21	chitin synthase 2
<i>CHS3</i>	-2.29	0.01	chitin synthase 3
<i>DLD3</i>	-2.80	0.48	lactate metabolism
<i>ERG5</i>	-2.85	0.18	cytochrome P450 involved in C-22 denaturation of the ergosterol side-chain
<i>FAA3</i>	-2.65	0.30	Acyl CoA synthase
<i>FEN1</i>	-2.70	0.36	Probable subunit of 1,3-beta-glucan synthase\; homolog of ELO1
<i>GLT1</i>	-2.22	0.14	Glutamate synthase (NADPH)
<i>GPII3</i>	-2.75	0.54	Glycosylphosphatidylinositol GPI biosynthesis
<i>MDH2</i>	-2.14	0.02	cytosolic malate dehydrogenase
<i>PMT6</i>	-2.57	0.32	dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase
<i>TSC10</i>	-2.61	0.24	catalyzes the second step in the synthesis of phytosphingosine
Amino Acid Metabolism			

<i>HMT1</i>	-4.37	0.71	nuclear protein arginine methyltransferase (mono- and asymmetrically dimethylating enzyme)
<i>ILV5</i>	-5.96	0.22	acetohydroxyacid reductoisomerase, branched-chain amino acid biosynthesis
Translation			
<i>AEP2</i>	-3.23	0.70	Required for the translation of OLI1 mRNA.
<i>CLU1</i>	-2.91	0.53	CLU1 is similar to the Dictyostelium cluA gene, translation initiation factor
<i>GCN2</i>	-2.43	0.00	eukaryotic initiation factor 2 alpha (eIF2-alpha) kinase
<i>NIP1</i>	-3.14	0.61	Protein required for nuclear import, translation initiation factor
RNA Processing			
<i>CFT1</i>	-2.07	0.05	Component of pre-mRNA cleavage factor II (CFII); 150-kDa protein associated with polyadenylation factor 1 (PF I)
<i>CBP1</i>	-2.15	0.11	Protein required for COB mRNA stability or 5 processing
<i>DAT1</i>	-2.53	0.31	datin, an oligo(dA).oligo(dT)-binding protein
<i>DBP7</i>	-3.89	0.04	putative RNA helicase
<i>DIP2</i>	-2.45	0.34	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>DUS1</i>	-3.03	0.39	tRNA dihydrouridine synthase
<i>IFH1</i>	-3.62	0.38	has a weak RNA-dependent ATPase activity which is not specific for rRNA
<i>LOS1</i>	-2.74	0.27	Nuclear pore protein involved in pre-tRNA splicing
<i>NUP145</i>	-2.47	0.22	Nuclear pore complex protein with GLFG motif
<i>NUP170</i>	-2.15	0.09	Nucleoporin highly similar to Nup157p and to mammalian Nup155p (nup170 mutant can be complemented with NUP155)
<i>PAN2</i>	-2.52	0.25	135-kDa protein that is subunit of poly(A) ribonuclease
<i>RCL1</i>	-3.88	0.61	putative RNA 3'-terminal phosphate cyclase
<i>REB1</i>	-2.41	0.16	RNA polymerase I enhancer binding protein
<i>RRP12</i>	-2.38	0.04	Required for normal pre-rRNA processing
<i>RRP9</i>	-2.89	0.10	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>SEN34</i>	-2.24	0.05	34kDa subunit of the tetrameric tRNA splicing endonuclease
<i>SOF1</i>	-3.63	0.51	56 kDa nucleolar snRNP protein that shows homology to beta subunits of G-proteins and

			the splicing factor Prp4
<i>SPB1</i>	-3.97	0.00	Methyltransferase
<i>SRP40</i>	-2.30	0.22	nucleolar protein that is immunologically and structurally related to rat Nopp140
<i>SUV3</i>	-2.29	0.18	putative ATP-dependent helicase
<i>TIF4631</i>	-2.42	0.29	mRNA cap-binding protein (eIF-4F), 150K subunit , highly homologous to Tif4632p, homologs of mammalian p220
<i>TR(ACG)D</i>	-3.72	1.25	TR(ACG)D tRNA-Arg
<i>UTP15</i>	-3.39	0.32	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>UTP18</i>	-2.02	0.01	part of small ribosomal subunit SSU processosome contains U3 snoRNA
<i>UTP9</i>	-3.16	0.32	part of small ribosomal subunit SSU processosome contains U3 snoRNA
Ribosomal Proteins			
<i>RPL22B</i>	-2.34	0.22	Ribosomal protein L22B (L1c) (rp4) (YL31)
<i>RPS28B</i>	-3.71	0.45	Ribosomal protein S28B (S33B) (YS27)
<i>RPS28B</i>	-3.29	0.42	Ribosomal protein S28B (S33B) (YS27)
<i>RPS9A</i>	-4.73	0.33	Ribosomal protein S9A (S13) (rp21) (YS11)
<i>RPS9A</i>	-2.28	0.07	Ribosomal protein S9A (S13) (rp21) (YS11)
Transport			
<i>BAP3</i>	-2.33	0.09	Valine transporter
<i>CCH1</i>	-3.43	0.42	putative calcium channel
<i>DIP5</i>	-4.81	0.69	dicarboxylic amino acid permease
<i>ENA2</i>	-3.18	0.00	plasma membrane protein\; putative Na ⁺ pump\; P-type ATPase
<i>ENA5</i>	-2.77	0.39	P-type ATPase involved in Na ⁺ efflux
<i>FCY2</i>	-2.51	0.16	purine-cytosine permease
<i>FUII</i>	-2.11	0.01	uridine permease
<i>HNMI</i>	-2.41	0.09	Transporter (permease) for choline and nitrogen mustard\; share homology with UGA4
<i>HXT1</i>	-3.00	0.40	High-affinity hexose (glucose) transporter
<i>IST2</i>	-3.04	0.63	Similar to calcium and sodium channel proteins
<i>MCH5</i>	-3.20	0.10	similarity to human X-linked PEST-containing transporter
<i>MEP3</i>	-4.00	0.36	NH ₄ ⁺ transporter, highly similar to Mep1p and Mep2p
<i>OPT1</i>	-2.53	0.09	oligopeptide transporter
<i>PMR1</i>	-2.35	0.07	Ca ⁺⁺ -Pump, ATPase
<i>PTR2</i>	-3.90	1.40	Peptide transporter
<i>SNF3</i>	-2.71	0.44	glucose transporter
<i>SUT1</i>	-2.47	0.13	Involved in sterol uptake

<i>TAT1</i>	-2.57	0.06	Probable amino acid transport protein
<i>TAT2</i>	-2.14	0.00	Tryptophan permease, high affinity
<i>VHT1</i>	-3.03	0.29	similarity to <i>P.putida</i> phthalate transporter
<i>YOR1</i>	-2.65	0.15	ABC transporter
Unknown			
<i>FRE7</i>	-4.91	0.77	similar to FRE2
<i>NBR016C</i>	-2.59	0.23	non-annotated SAGE orf
<i>NBR054C</i>	-8.99	5.54	non-annotated SAGE orf
<i>NDD1</i>	-2.66	0.47	hypothetical protein
<i>NGL019W</i>	-2.59	0.18	non-annotated SAGE orf
<i>NGR109C</i>	-2.25	0.12	non-annotated SAGE orf
<i>NGR122W</i>	-2.30	0.20	non-annotated SAGE orf
<i>NHL005C</i>	-2.69	0.05	non-annotated SAGE orf
<i>NIR009W</i>	-5.63	1.29	non-annotated SAGE orf
<i>NKL008W</i>	-2.39	0.18	non-annotated SAGE orf
<i>NKL020C</i>	-3.33	1.09	non-annotated SAGE orf
<i>NLR003C</i>	-2.94	0.58	non-annotated SAGE orf
<i>NMR057W</i>	-5.06	1.48	non-annotated SAGE orf
<i>NNL039W</i>	-2.75	0.05	non-annotated SAGE orf
<i>NNL045W</i>	-2.42	0.14	non-annotated SAGE orf
<i>NNL056W</i>	-2.46	0.16	non-annotated SAGE orf
<i>NNR003W</i>	-2.35	0.22	non-annotated SAGE orf
<i>NOG1</i>	-3.20	0.33	similar to <i>M.jannaschii</i> GTP-binding protein, GTP1/OBG-family, similarity to other GTP-binding proteins
<i>NOG2</i>	-2.94	0.35	strong similarity to human breast tumor associated autoantigen
<i>NOR077W</i>	-3.84	0.86	non-annotated SAGE orf
<i>NOR079W</i>	-3.69	0.07	non-annotated SAGE orf
<i>NOR079W</i>	-4.57	0.89	non-annotated SAGE orf
<i>NPL004W</i>	-2.25	0.13	non-annotated SAGE orf
<i>NPL022C</i>	-2.94	0.01	non-annotated SAGE orf
<i>NPR023C</i>	-3.10	0.11	non-annotated SAGE orf
<i>YAL046C</i>	-2.14	0.02	hypothetical protein
<i>YBL081W</i>	-2.30	0.14	hypothetical protein
<i>YBR267W</i>	-2.99	0.29	Probable Zn-finger protein (C2H2 type)
<i>YCG1</i>	-2.61	0.28	weak similarity to <i>S.pombe</i> hypothetical protein SPAC1B9
<i>YCL063W</i>	-2.35	0.08	weak similarity to yeast translation regulator Gcd6p
<i>YDL211C</i>	-2.99	0.29	similarity to hypothetical protein YNL176c
<i>YDR089W</i>	-2.36	0.07	weak similarity to <i>Streptococcus</i> transposase
<i>YDR119W</i>	-3.05	0.33	similarity to <i>B.subtilis</i> tetracyclin resistance
<i>YDR326C</i>	-3.42	0.73	strong similarity to YHR080c, similarity to YFL042c and YLR072w

<i>YDR514C</i>	-2.93	0.26	strong similarity to hypothetical protein YCL036w
<i>YER064C</i>	-2.13	0.07	similarity to hypothetical protein YIL056w
<i>YER113C</i>	-3.77	0.83	similarity to Emp70p
<i>YGL101W</i>	-3.08	0.41	strong similarity to hypothetical protein YBR242w
<i>YGL139W</i>	-2.81	0.25	strong similarity to hypothetical protein YPL221w
<i>YGR071C</i>	-3.11	0.60	similarity to hypothetical protein YLR373c
<i>YGR079W</i>	-2.89	0.31	hypothetical protein
<i>YGR090W</i>	-3.42	0.03	hypothetical protein
<i>YGR150C</i>	-3.03	0.49	hypothetical protein
<i>YHPI</i>	-4.45	0.36	strong similarity to Yox1p
<i>YHR036W</i>	-3.97	0.83	similarity to hypothetical protein YGL247w
<i>YHR130C</i>	-3.15	0.93	weak similarity to T.brucei H ⁺ -transporting ATP synthase
<i>YHR149C</i>	-2.62	0.06	similarity to hypothetical protein YGR221c
<i>YIL091C</i>	-2.46	0.22	weak similarity to spt5p
<i>YIL158W</i>	-2.80	0.24	similarity to hypothetical protein YKR100c
<i>YJL181W</i>	-2.54	0.38	similarity to hypothetical protein YJR030c
<i>YJL193W</i>	-2.56	0.09	similarity to Sly41p
<i>YKR017C</i>	-2.63	0.01	similarity to human hypothetical KIAA0161 protein
<i>YLL012W</i>	-2.99	0.08	similarity to triacylglycerol lipases
<i>YLR218C</i>	-2.19	0.01	hypothetical protein
<i>YLR407W</i>	-2.78	0.09	hypothetical protein
<i>YLR419W</i>	-2.17	0.03	similarity to helicases
<i>YML018C</i>	-3.67	0.73	similarity to YDR438w
<i>YML059C</i>	-3.75	0.10	similarity to C.elegans ZK370.4 protein
<i>YMR003W</i>	-2.56	0.14	hypothetical protein
<i>YMR010W</i>	-2.35	0.15	weak similarity to hypothetical protein YDR352w
<i>YNL201C</i>	-2.68	0.46	involved in regulation of carbon metabolism
<i>YNL275W</i>	-2.69	0.10	similarity to human band 3 anion transport protein
<i>YNR009W</i>	-4.46	1.04	hypothetical protein
<i>YOL078W</i>	-2.80	0.56	hypothetical protein
<i>YOR062C</i>	-2.09	0.05	strong similarity to YKR075c
<i>YOR073W</i>	-3.20	0.35	hypothetical protein
<i>YOR129C</i>	-2.55	0.01	hypothetical protein
<i>YOR291W</i>	-2.41	0.13	similarity to cation translocating ATPases
<i>YOR315W</i>	-12.31	1.01	hypothetical protein
<i>YOR342C</i>	-2.98	0.47	weak similarity to YAI037w
<i>YOR390W</i>	-3.89	0.13	nearly identical to YPL279c
<i>YPL113C</i>	-3.78	0.80	similarity to glycerate dehydrogenases
<i>YPL141C</i>	-4.22	0.36	strong similarity to protein kinase Kin4p

<i>YPR003C</i>	-2.44	0.09	similarity to sulphate transporter proteins
<i>YPR031W</i>	-4.40	0.14	similarity to human zinc-finger protein BR140
<i>ALK1</i>	-3.21	0.33	Protein serine/threonine kinase activity
<i>AQR1</i>	-10.02	1.18	similarity to resistance proteins
<i>DNF3</i>	-2.73	0.37	similarity to ATPases
<i>DSE2</i>	-2.21	0.07	Ser-Thr rich protein, Daughter SpecificExpression 2
<i>DSE4</i>	-4.85	0.41	similarity to beta-glucan-elicitor receptor - Glycine max, Daughter Specific Expression 4
<i>DSN1</i>	-2.31	0.16	Dosage Suppressor of NNF1
<i>ECM7</i>	-2.48	0.29	ExtraCellular Mutant
<i>GFD2</i>	-2.47	0.14	Great for FULL DEAD box protein activity
<i>GIN1</i>	-3.33	0.23	similarity to Put3p and to hypothetical protein YJL206c, Gcn5 INdependent
<i>GIS4</i>	-2.82	0.50	hypothetical protein
<i>HLR1</i>	-4.36	0.78	similarity to Lre1p
<i>HSH155</i>	-2.22	0.13	strong similarity to hypothetical S.pombe and C.elegans proteins
<i>NRP1</i>	-2.62	0.13	Asparagine-rich protein
<i>PUF4</i>	-2.15	0.12	similarity to Drosophila pumilio protein and Mpt5p protein
<i>SBE22</i>	-2.98	0.66	functionally redundant and similar in structure to SBE2
<i>SPO73</i>	-2.45	0.24	hypothetical protein
<i>SSF2</i>	-2.22	0.12	high copy suppressor of G beta subunit temperature sensitive mutation
<i>SYT1</i>	-2.98	0.66	Suppressor of Ypt3
<i>TOS9</i>	-3.35	0.23	similarity to S.pombe pac2 protein
<i>VTSI</i>	-2.79	0.27	hypothetical protein
