

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

Gene name	Average Fold Change	S.E.M.	Description
Cell Stress			
<i>YRO2</i>	2.22	0.08	Homolog to HSP30 heat shock protein YRO1
<i>CTA1</i>	14.59	0.62	catalase A
<i>CTT1</i>	27.07	2.44	cytoplasmic catalase T
<i>CRS5</i>	3.15	0.46	Metallothionein-like protein, heavy metal sensitivity/resistance
<i>GPX1</i>	5.29	1.10	strong similarity to glutathione peroxidase
<i>GPX2</i>	4.43	1.65	Probable glutathione peroxidase
<i>GRE1</i>	2.71	0.10	Induced by osmotic stress
<i>GRE2</i>	10.77	1.60	induced by osmotic stress\; similar to dihydroflavonol 4-reductase from plants
<i>GTT2</i>	41.57	2.00	Glutathione transferase
<i>HSP26</i>	6.90	0.29	heat shock protein 26
<i>HSP30</i>	8.99	0.81	Protein induced by heat shock, ethanol, and entry into stationary phase\; located in plasma membrane
<i>HSP42</i>	3.45	0.34	Similar to HSP26\; expression is regulated by stress conditions
<i>HSP78</i>	2.48	0.30	Mitochondrial heat shock protein 78 kDa
<i>MGA1</i>	3.26	0.54	Mga1p shows similarity to heat shock transcription factor
<i>OXR1</i>	2.49	0.04	OXidation Resistance
<i>SNZ2</i>	2.47	0.23	Snooze: stationary phase-induced gene family
<i>SOD2</i>	4.51	1.10	Manganese-containing superoxide dismutase
<i>SSA3</i>	4.71	1.00	heat-inducible cytosolic member of the 70 kDa heat shock protein family
<i>SSA4</i>	8.31	0.02	member of 70 kDa heat shock protein family
<i>SSE2</i>	3.19	0.16	HSP70 family member, highly homologous to Sse1p
<i>SSQ1</i>	2.45	0.29	Hsp70 protein
<i>TSA2</i>	10.67	0.21	strong similarity to thiol-specific antioxidant proteins
<i>DDR2</i>	4.47	0.66	Multistress response protein
DNA repair/ Replication			
<i>DDI1</i>	2.44	0.17	DNA Damage Inducible
<i>LIF1</i>	3.57	0.01	Ligase Interacting Factor 1\; physically interacts with DNA ligase 4 protein (Lig4p)
<i>RAD14</i>	2.19	0.12	human xeroderma pigmentosum group A DNA

<i>ZIP2</i>	2.26	0.17	repair gene homolog Required for ZIPpering up meiotic chromosomes during chromosome synapsis
<i>LIN1</i>	2.39	0.01	LIN element of a link between sister chromatid cohesion, DNA replication and splicing
Signal Transduction			
<i>YPT53</i>	3.28	0.52	rab5-like GTPase involved in vacuolar protein sorting and endocytosis
<i>FRM2</i>	27.10	2.59	Protein involved in the integration of lipid signaling pathways with cellular homeostasis
<i>HAL5</i>	2.15	0.05	Protein kinase homolog, mutant is salt and pH sensitive
<i>IKS1</i>	3.82	0.63	probable serine/threonine kinase
<i>KSS1</i>	3.36	0.30	MAP protein kinase homolog involved in pheromone signal transduction
<i>MDG1</i>	4.24	1.32	multicopy suppressor of <i>bem1</i> mutation, may be involved in G-protein mediated signal transduction
<i>MTL1</i>	2.53	0.09	acts in concert with Mid2p to transduce cell wall stress signals
<i>REG2</i>	2.64	0.28	Possible regulatory subunit for the PP1 family protein phosphatase Glc7p
<i>TPK2</i>	3.00	0.13	cAMP-dependent protein kinase catalytic subunit
Transcription			
<i>ADA2</i>	2.68	0.43	member of ADA and SAGA, two transcriptional adaptor/HAT (histone acetyltransferase) complexes
<i>AFT2</i>	5.54	0.03	similarity to cell size regulation protein Rcs1p, Activator of Iron Fe Transcription
<i>CIN5</i>	13.87	0.86	bZIP protein, can activate transcription from a promoter containing a Yap recognition site
<i>MED8</i>	2.29	0.07	Member of RNA Polymerase II transcriptional regulation mediator
<i>PHD1</i>	2.39	0.31	putative transcription factor
<i>RDS1</i>	2.28	0.18	Transcription regulator
<i>ROX1</i>	4.31	0.21	site-specific DNA binding protein, repressor
<i>SPT10</i>	3.55	0.70	negative transcriptional regulator
<i>YAP7</i>	12.93	7.53	bZIP protein
Nucleotide Metabolism			
<i>CDD1</i>	2.62	0.40	Involved in cytidine and deoxycytidine

			metabolism
Degradation			
<i>YPS5</i>	4.89	1.78	GPI-anchored aspartic protease
<i>LAP4</i>	4.26	0.02	vacuolar aminopeptidase ysc1
Mitochondrial Maintenance			
<i>CCPI</i>	5.75	0.73	Cytochrome-c peroxidase
<i>CYC1</i>	6.54	1.15	iso-1-cytochrome c
<i>GLO4</i>	3.62	0.01	Mitochondrial glyoxylase-II
<i>ISU2</i>	8.86	0.70	NifU-like protein A, iron homeostasis, mitochondrial matrix
<i>MMM1</i>	2.27	0.19	mitochondrial outer membrane protein
<i>MRM2</i>	3.13	0.04	Mitochondrial rRNA Methyltransferase
<i>MRS4</i>	5.23	0.65	mitochondrial carrier protein, highly homologous to Mrs3p
<i>NFU1</i>	2.98	0.14	NifU-like protein B, iron homeostasis, mitochondrial matrix
<i>OM45</i>	3.24	0.06	45-kDa mitochondrial outer membrane protein
Cell Cycle			
<i>APC9</i>	2.12	0.08	subunit of the anaphase promoting complex (APC)
<i>CDC31</i>	2.33	0.14	calcium-binding protein component of spindle pole bodies, localizes to half-bridges and interacts with KAR1
<i>DOC1</i>	3.43	0.27	Doc1p and Cdc26p are associated with the anaphase-promoting complex and are involved in the degradation of Clb2p
Cell Growth/ Maintenance			
<i>ERO1</i>	3.12	0.90	required for protein disulfide bond formation in the ER
<i>ICY2</i>	5.30	0.73	Interacting with the cytoskeleton Involved in chromatin organization and nuclear transport
<i>PEP12</i>	2.76	0.09	integral membrane protein\; c-terminal TMD\; located in endosome
<i>PRM8</i>	5.09	1.41	pheromone responsive
<i>PRM9</i>	4.82	0.26	pheromone responsive
<i>RAV2</i>	2.18	0.10	Regulator of H ⁺ -ATPase in Vacuolarmembrane
<i>VPS24</i>	2.22	0.00	endosomal Vps protein complex subunit
Metabolism			

<i>AAD4</i>	18.83	2.22	Hypothetical aryl-alcohol dehydrogenase
<i>ALD3</i>	6.70	0.06	Aldehyde Dehydrogenase (NAD(P)+)
<i>CDA1</i>	12.84	2.49	Chitin Deacetylase
<i>CEM1</i>	2.33	0.15	Protein homologous to beta-keto-acyl synthase, hexadecanal biosynthesis
<i>DAL7</i>	3.12	0.18	Malate synthase 2
<i>DIT1</i>	3.47	0.94	first enzyme in dityrosine synthesis
<i>DIT2</i>	12.69	2.70	Cytochrome P450 56, Dit2p catalyzes oxidation of N-formyl tyrosine to N,N-bisformyl dityrosine in vitro
<i>FBP26</i>	2.43	0.12	Fructose-2,6-bisphosphatase
<i>GCY1</i>	2.41	0.08	Similar to mammalian aldo\keto reductases
<i>GLC3</i>	2.51	0.05	1,4-glucan-6-(1,4-glucano)-transferase
<i>GND2</i>	6.97	1.36	6-phosphogluconate dehydrogenase
<i>MLS1</i>	12.08	6.79	carbon-catabolite sensitive malate synthase
<i>NIT1</i>	12.06	3.96	Nit1 nitrilase
<i>OYE3</i>	13.61	6.13	NAD(P)H dehydrogenase
<i>PHM6</i>	5.69	1.00	Phosphate metabolism; transcription is regulated by PHO system
<i>RIB1</i>	3.73	0.02	GTP cyclohydrolase II
<i>RMA1</i>	2.86	0.39	probable folyl-polyglutamate synthetase
<i>SUC2</i>	2.58	0.35	invertase (sucrose hydrolyzing enzyme)
<i>TKL2</i>	5.89	1.50	transketolase, homologous to tk11
<i>TMT1</i>	4.08	0.05	Trans-aconitate Methyltransferase 1
Amino Acid Metabolism			
<i>LYS7</i>	2.76	0.27	Homocitrate
<i>SDL1</i>	17.11	10.24	L-serine dehydratase
<i>URA10</i>	3.25	0.37	Orotate phosphoribosyltransferase 2
<i>URA8</i>	2.98	0.49	CTP synthase
RNA Processing			
<i>IST3</i>	2.59	0.24	U2 snRNP associated protein
<i>LUC7</i>	2.06	0.03	Living Under Cap-binding complex expression, mRNA splice site selection
<i>NBP35</i>	2.82	0.50	35 kDa nucleotide binding protein
<i>SNR57</i>	2.23	0.12	SNR57 snRNA
<i>SNR6</i>	2.18	0.01	SNR6 snRNA
<i>SNR62</i>	4.94	2.06	SNR62 snRNA
<i>SRN2</i>	2.23	0.15	suppressor of rna1-1 mutation
Transport			
<i>FLR1</i>	14.32	1.93	Major Facilitator Transporter
<i>MCH4</i>	2.89	0.73	similarity to monocarboxylate transporter

			proteins
<i>MUP3</i>	5.70	0.55	very low affinity methionine permease
<i>SUL1</i>	2.36	0.25	Probable sulfate transport protein
Unknown			
<i>FUN19</i>	3.25	0.53	Function unknown now
<i>FYV10</i>	2.62	0.30	hypothetical protein
<i>gAR04_0</i>	2.39	0.23	Saccharomyces cerevisiae chromosome I, Found forward in NC_001133 between 208649 and 209648
<i>gCR02_1</i>	2.95	0.08	Saccharomyces cerevisiae chromosome III, Found forward in NC_001135 between 178526 and 179525
<i>gCR03_2</i>	3.92	1.42	Saccharomyces cerevisiae chromosome III, Found forward in NC_001135 between 277986 and 278985
<i>gIL01_2</i>	3.93	1.10	Saccharomyces cerevisiae chromosome IX, Found forward in NC_001141 between 11696 and 12695
<i>gJL08_1</i>	2.18	0.10	Saccharomyces cerevisiae chromosome X, Found forward in NC_001142 between 425301 and 426300
<i>gJR13_4</i>	3.56	1.14	Saccharomyces cerevisiae chromosome X, Found forward in NC_001142 between 633774 and 634773
<i>gLR03_6</i>	4.19	0.49	Saccharomyces cerevisiae chromosome XII, Found forward in NC_001144 between 194164 and 194675
<i>gLR11_0</i>	4.11	1.52	Saccharomyces cerevisiae chromosome XII, Found forward in NC_001144 between 965554 and 966553
<i>gLR14_1</i>	10.99	5.32	Saccharomyces cerevisiae chromosome XII, Found forward in NC_001144 between 1043294 and 1044293
<i>gLR14_2</i>	6.07	1.36	Saccharomyces cerevisiae chromosome XII, Found forward in NC_001144 between 1044294 and 1045293
<i>gNL06_1</i>	8.59	0.75	Saccharomyces cerevisiae chromosome XIV, Found forward in NC_001146 between 310454 and 311453
<i>gNL06_2</i>	5.65	2.01	Saccharomyces cerevisiae chromosome XIV, Found forward in NC_001146 between 311454 and 312453
<i>gNR09_4</i>	7.83	4.75	Saccharomyces cerevisiae chromosome XIV, Found forward in NC_001146 between 685191 and 686190

<i>gNR09_5</i>	5.22	2.36	Saccharomyces cerevisiae chromosome XIV, Found forward in NC_001146 between 686191 and 686613
<i>gNR10_1</i>	2.62	0.40	Saccharomyces cerevisiae chromosome XIV, Found forward in NC_001146 between 762618 and 763617
<i>gOL02_4</i>	52.46	24.23	Saccharomyces cerevisiae chromosome XV, Found forward in NC_001147 between 173973 and 174972
<i>gPR13_0</i>	16.32	10.88	Saccharomyces cerevisiae chromosome XVI, Found forward in NC_001148 between 759478 and 760477
<i>NAL013C</i>	2.95	0.13	non-annotated SAGE orf
<i>NBL011C</i>	2.50	0.08	non-annotated SAGE orf
<i>NGL026C</i>	3.82	0.36	non-annotated SAGE orf
<i>NJR008W</i>	3.47	0.27	non-annotated SAGE orf
<i>NJR009W</i>	4.09	0.57	non-annotated SAGE orf
<i>NLR116W</i>	8.09	3.23	non-annotated SAGE orf
<i>NMA2</i>	2.80	0.02	strong similarity to hypothetical protein YLR328w
<i>NMA2</i>	2.63	0.43	strong similarity to hypothetical protein YLR328w
<i>NNL036W</i>	7.74	2.07	non-annotated SAGE orf
<i>NNL044C</i>	11.66	3.91	non-annotated SAGE orf
<i>NOL042W</i>	8.32	4.58	non-annotated SAGE orf
<i>NOL048W</i>	2.56	0.30	non-annotated SAGE orf
<i>NOR060C</i>	3.56	1.00	non-annotated SAGE orf
<i>NPR004C</i>	2.70	0.01	non-annotated SAGE orf
<i>YAL037c-a</i>	8.92	3.55	identified by SAGE
<i>YAL061W</i>	14.72	8.34	similarity to alcohol/sorbitol dehydrogenase
<i>YAR023C</i>	3.28	0.31	membrane protein
<i>YBL049W</i>	3.34	0.54	hypothetical protein
<i>YBL086C</i>	2.75	0.18	involved in sugar metabolism
<i>YBR047W</i>	6.63	0.73	hypothetical protein
<i>YBR101C</i>	3.64	0.16	weak similarity to S.pombe hypothetical protein SPBC3B9.01
<i>YBR116C</i>	2.77	0.33	questionable ORF
<i>YBR116C</i>	2.61	0.47	questionable ORF
<i>YBR255W</i>	3.15	0.56	hypothetical protein
<i>YCR007C</i>	4.91	1.34	strong similarity to subtelomeric encoded proteins
<i>YCR068w-a</i>	6.88	3.43	similarity to starvation induced pSI-7 protein of C. fluvum
<i>YCR102C</i>	26.94	3.77	Alcohol dehydrogenase
<i>YDL025C</i>	4.75	0.23	ser/thr protein kinase of the DEAD/DEAH box family

<i>YDL091C</i>	2.33	0.20	weak similarity to mouse FAF1 protein
<i>YDL204W</i>	4.28	0.21	similarity to hypothetical protein YDR233c
<i>YDL218W</i>	61.79	18.50	weak similarity to hypothetical protein YNR061c
<i>YDR003W</i>	4.40	0.48	strong similarity to hypothetical protein YBR005w
<i>YDR042C</i>	3.91	1.00	hypothetical protein
<i>YDR048C</i>	6.54	2.70	questionable ORF
<i>YDR066C</i>	3.08	0.31	similarity to hypothetical protein YER139c
<i>YDR070C</i>	9.22	0.03	hypothetical protein
<i>YDR132C</i>	17.06	2.15	strong similarity to hypothetical protein YLR108c
<i>YDR222W</i>	3.04	0.09	strong similarity to hypothetical protein YLR225c
<i>YDR278C</i>	2.64	0.51	hypothetical protein
<i>YDR374C</i>	2.33	0.20	similarity to hypothetical A. thaliana protein BAC F21M12
<i>YDR533C</i>	3.95	0.20	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c
<i>YER067W</i>	5.18	0.32	strong similarity to hypothetical protein YIL057c
<i>YER079W</i>	3.91	0.31	hypothetical protein
<i>YERCDELTA26</i>	7.79	4.03	YERCDELTA26 Ty1 LTR
<i>YFL057C</i>	19.50	2.94	strong similarity to aryl-alcohol dehydrogenases
<i>YGL004C</i>	3.66	0.53	weak similarity to Tup1p
<i>YGL108C</i>	3.29	0.79	weak similarity to hypothetical S.pombe protein
<i>YGL114W</i>	3.13	0.64	weak similarity to H.influenzae permease
<i>YGR011W</i>	2.53	0.43	questionable ORF
<i>YGR015C</i>	2.58	0.45	similarity to hypothetical protein YGR031w
<i>YGR043C</i>	5.25	0.18	strong similarity to transaldolase
<i>YGR161C</i>	4.12	0.44	hypothetical protein
<i>YGR223C</i>	2.91	0.35	weak similarity to hypothetical protein YFR021w
<i>YHL010C</i>	2.88	0.45	similarity to C.elegans hypothetical protein
<i>YHLWDELTA2</i>	3.95	0.07	YHLWDELTA2 Ty1 LTR
<i>YHR029C</i>	2.59	0.10	Thymidylate synthase (putative\; weak)
<i>YHR048W</i>	9.99	2.31	similarity to multidrug resistance proteins
<i>YHR087W</i>	4.35	0.42	hypothetical protein
<i>YHR097C_ex2</i>	3.11	0.31	strong similarity to hypothetical protein YDR348c
<i>YHR126C</i>	5.02	0.79	hypothetical protein
<i>YHR159W</i>	3.84	0.17	hypothetical protein
<i>YHR199C</i>	2.81	0.28	strong similarity to hypothetical protein YHR198c
<i>YIL007C</i>	2.47	0.17	similarity to C.elegans hypothetical protein

<i>YIL087C</i>	3.23	0.68	hypothetical protein
<i>YIL100W</i>	3.15	0.41	similarity to mouse Gcap1 protein and fruit fly Bkm-like sex-determining region hypothetical protein CS314
<i>YIL165C</i>	8.21	1.51	putative pseudogene
<i>YIL167W</i>	3.78	0.59	serine dehydratase
<i>YJL048C</i>	5.22	1.66	similarity to hypothetical protein YBR273c
<i>YJL144W</i>	9.93	2.22	hypothetical protein
<i>YJLWTAU4</i>	2.35	0.01	YJLWTAU4 Ty4 LTR
<i>YJR008W</i>	4.36	0.43	similarity to <i>S.pombe</i> hypothetical protein
<i>YJR096W</i>	2.69	0.21	similarity to <i>Corynebacterium</i> 2,5-diketo-D-gluconic acid reductase and aldehyde reductases
<i>YJU2</i>	13.86	9.18	similarity to <i>C.elegans</i> hypothetical proteins
<i>YJU3</i>	2.28	0.11	weak similarity to <i>E.coli</i> hypothetical protein
<i>YKL023W</i>	3.12	0.30	weak similarity to human cyclin II
<i>YKL044W</i>	4.20	1.59	hypothetical protein
<i>YKL070W</i>	3.85	0.34	similarity to <i>B.subtilis</i> transcriptional regulatory protein
<i>YKL071W</i>	49.39	1.54	weak similarity to <i>A.parasiticus</i> nor-1 protein
<i>YKL086W</i>	52.62	7.52	hypothetical protein
<i>YKL107W</i>	12.52	3.78	weak similarity to <i>S.antibioticus</i> probable oxidoreductase
<i>YKL162C</i>	2.77	0.32	hypothetical protein
<i>YLL055W</i>	11.20	0.29	similarity to Dal5p
<i>YLL056C</i>	20.52	3.04	weak similarity to <i>Y.pseudotuberculosis</i> CDP-3,6-dideoxy-D-glycero-L-glycero-4-hexulose-5-epimerase
<i>YLL057C</i>	3.39	0.10	similarity to <i>E.coli</i> dioxygenase
<i>YLL059C</i>	8.32	1.77	hypothetical protein
<i>YLR108C</i>	6.39	0.43	strong similarity to YDR132c
<i>YLR164W</i>	4.85	1.50	strong similarity to Sdh4p
<i>YLR168C</i>	2.14	0.07	probably involved in intramitochondrial protein sorting
<i>YLR193C</i>	5.05	0.34	similarity to <i>G.gallus</i> px19 and Msf1p
<i>YLR251W</i>	4.00	0.11	similarity to peroxisomal rat membrane protein PMP22
<i>YLR252W</i>	4.08	0.37	questionable ORF
<i>YLR271W</i>	2.69	0.00	hypothetical protein
<i>YLR297W</i>	2.42	0.05	weak similarity to <i>Vibrio vulnificus</i> VvpC protein
<i>YLR312C</i>	2.62	0.24	hypothetical protein
<i>YLR327C</i>	3.96	0.01	strong similarity to Stf2p
<i>YLR346C</i>	6.40	1.45	weak similarity to YGR035c
<i>YLR460C</i>	21.00	5.13	similarity to <i>C.carbonum</i> toxD protein
<i>YLRWSIGMA3</i>	2.59	0.13	YLRWSIGMA3 Ty3 LTR

<i>YML003W</i>	3.68	1.02	hypothetical protein
<i>YML087C</i>	6.36	0.70	strong similarity to YML125c, similarity to cytochrome-b5- and nitrate reductases
<i>YML131W</i>	3.77	0.60	similarity to human leukotriene b4 12-hydroxydehydrogenase
<i>YMR084W</i>	25.03	11.07	putative pseudogene
<i>YMR085W</i>	43.61	5.39	putative pseudogene
<i>YMR090W</i>	7.99	0.43	strong similarity to B. subtilis conserved hypothetical protein yhfK
<i>YMR135C</i>	2.21	0.11	hypothetical protein
<i>YMR181C</i>	2.25	0.04	similarity to YPL229w
<i>YMR265C</i>	4.42	0.41	hypothetical protein
<i>YMRWDELTA21</i>	3.55	0.51	YMRWDELTA21 Ty1 LTR
<i>YNL077W</i>	3.09	0.40	similarity to dnaJ protein homolog YDJ1
<i>YNL092W</i>	2.63	0.02	similarity to hypothetical C. elegans proteins Y48E1C.2 and Y48E1C.c
<i>YNL134C</i>	6.41	0.18	similarity to C.carbonum toxD gene
<i>YNL144C</i>	2.26	0.01	similarity to YHR131c
<i>YNL194C</i>	80.16	48.92	strong similarity to YDL222c and similarity to Sur7p
<i>YNL195C</i>	4.87	0.52	hypothetical protein
<i>YNL260C</i>	8.16	1.21	hypothetical protein
<i>YNL305C</i>	2.24	0.06	similarity to C-term. of A.nidulans regulatory protein (qutR)
<i>YNR034w-a</i>	5.66	0.40	hypothetical protein
<i>YNR068C</i>	3.16	0.21	similarity to Bull1p
<i>YNR069C</i>	3.69	0.30	similarity to central part of Bull1p
<i>YNR073C</i>	2.32	0.02	strong similarity to E.coli D-mannonate oxidoreductase, identical to YEL070w
<i>YOL029C</i>	3.04	0.59	hypothetical protein
<i>YOL032W</i>	6.94	0.43	hypothetical protein
<i>YOL150C</i>	3.57	0.33	questionable ORF
<i>YOL153C</i>	4.66	0.47	strong similarity to Cps1p
<i>YOLWDELTA10</i>	2.33	0.01	YOLWDELTA10 Ty1 LTR
<i>YOR060C</i>	4.24	1.74	hypothetical protein
<i>YOR173W</i>	3.15	0.46	strong similarity to YLR270w
<i>YOR223W</i>	2.21	0.04	protein of unknown function
<i>YOR225W</i>	3.49	0.18	questionable ORF
<i>YOR255W</i>	5.88	2.86	hypothetical protein
<i>YPL166W</i>	4.22	1.23	weak similarity to paramyosins
<i>YPL247C</i>	2.33	0.20	similarity to human HAN11 protein and petunia an11 protein
<i>YPLWDELTA11</i>	2.37	0.22	YPLWDELTA11 Ty1 LTR
<i>YPLWDELTA6</i>	6.02	0.58	YPLWDELTA6 Ty1 LTR
<i>YPR012W</i>	2.35	0.17	hypothetical protein
<i>YPR093C</i>	10.62	2.94	weak similarity to zinc-finger proteins

<i>YPR116W</i>	17.75	8.73	hypothetical protein
<i>YPR127W</i>	4.88	0.21	similarity to C-term. of <i>N.tabacum</i> auxin-induced protein
<i>YPR158W</i>	2.24	0.14	similarity to YGR142w
<i>YPR174C</i>	3.54	0.33	weak similarity to Nbp1p
<i>YPRCTAU3</i>	2.62	0.14	YPRCTAU3 Ty4 LTR
<i>ARR2</i>	7.17	1.75	Required for arsenate but not for arsenite resistance
<i>ARR3</i>	32.42	18.70	involved in arsenite transport
<i>BTN2</i>	8.62	0.46	Gene/protein whose expression is elevated in a <i>btn1</i> minus/ <i>Btn1p</i> lacking yeast strain.
<i>CRR1</i>	4.21	1.61	similarity to UTR2 protein
<i>DRE2</i>	4.48	0.48	weak similarity to <i>C.elegans</i> hypothetical protein
<i>ECM13</i>	3.10	0.52	ExtraCellular Mutant
<i>ECM4</i>	5.09	0.73	ExtraCellular Mutant
<i>JIP4</i>	4.45	0.83	hypothetical protein
<i>PIN3</i>	2.93	0.61	similarity to chicken growth factor receptor-binding protein GRB2 homolog
<i>RTA1</i>	2.15	0.12	involved in 7-aminocholesterol resistance
<i>SDF1</i>	2.33	0.05	similarity to <i>C.elegans</i> C02C2.6 protein
<i>SDS24</i>	2.39	0.03	Similar to <i>S. pombe</i> SDS23, suppresses DIS2, localized to the nucleus
<i>SDS3</i>	3.63	1.26	Functions are similar to those of SIN3 and RPD3
<i>SOL1</i>	3.91	0.31	similarity to glucose-6-phosphate dehydrogenase non-catalytic domains\; homologous to Sol2p and Sol3p
<i>SOL4</i>	3.59	0.29	similar to SOL3
<i>SPI1</i>	3.49	0.41	Stationary Phase Induced; strongly expressed during stationary phase, and transcription is dependent on MSN2/MSN4.
<i>TAH11</i>	2.50	0.14	weak similarity to <i>Xenopus</i> vimentin 4
<i>TIS11</i>	2.95	0.00	zinc finger containing homolog of mammalian TIS11, glucose repressible gene
<i>UGX2</i>	2.52	0.38	protein of unknown function
<i>MSC1</i>	3.32	0.32	C-terminal part starting with aa 262 cause growth inhibition when overexpressed
