

Up regulated genes in BER/NER-defective cells following 0.125mM H₂O₂ exposure for 30 minutes

Gene name	Average Fold Change	S.E.M.	Gene Description
Cell Stress			
<i>DDR2</i>	5.01	1.00	Multistress response protein
<i>TSA2</i>	16.62	3.91	thioredoxin peroxidase
<i>TRR1</i>	2.64	0.18	thioredoxin reductase
<i>SNZ2</i>	3.51	0.62	Snooze, stationary phase induced gene family
<i>GTT2</i>	26.19	10.67	glutathione transferase
<i>GRE2</i>	8.03	3.12	NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase)
<i>GPX2</i>	9.95	1.96	Phospholipid hydroperoxide glutathione peroxidase
<i>CTA1</i>	8.43	3.21	catalase A
<i>SOD2</i>	4.46	0.24	manganese-containing superoxide dismutase
Signal Transduction			
<i>SMK1</i>	42.15	12.70	MAP kinase, involved in sporulation
<i>MDG1</i>	3.36	1.00	involved in G-protein mediated signal transduction
<i>FRM2</i>	38.14	6.37	involved in integration of lipid signaling with cellular homeostasis
Degradation			
<i>LAP4</i>	3.07	.046	vacuolar aminopeptidase ysc1
Mitochondrial Maintenance			
<i>PRX1</i>	5.43	0.78	mitochondrial isoform of thioredoxin peroxidase
<i>MRS4</i>	2.94	0.44	RNA splicing, mitochondrial carrier protein
<i>ISU2</i>	4.10	0.71	involved in iron homeostasis
<i>FRE1</i>	3.21	0.46	ferric and cupric reductase, iron homeostasis
<i>CYT2</i>	2.45	0.23	cytochrome c1 heme lyase
<i>CYC1</i>	11.33	1.39	iso-1-cytochrome c
<i>CCP1</i>	8.77	0.93	cytochrome-c peroxidase
Metabolism			
<i>YCR102C</i>	15.75	7.55	alcohol dehydrogenase
<i>YDL124W</i>	2.38	0.20	similarity to aldose reductases
<i>YFL057C</i>	19.57	5.26	similarity to aryl-alcohol dehydrogenases
<i>ZWF1</i>	3.06	0.55	glucose-6-phosphate dehydrogenase
<i>PGM2</i>	2.43	0.20	Phosphoglucomutase

<i>OYE3</i>	16.99	4.03	NADPH dehydrogenase
<i>GCY1</i>	2.47	0.33	similar to mammalian aldo/keto reductases
<i>AAD4</i>	19.08	5.14	hypothetical aryl-alcohol dehydrogenase
Transport			
<i>FLR1</i>	21.19	7.74	transporter in nuclear pore
<i>ATR1</i>	4.63	0.84	multidrug transport protein
Unknown			
<i>NJR005C</i>	14.21	3.83	non-annotated SAGE orf
<i>NJR008W</i>	2.17	0.13	non-annotated SAGE orf
<i>NHR002C</i>	4.29	0.84	non-annotated SAGE orf
<i>YOR121C</i>	2.23	0.21	questionable orf
<i>YLR460C</i>	7.63	3.45	similarity to C.carbonum toxD protein
<i>YML131W</i>	4.55	0.74	similarity to human leukotriene b4 12hydroxydehydrogenase
<i>YMR090W</i>	6.25	0.93	similarity to B.subtilis hypothetical protein yhfK
<i>YNL134C</i>	5.76	1.00	similarity to C.carbonum toxD gene
<i>YBR047W</i>	2.40	0.10	hypothetical protein
<i>YDL218W</i>	61.80	19.93	similarity to hypothetical protein YNR061C
<i>YDR533C</i>	2.94	0.09	similarity to YPL280w, YOR391C, and YMR322C
<i>YHR029C</i>	2.49	0.21	Unknown ORF
<i>YJL045W</i>	2.43	0.28	similarity to succinate dehydrogenase flavoprotein
<i>YKL086W</i>	56.92	10.08	hypothetical protein
<i>YKL071W</i>	34.73	14.89	similarity to A.parasiticus nor-1 protein
<i>YLL056C</i>	4.81	1.51	similarity to Y.Pseudotuberculosis CDP-3,6-dideoxy-D-glycero-L-glycero-4- hexulose-5-epimerase
<i>YLR164W</i>	4.96	0.32	strong similarity to Sdh4p
<i>YLR311C</i>	4.60	0.97	similarity to S.tarentolae cryptogene protein G4
<i>ECM4</i>	6.50	0.90	extracellular mutant
<i>BOP2</i>	2.94	0.40	bypass of PAM1
<i>ARR2</i>	3.12	0.32	required for arsenate but not for arsenite resistance