

Up regulated genes in WT cells following 0.25mM H₂O₂ exposure for 60 minutes

Gene name	Average Fold Change	S.E.M.	Description
Cell Stress			
<i>HSP12</i>	19.93	5.94	12 kDa heat shock protein
<i>HSP26</i>	8.36	0.67	heat shock protein 26
<i>GTT1</i>	6.54	0.97	Glutathione transferase
<i>GTT2</i>	4.95	2.06	Glutathione transferase
<i>TRX2</i>	5.32	0.73	thioredoxin
<i>TRR1</i>	3.03	0.53	Thioredoxin reductase
<i>YBL064C</i>	11.04	1.92	Homolog to thiol-specific antioxidant
<i>TSA2</i>	121.07	9.64	strong similarity to thiol-specific antioxidant proteins
<i>GPX2</i>	4.41	1.42	Probable glutathione peroxidase
<i>SOD2</i>	3.68	0.85	Manganese-containing superoxide dismutase
<i>SOD1</i>	2.44	0.20	Cu, Zn superoxide dismutase
DNA Repair/ Replication			
<i>HUG1</i>	10.98	1.74	induced by Mec1 signaling, suppressor of mec1 lethality
<i>RAD51</i>	2.21	0.12	RecA homolog\; involved in recombination
<i>RNR4</i>	2.93	0.05	Ribonucleotide Reductase
<i>RNR3</i>	25.28	10.15	Ribonucleotide reductase large subunit
<i>RNR2</i>	4.17	0.59	Ribonucleotide reductase small subunit
<i>DDR48</i>	4.47	0.13	DNA-damage responsive protein
Signal Transduction			
<i>GSP2</i>	4.64	0.30	GTP binding protein maintenance of nuclear organization a small nuclear GTPase of the ras superfamily
<i>FRM2</i>	5.35	0.69	Protein involved in the integration of lipid signaling pathways with cellular homeostatis
Degradation			
<i>UBI4</i>	4.95	0.16	ubiquitin
<i>LAP4</i>	3.90	0.65	vacuolar aminopeptidase ysc1
Mitochondrial Maintenance			
<i>FET3</i>	2.47	0.34	multicopper oxidase
<i>IDH1</i>	3.14	0.36	alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1

<i>MRP8</i>	2.43	0.17	mitochondrial ribosomal protein
<i>CYC1</i>	4.05	1.49	iso-1-cytochrome c
<i>CIT2</i>	2.71	0.32	non-mitochondrial citrate synthase
<i>CYT2</i>	2.43	0.28	cytochrome c1 heme lyase
<i>STF1</i>	3.07	0.43	ATPase stabilizing factor
<i>STF2</i>	2.84	0.39	ATP synthesis coupled proton transport
<i>NCA3</i>	3.55	0.69	With NCA2, regulates proper expression of subunits 6 (Atp6p) and 8 (Atp8p) of the Fo-F1 ATP synthase
<i>FIS1</i>	2.76	0.32	involved in mitochondrial division
<i>SMF3</i>	4.71	2.60	strong similarity to SMF2 protein, involved in iron transport
Cell Cycle			
<i>PCL5</i>	2.75	0.33	G1/S cyclin (weak)
Cell Growth/Maintenance			
<i>TIP1</i>	2.70	0.24	cell wall mannoprotein
Metabolism			
<i>HOR2</i>	3.23	0.32	DL-glycerol-3-phosphatase
<i>ALD3</i>	3.68	0.45	Aldehyde Dehydrogenase (NAD(P)+)
<i>OPI3</i>	4.65	1.36	Methylene-fatty-acyl-phospholipid synthase
<i>TDH1</i>	14.21	4.80	Glyceraldehyde-3-phosphate dehydrogenase 1
<i>HXK1</i>	5.83	0.71	Hexokinase I (PI) (also called Hexokinase A)
<i>GLK1</i>	2.80	0.54	Glucokinase
<i>PGM2</i>	4.13	0.54	Phosphoglucomutase
<i>OLE1</i>	5.16	0.26	delta-9-fatty acid desaturase
<i>GCY1</i>	7.01	1.54	Similar to mammalian aldo\keto reductases
<i>OYE3</i>	5.37	0.31	NAD(P)H dehydrogenase
<i>GND2</i>	6.35	2.91	6-phosphogluconate dehydrogenase
<i>YPR1</i>	3.26	0.62	homologous to the aldo-keto reductase protein family
<i>YEL047C</i>	2.22	0.05	fumarate reductase (NADH) activity
<i>YGL039W</i>	4.32	0.45	Oxidoreductase
Transport			
<i>PHO84</i>	2.61	0.11	inorganic phosphate transporter, transmembrane protein
<i>PDR10</i>	4.30	1.75	Putative ABC transporter highly similar to Pdr5p
<i>ARN1</i>	4.29	0.94	Siderophore transporter for triacetylfulsarinine C
<i>SIT1</i>	2.97	0.17	Ferrioxamine B transporter
<i>FIT3</i>	6.28	0.62	siderochrome transport
<i>FIT2</i>	22.54	1.61	siderochrome transport

Unknown			
<i>SPL2</i>	3.44	0.56	Protein with similarity to cyclin-dependent kinase inhibitors, overproduction suppresses a <i>plc1</i> null mutation
<i>YML131W</i>	3.38	0.35	similarity to human leukotriene b4 12-hydroxydehydrogenase
<i>MSC1</i>	3.77	0.17	C-terminal part starting with aa 262 cause growth inhibition when overexpressed
<i>YMR090W</i>	17.72	4.38	strong similarity to <i>B. subtilis</i> conserved hypothetical protein <i>yhfK</i>
<i>YMR173W-A</i>	5.04	1.14	questionable ORF
<i>YMR196W</i>	3.71	0.61	hypothetical protein
<i>YMR315W</i>	3.55	0.35	hypothetical protein
<i>NMR009W</i>	3.13	0.33	non-annotated SAGE orf
<i>YNL208W</i>	4.07	0.63	weak similarity to <i>Colletotrichum gloeosporioides</i> nitrogen starvation-induced glutamine rich protein
<i>YNL134C</i>	5.99	0.60	similarity to <i>C.carbonum</i> <i>toxD</i> gene
<i>YOL101C</i>	9.07	0.15	similarity to <i>YOL002c</i> and <i>YDR492w</i>
<i>PHO36</i>	2.51	0.16	strong similarity to <i>YDR492w</i> and <i>S.pombe</i> hypothetical protein
<i>YOR338W</i>	4.84	2.07	similarity to <i>YAL034c</i>
<i>YPR127W</i>	2.88	0.40	similarity to C-term. of <i>N.tabacum</i> auxin-induced protein
<i>YBR085c-a</i>	2.76	0.02	hypothetical protein
<i>YCL042W</i>	5.44	3.02	hypothetical protein
<i>YCL049C</i>	2.35	0.06	hypothetical protein
<i>YDL124W</i>	4.77	1.04	similarity to aldose reductases
<i>PST2</i>	3.16	0.48	strong similarity to <i>S.pombe</i> <i>obr1</i>
<i>YDR533C</i>	4.98	0.66	strong similarity to hypothetical proteins <i>YPL280w</i> , <i>YOR391c</i> and <i>YMR322c</i>
<i>YFL057C</i>	4.31	1.33	strong similarity to aryl-alcohol dehydrogenases
<i>YGL121C</i>	3.57	0.82	hypothetical protein
<i>YHR029C</i>	2.70	0.50	Thymidylate synthase (putative\; weak)
<i>YHR087W</i>	3.09	0.62	hypothetical protein
<i>YGLCDELTA5</i>	2.68	0.31	<i>YGLCDELTA5</i> Ty1 LTR
<i>PRY1</i>	2.75	0.39	Similar to plant PR-1 pathogen related proteins
<i>NJL020C</i>	5.14	0.79	non-annotated SAGE orf
<i>YKL151C</i>	3.07	0.33	similarity to <i>C.elegans</i> hypothetical protein R107.2
<i>YKL086W</i>	17.33	14.44	hypothetical protein
<i>YKL071W</i>	9.83	3.13	weak similarity to <i>A.parasiticus</i> <i>nor-1</i> protein
<i>YKR046C</i>	4.74	0.90	hypothetical protein
<i>ECM4</i>	12.83	2.07	ExtraCellular Mutant
<i>TFS1</i>	4.30	0.56	suppressor of <i>cdc25</i>
<i>YLR270W</i>	3.08	0.14	strong similarity to <i>YOR173w</i>