

Supplemental Table 1. Number of microarray experiments for different conditions

Experiment	Low HP					Medium HP				High HP				Md			TBH		
	0	5	15	30	60	5	15	30	60	5	15	30	60	0	15	60	0	15	60
wild-type	16	4	4	4	4	4	4	4	4	4	4	4	4	4	2	2	4	2	2
<i>pap1</i>	2	0	2	0	2	0	2	0	2	0	0	0	0	0	2	2	0	2	2
<i>prp1</i>	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0
<i>pap1 atf1</i>	1	0	1	0	1	0	1	0	1	0	1	0	1	0	0	0	0	0	0
<i>atf1</i>	2	0	2	0	2	0	2	0	2	0	1	0	1	0	0	0	1	1	1
<i>sty1</i>	2	0	2	0	2	0	2	0	2	0	1	0	1	0	0	0	0	2	2
<i>pmk1</i>	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	1	1
<i>hsr1</i>	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0

Supplemental Table 2. Genes that are induced in all four oxidative stress conditions.

<i>Gene name</i>	<i>Annotation</i>
<i>bfr1</i>	ABC transporter involved in multidrug resistance
<i>caf5</i>	MFS multidrug efflux transporter
<i>ctt1</i>	Catalase
<i>gst1</i>	Glutathione S-transferase
<i>gst2</i>	Glutathione S-transferase
<i>meu8</i>	Predicted aldehyde dehydrogenase
<i>mfs1</i>	MFS membrane transporter
<i>obr1</i>	Ubiquitinated histone-like protein
<i>ppk8</i>	Predicted protein kinase
SPAC11D3.05	Membrane transporter
SPAC11D3.13	Member of the DJ-1 or PfpI family
SPAC1399.01c	Member of purine permease family of membrane transporters
SPAC1F8.04c	Protein with amidohydrolase family domain
SPAC23D3.05c	Alcohol dehydrogenase pseudogene
SPAC2E1P3.01	Member of zinc-binding dehydrogenase family
SPAC513.06c	Member of oxidoreductase family
SPAC513.07	Predicted alpha-acetoxy ketone reductase
SPAC5H10.05c	Protein with domain found in NAD(P)H2 dehydrogenases
SPAC6G10.03c	Protein with hydrolase fold domain
SPAC869.02c	Predicted nitric oxide oxidoreductase
SPAP27G11.09c	Protein with high similarity to GTP cyclohydrolase (riboflavin synthesis)
SPAPB24D3.08c	Member of the zinc-binding dehydrogenase family
SPBC1271.07c	Predicted N-acetyltransferase
SPBC1773.06c	Member of the zinc-binding dehydrogenase family
SPBC17D11.03c	Member of the bacterial carboxymuconolactone decarboxylase family
SPBC215.10	Protein of unknown function
SPBC215.11c	Protein with aldo-keto reductase family domain
SPBC23G7.10c	Predicted NADH-dependent flavin oxidoreductase
SPBC2A9.02	Protein of unknown function
SPBC409.13	Predicted dimethyl-ribityllumazine synthase (riboflavin synthesis)
SPCC18B5.02c	Cinnamoyl-coa reductase pseudogene
SPCC24B10.20	Predicted short chain dehydrogenase
SPCC4B3.06c	Predicted NADPH-dependent FMN reductase
SPCC576.02	Member of aspartate and glutamate racemases family
SPCC663.06c	Protein containing a short chain dehydrogenase domain
SPCC663.07c	Short chain dehydrogenase pseudogene
SPCC663.08c	Protein containing a short chain dehydrogenase domain
<i>srx1</i>	Sulfiredoxin that catalyzes reduction of oxidized Tpx1p
<i>tpx1</i>	Peroxiredoxin
<i>trr1</i>	Thioredoxin reductase
<i>trx1</i>	Thioredoxin

List of the 41 core genes that were induced at least 1.5-fold in all four oxidative stress conditions and whose profiles are shown in Figure 5A. Annotations are based on *S. pombe* GeneDB at <http://www.genedb.org/genedb/pombe/index.jsp>.