SUPPLEMENTARY INFORMATION

Supplementary Table S1.
An excel table listing all proteins that were identified from at least two independent cultures from the same strain. For the sake of clarity only the columns containing Sequest score of proteins are visible for the independent cultures of each strain. However the % coverage and number of unique peptides for each protein from each independent culture and from each strain can be examined by adjusting column width. Rows highlighted in tan are proteins that have been identified from peptides that do not contain a cysteine residue.

Major Columns:
A, lists accession numbers
B, amino acids in protein
C, protein description
D, % coverage
E, number of unique peptides detected

Likewise the information for each unique peptide detected from each protein can be examined by opening the (+) button in column 1. The information includes:

- The sequence of each unique peptide
- The number of proteins in *S. cerevisiae* that contain the peptide sequence
- The number of protein groups
- Activation type (all CID)
- Δ score
- Sequest rank for peptide
- Peptide charge
- MH+ [Da]
- ΔM [ppm]
- First scan
- Last scan
- Retention time
- Number of ions matched
- Peptide modifications [e.g. destreak on cys residues signifies the cys was reversibly oxidised and reduced by mercaptoethanol]
- Probability
- xCorr of individual peptides.

This can be embedded again by using the (–) button in column 1.
A selection and classification of proteins with differential redox patterns among the dour strains is summarized in Table 2.

Supplementary Table S2
An Excel file with expression analysis of the mutant strains as compared to wild type. Two independent experiments were performed and dye swapping was carried out. Average intensity measurements were compared between the three mutant strains and *WT* and ratios are represented. Significant ratios below 0.5 and above 2 for down- and up-regulation are coloured in green and red, respectively. Major columns: A, lists Gene name as in SGD; B, ORF code; G, L and Q intensity ratio of Δ*GRX2*, Δ*PRX1* and Δ*GRX*/Δ*PRX1* relative to *WT*, respectively. A selection and classification of genes with significant changes in expression levels is summarized in Table 3.