



Supplementary Figure 1: Hierarchical clustering analysis of the expression profiles of 972 genes that show a statistically significant change 10-30 min of Heat Shock (HS), Osmotic Shock (OS) or Oxidative Stress (XS). Each gene is represented by a single block which is colored according to its change in transcript abundance after 10, 30 or 60 min of stress. Upregulated genes are in red while downregulated genes are in green. Genes are clustered according to the similarity in their expression profile i.e. genes that respond in a similar manner will be located closer to each other. The similarity between the expression profiles is illustrated by the dendrogram on the left.