

SUPPORTING INFORMATION FOR PUBLICATION

FOR

The phosphoproteome response to dithiothreitol reveals unique versus shared features of *Saccharomyces cerevisiae* stress responses

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Dataset S1: Processed data. \log_2 (fold change) in phosphopeptide abundance or phosphopeptide abundance normalized to changes in protein abundance, where indicated. The file also annotates peptides with significant changes in wild-type and mutant strains, according to that described in the Methods.

Supporting Material S1: Module Constituents. The file lists phosphopeptide constituents of modules identified in the paper.

Supporting Material S2: Shared-interactor kinases. A list of kinases identified as shared interactors for each module, at an FDR of 0.02 or 0.05 (where 1 = significant at that threshold, last columns). The file includes the number of module constituents that interact with a listed SI (k), the number of proteins in that module (n), the total number of proteins that interact with the SI in the background dataset (M), the total number of proteins in the background dataset (N), the p-value from the hypergeometric test, and peptides called significant at an FDR of 0.02 or 0.05.

Supporting Material S3: Functional enrichments.

Supporting Material S4: Cytoscape .sif file of modules, constituent peptides belonging to each module, and kinase/phosphatase shared interactors. Nodes are color coded for induced (yellow) or repressed (blue) modules, kinases (magenta), and phosphatases (light green).

Supporting Material S5: Source data for Figure 1B.

Supporting Material S6: Source data for Figure 4B.