

Quantitative global proteomics of yeast PBP1 deletion mutants and their stress responses identifies glucose metabolism, mitochondrial, and stress granule changes

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Supporting information

Supplemental Table 1 – Original MaxQuant output files of all identified protein groups, including LFQ intensities, sequence coverage, and PEP.

Supplemental Table 2 – Specific comparisons of strains and stress conditions as indicated on individual sheets, using only valid values.

Supplemental Figure 1 – The Pearson correlation between SM, DB, and BY strains without stress and the two stress conditions heat and NaN3 in scatter plots, indicating biological replicates.