

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Absolute protein and mRNA abundances in yeast chemostat cultures.

File Name: Supplementary Data 2

Description: Proteome and transcriptome allocation to different GO-slim processes. Genes are allowed to map to multiple GO-slim terms

File Name: Supplementary Data 3

Description: Detailed breakdown of proteome-transcriptome relationship by 6 functional categories.

File Name: Supplementary Data 4

Description: Measured metabolic flux of yeast chemostat cultures.

File Name: Supplementary Data 5

Description: Proportion of genes in each GO-slim process that are differentially allocated between different conditions.

File Name: Supplementary Data 6

Description: Exchange flux constraints used for flux balance analysis and flux variability analysis.

File Name: Supplementary Data 7

Description: Relative usage of metabolic superpathways. SGD superpathways containing at least 5 genes and with non-zero simulated flux are examined.

File Name: Supplementary Data 8

Description: Model-calculated enzyme exchange and measured enzyme abundance for each enzyme in SGD superpathways containing at least 5 genes and with non-zero simulated flux.

File Name: Supplementary Data 9

Description: Relative isozyme expression. Values represent the % of all isozymes capable of catalyzing the given reaction. Reactions are those in Yeast8.1 that contains an "or" argument in the gene association rule.

File Name: Supplementary Data 10

Description: Protein synthesis efficiency of yeast. "Group" corresponds to Fig 4c; 1=Early modulation; 2=Intermediate; 3=Late modulation; 4=No modulation.

File Name: Supplementary Data 11

Description: Validation of iBAQ-based ribosomal protein quantification by targeted quantitative proteomics.

File Name: Supplementary Data 12

Description: Ribosomal protein abundance, measured by iBAQ and adjusted by targeted quantitative proteomics.