

Supplemental Data to accompany the article by Jesch *et al.* “Genome Wide Analysis Reveals Inositol, not Choline, as the Major Effector of Ino2p-Ino4p and Unfolded Protein Response Target Gene Expression in Yeast” published in the *Journal of Biological Chemistry*.

Each workbook in the spreadsheet corresponds to the seven experiments performed in the study shown in Table I and outlined below:

Experiment	Experimental sample	Reference sample
1	Wild type I+C-	Wild type I-C-
2	Wild type I-C+	Wild type I-C-
3	Wild type I+C+	Wild type I-C-
4	Wild type I+C+	Wild type I-C+
5	<i>opi1</i> Δ I+C-	Wild type I+C-
6	<i>opi1</i> Δ I-C-	Wild type I-C-
7	<i>opi1</i> Δ I+C-	<i>opi1</i> Δ I-C-

I+ or I- refers to the presence or absence of 75 μ M inositol or 0 μ M inositol.

C+ or C- refers to the presence or absence of 1 mM choline.

Glossary of Terms:

“t” indicates the t-value for each gene. The t-value was computed as described in the “Experimental Procedures”. For this article, a gene with a p-value ≤ 0.025 was chosen as significantly regulated, corresponding to a t-value ≥ 4.303 . For a less rigorous cutoff, a t-value ≥ 2.92 corresponds to a p-value ≤ 0.05 . For a more rigorous statistical cutoff, a t-value ≥ 6.965 corresponds to a p-value ≤ 0.01 .

“Ratio” indicates the magnitude of differential expression of the “experimental” sample verses the “reference” sample. The + or – sign indicates up or down regulation, respectively.

Expression ratios for genes are included only for those spots on microarrays whose intensity was measured in all three replicates.

“SGD ID” is a hyperlink to the Saccharomyces genome database (SGD) for each gene.

Each gene is functionally annotated from data downloaded from the SGD (<http://www.yeastgenome.org>).