Supplemental Data to accompany Jesch *et al.,* "Multiple Endoplasmic Reticulum-to-Nucleus Signaling Pathways Coordinate Phospholipid Metabolism with Gene Expression by Distinct Mechanisms" published in the *Journal of Biological Chemistry*. The data are organized into three worksheets.

Inositol-regulated genes

Lists the 712 genes selected for analysis. The expression ratio and *p* value at each time point following the addition of inositol for each gene are listed. The averaged fold expression for each gene is reported as $\log_2$ [individual time point (min)/0 min reference]. The *p* value was calculated as described in "Experimental Procedures".

Each gene was grouped into one of 28 clusters numbered 1 through 28 as described in "Experimental Procedures" and subsequently grouped into one of five superclusters numbered I through V using criteria described in "Results".

Each listed gene includes the transcription factor(s) shown by Harbison *et al*. (2004) to bind that gene. Note that this only includes transcription factors whose gene associations are enriched in our dataset. See **Enriched TFs** worksheet for enriched transcription factors.

Genes identified as UPR targets by Travers *et al*., (2000) are labeled "UPR".

All ORFs

Lists the expression ratio and *p* value at each time point following the addition of inositol for 5991 open reading frames (ORFs) that passed our initial quality control criteria. The averaged fold expression for each gene is reported as $\log_2$ [individual time point (min)/0 min reference]. The *p* value was calculated as described in "Experimental Procedures".

Enriched TFs

Lists the set of transcription factors identified by Harbison *et al*. (2004) that are enriched in our dataset. The fold enrichment for each transcription factor was calculated by dividing the fraction gene occupancy for inositol-regulated genes (X) by the total gene occupancy across the genome (Y). A transcription factor with a ratio of greater than 1 was considered enriched.

References:

Harbison, C. T., Gordon, D. B., Lee, T. I., Rinaldi, N. J., Macisaac, K. D., Danford, T. W., Hannett, N. M., Tagne, J. B., Reynolds, D. B., Yoo, J., Jennings, E. G., Zeitlinger, J., Pokholok, D. K., Kellis, M., Rolfe, P. A., Takusagawa, K. T., Lander, E. S., Gifford, D. K., Fraenkel, E., and Young, R. A. (2004) *Nature* **431**, 99-104.

Travers, K. J., Patil, C. K., Wodicka, L., Lockhart, D. J., Weissman, J. S., and Walter, P. (2000) *Cell* **101**, 249-258