Supplementary Table S6

References for Data Used for P-value Calculations

Biological Property	Reference
Nuclear location	Casolari, J. M. et al. Genome-wide localization of the nuclear transport machinery couples transcriptional status and nuclear organization. *Cell* **117**, 427-39 (2004).
Chromosomal Location	genome-ftp.stanford.edu/chromosomal_feature/SGD_features.tab
Transcription Factor Binding	Harbison, C. T. et al. Transcriptional regulatory code of a eukaryotic genome. *Nature* **431**, 99-104 (2004).
TATA Box	Huisinga, K. L. & Pugh, B. F. A genome-wide housekeeping role for TFIID and a highly regulated stress-related role for SAGA in *Saccharomyces cerevisiae*. *Mol. Cell* **13**, 573-85 (2004).
SAGA/TFIID	Basehoar, A. D., Zanton, S. J. & Pugh, B. F. Identification and distinct regulation of yeast TATA box-containing genes. *Cell* **116**, 699-709 (2004).
INO80/SWR1	Mizuguchi, G. et al. ATP-driven exchange of histone H2AZ variant catalyzed by SWR1 chromatin remodeling complex. *Science* **303**, 343-8 (2004).
SWI/SNF	Sudarsanam, P., Iyer, V. R., Brown, P. O. & Winston, F. Whole-genome expression analysis of snf/swi mutants of *Saccharomyces cerevisiae*. *Proc. Natl. Acad. Sci. USA* **97**, 3364-9 (2000).
ISW2/RPD3/SIN3/UME6	Fazzio, T. G. et al. Widespread collaboration of Isw2 and Sin3-Rpd3 chromatin remodeling complexes in transcriptional repression. *Mol. Cell. Biol*. **21**, 6450-60 (2001).
HDA1	Robyr, D. et al. Microarray deacetylation maps determine genome-wide functions for yeast histone deacetylases. *Cell* **109**, 437-46 (2002).
ESA1	Robert, F. et al. Global position and recruitment of HATs and HDACs in the yeast genome. *Mol. Cell* **16**, 199-209 (2004).
mRNA half life	Wang, Y. et al. Precision and functional specificity in mRNA decay. *Proc. Natl. Acad. Sci. USA* **99**, 5860-5 (2002).
mRNA Copy Number	Wang, Y. et al. Precision and functional specificity in mRNA decay. *Proc. Natl. Acad. Sci. USA* **99**, 5860-5 (2002).
CAI Score	genome-ftp.stanford.edu/protein_info/protein_properties.tab
Ribosome Density	Arava, Y. et al. Genome-wide analysis of mRNA translation profiles in *Saccharomyces cerevisiae*. *Proc. Natl. Acad. Sci. USA* **100**, 3889-94 (2003).
Number of Proteins/mRNA	Fraser, H. B., Hirsh, A. E., Giaever, G., Kumm, J. & Eisen, M. B. Noise minimization in eukaryotic gene expression. *PLoS Biol*. **2**, e137 (2004).

Supplementary Table S6, continued.

Biological Property	Reference
Protein Copy Number	This work.
	Ghaemmaghami, S. et al. Global analysis of protein expression in yeast. *Nature* **425**, 737-41 (2003).
Protein Half-life	Belle et al. Manuscript Submitted
Protein Cellular Location	Huh, W. K. et al. Global analysis of protein localization in budding yeast. *Nature* **425**, 686-91 (2003).
Protein-Protein Interactions	Fraser, H. B., Hirsh, A. E., Giaever, G., Kumm, J. & Eisen, M. B. Noise minimization in eukaryotic gene expression. *PLoS Biol*. **2**, e137 (2004).
	Balakrishnan, R., Christie, K. R., Costanzo, M. C., Dolinski, K., Dwight, S. S., Engel, S. R., Fisk, D. G., Hirschman, J. E., Hong, E. L., Nash, R., Oughtred, R., Skrzypek, M., Theesfeld, C. L., Binkley, G., Lane, C., Schroeder, M., Sethuraman, A., Dong, S., Weng, S., Miyasato, S., Andrada, R., Botstein, D., and Cherry, J. M. "*Saccharomyces* Genome Database" http://www.yeastgenome.org/
Essentiality	Fraser, H. B., Hirsh, A. E., Giaever, G., Kumm, J. & Eisen, M. B. Noise minimization in eukaryotic gene expression. *PLoS Biol*. **2**, e137 (2004).
	genome-ftp.stanford.edu/data_download/literature_curation/phenotypes.tab