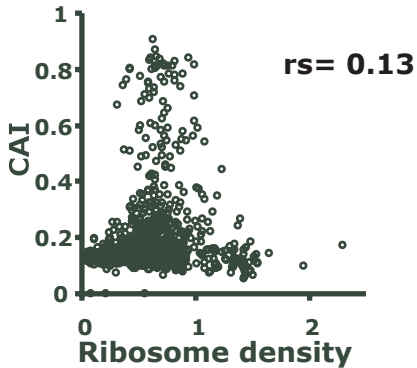


Supplemental Figure 6

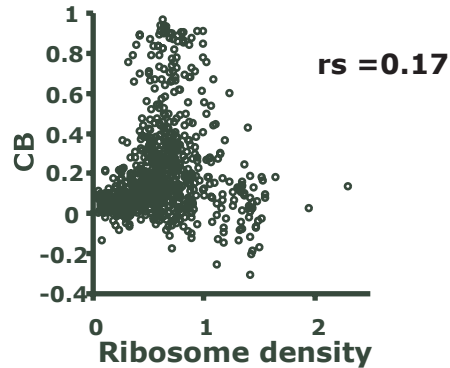
Testing mRNA features that may affect ribosome density.

Below are a series of scatter plots for the 739 genes with well-defined peaks fraction. Ribosome densities for the individual mRNAs are plotted on the x-axis versus codon usage indices (A), mRNA abundance (B) and mRNA half time. For each plot, the Spearman rank correlation (r_s) is presented.

A). Scatter plot of Ribosome density versus two different codon usage indices.

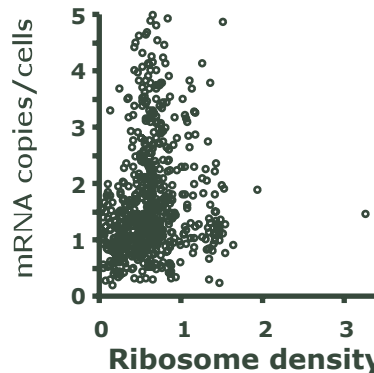
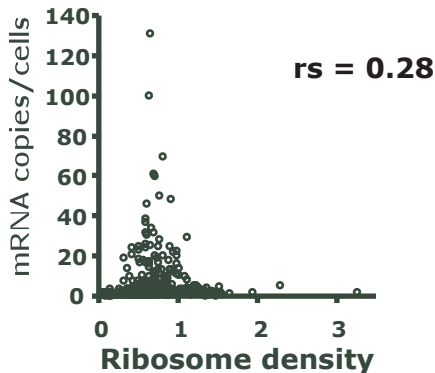


Scatter plot of density values for the genes in the 739 data set and the codon adaptation index (Sharp and Li, NAR 1987 15 281-295). Values were taken from YPD, July 20 2000 update.



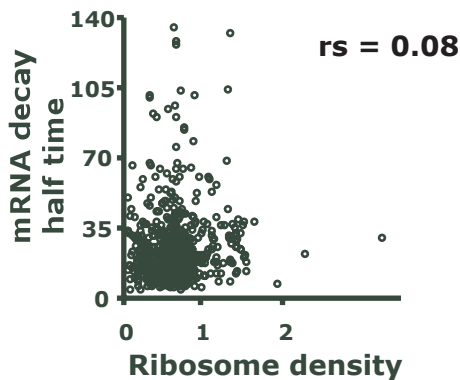
Scatter plot of density values for the genes in the 739 data set and their Codon Bias values (Bennetzen and Hall, JBC 1982, 257 3026-3031). Values were taken from YPD, July 20 2000 update.

B). Scatter plot of Ribosome density versus mRNA abundance.



Scatter plot of ribosome density values for the genes in the 739 data set and mRNA abundance (expressed as copies/cell). Details of the determination of abundance values are at the Protocols link. The left panel includes all genes and the right panel is a zoom-in for the region from 0 to 5.

C). Scatter plot of ribosome density versus mRNA decay half-time.



Scatter plot of ribosome density values for the genes in the 739 data set and their decay half-time (Wang Y. et. al. PNAS 2002, 99 5860-5865).