Data S1: Transcription levels correlate with expression levels in *S. cerevisiae*

We compared the level of reads per billion (RPKM) obtained under our study to that of gene expression corresponding to a previous study (Albert et al. 2014) in which they used ribosomal profiling to determine the number of mRNA molecules that are translated genome wide. In total, we compared the levels of expression for 4682 genes. We found a very strong correlation between both measures of gene expression (Fig S1, Spearman´s correlation: $\rho = 0.77$, $P < 2.2 \times 10^{-16}$).

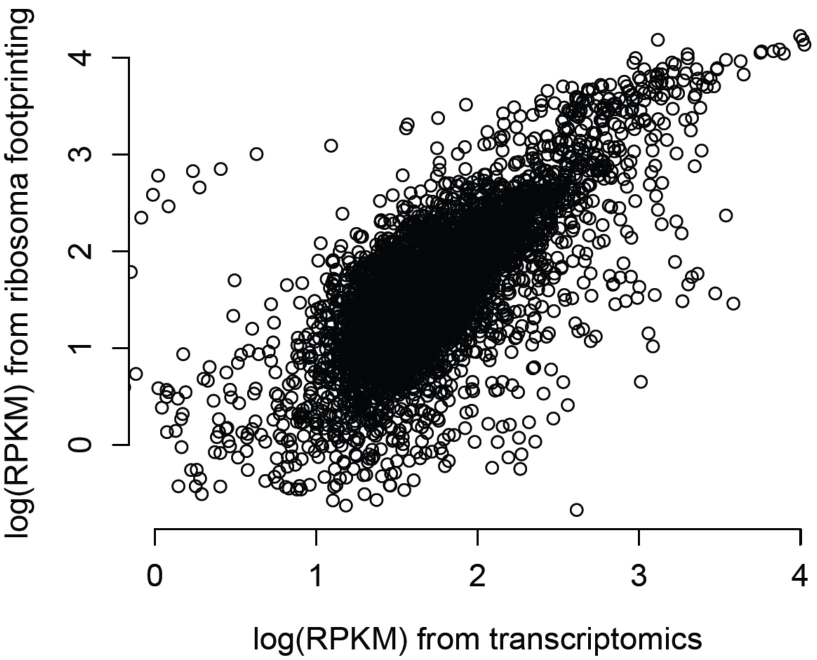

Figure S1. The number of reads per billion (RPKM) obtained from transcriptomic data correlates significantly with that from ribosomal profiling data. The RPKM values are represented in logarithmic scale. We obtained ribosomal profiling RPKMs for 4682 genes from a previous study for yeast growing in rich growth media.

Comparison of these with the transcriptomic data revealed a significant correlation (Spearman´s correlation: $\rho = 0.77$, $P < 2.2 \times 10^{-16}$), such that genes with high RPKMs in the transcriptomic data correspond to those with high RPKMs in the ribosomal profiling data, and vice versa.