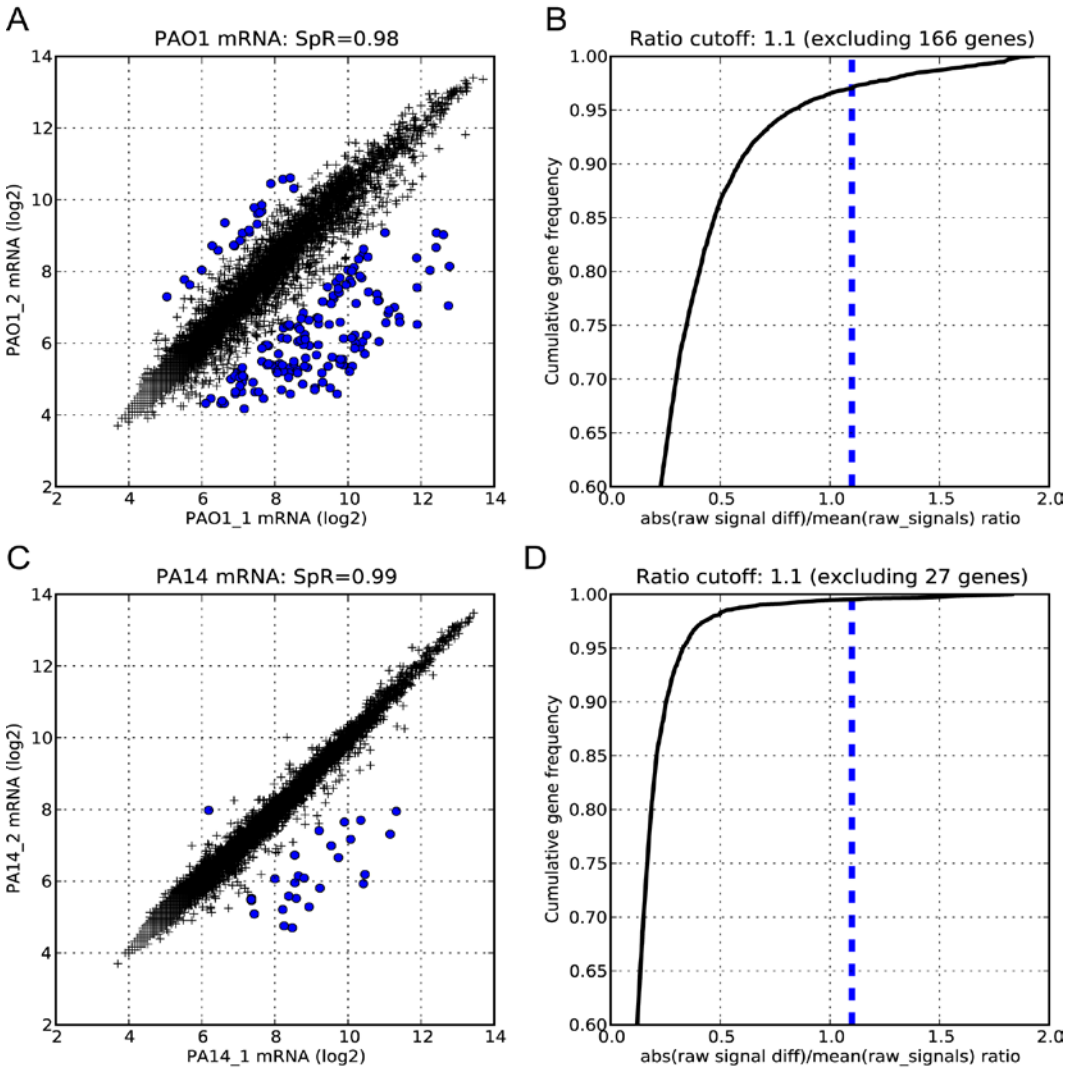
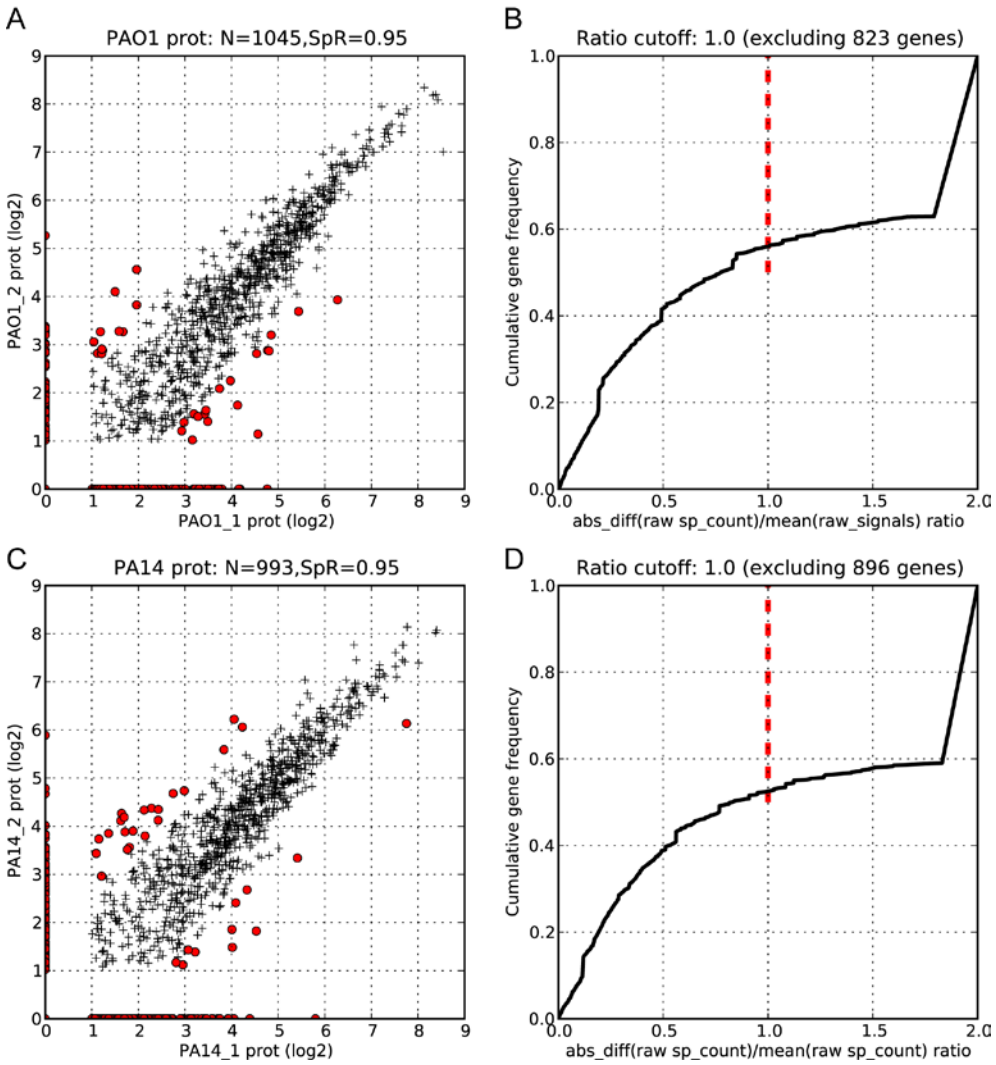
Supplementary Information



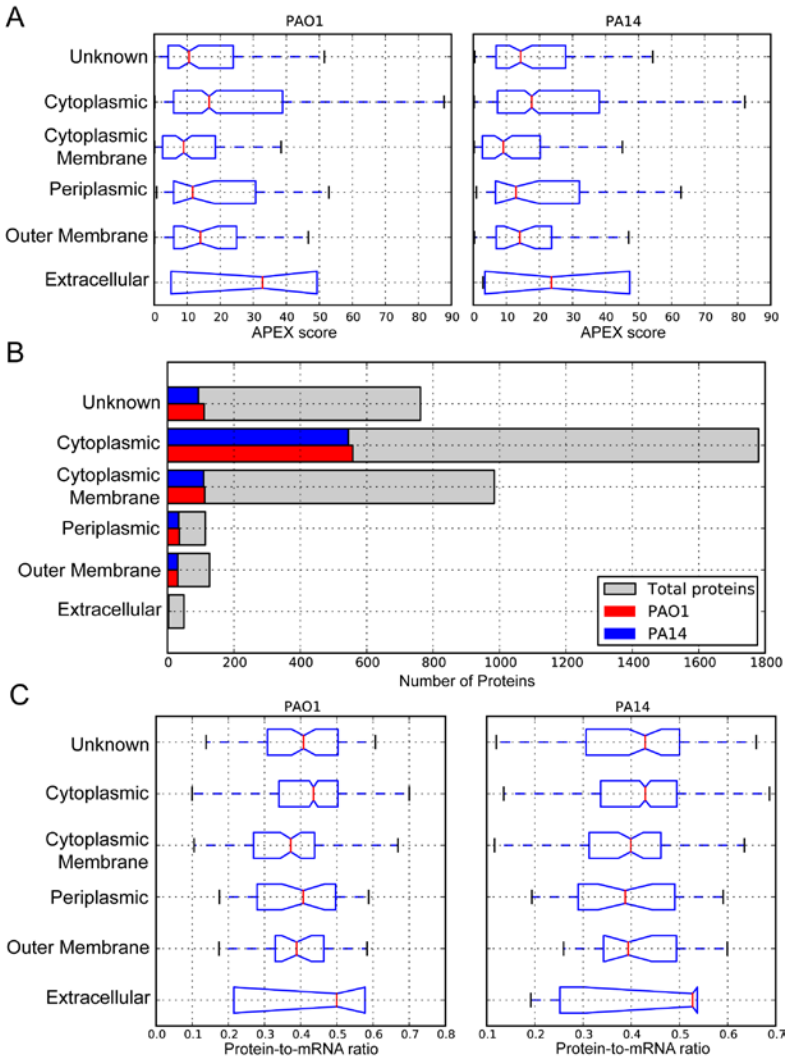
Supplementary Figure 1. mRNA abundances correlate highly between biological replicates. (A) mRNA abundance between two biological replicates of PAO1. Blue circles represent genes showing inconsistent abundances between replicates based on the inconsistency factor, which was calculated as the absolute difference between replicates divided by their mean. (B) Cumulative frequency of PAO1 genes according to the inconsistency factor.

The blue dashed line indicates the cutoff used in this study to remove inconsistent data for further analysis (marked as ‘Outlier’ in supplemental tables). (C) mRNA abundance between two biological replicates of PA14. Data was analyzed as (A). (D) Cumulative fraction of PA14 genes according to the inconsistency factor. Data was analyzed as (B).



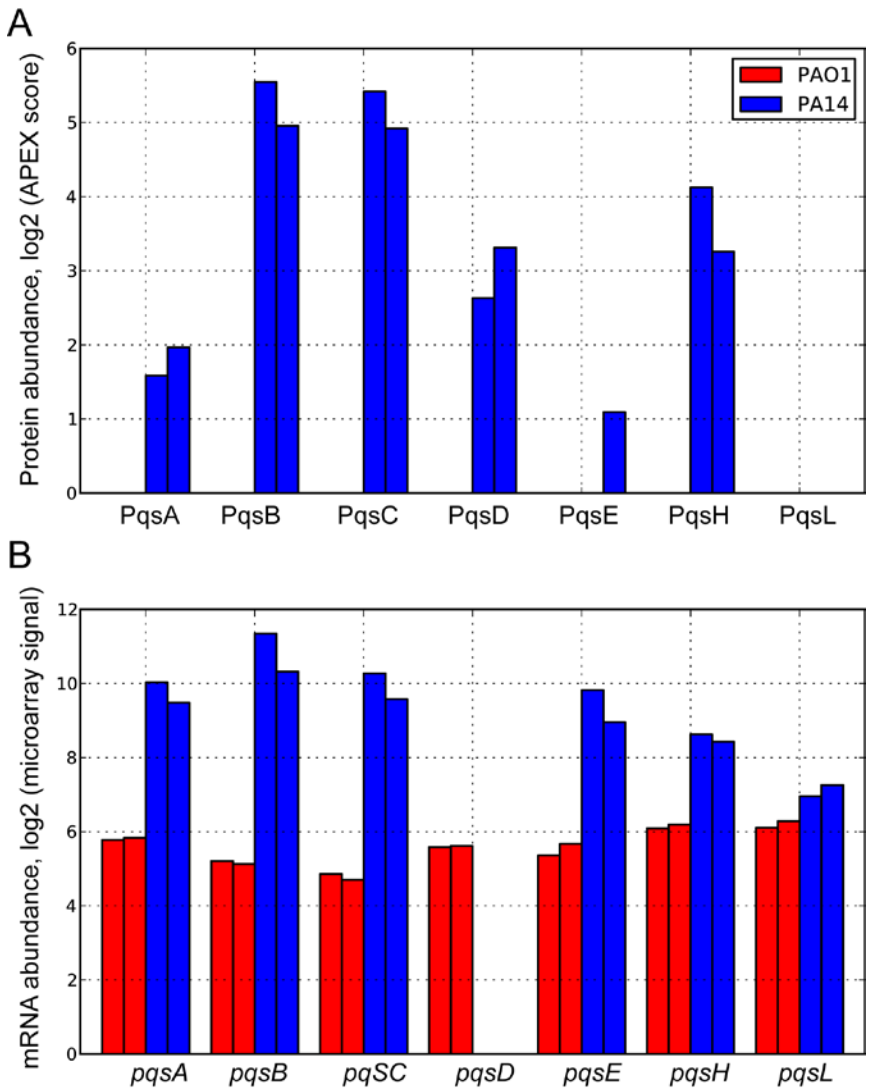
Supplementary Figure 2. Protein abundances correlate highly between biological replicates. (A) Protein abundance between two biological replicates of PAO1. Red circles represent genes showing inconsistent abundances between replicates based on the inconsistency factor, which was calculated as the absolute difference between replicates divided by their mean. (B) Cumulative frequency of PAO1 genes according to the inconsistency factor. The red dashed line indicates the cutoff used in this study toremove inconsistent data for further

analysis. (C) Protein abundance between two biological replicates of PA14. Data was analyzed as (A). (D) Cumulative fraction of PA14 genes according to the inconsistency factor. Data was analyzed as (B).

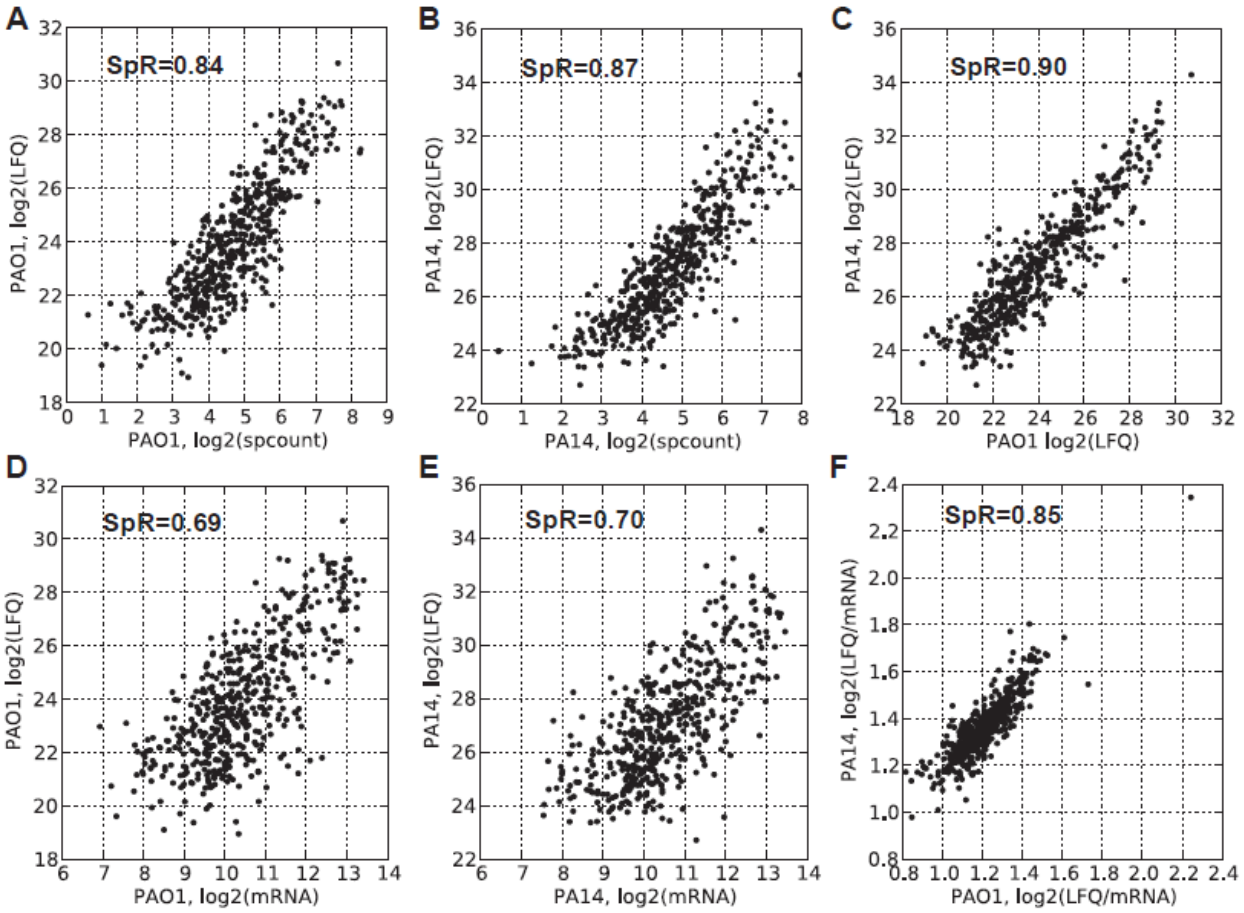


Supplementary Figure S3. Abundance distributions of proteins localized in different cellular compartments. (A) Distributions of protein abundances (APEX scores) for proteins localized in different cellular compartments. The red line indicates the median abundance of proteins in each compartment; whiskers mark 1.5 times the inter-quartile range (IQR). Outliers outside 1.5 IQR are not shown. (B) Numbers of observed proteins localized in each cellular

compartment. The grey bars represent the total numbers of proteins localized in each cellular compartment in PAO1. (C) Distributions of protein-per-mRNA ratios for proteins localized in different cellular compartments. The red lines indicate median protein-per-mRNA ratios of proteins in each compartment; whiskers mark 1.5 times inter-quartile range (IQR). Outliers outside 1.5 IQR are not shown.



Supplementary Figure S4. Expression of *pqs* (4-quinolone) genes. (A) Protein abundance. (B) mRNA abundance. Each pair of bars shows data from the two biological replicates for a given strain. It should be noted that the mRNA abundance of *pqsD* in PA14 (PA14_51390) is not reported, because there are no microarray probes mapped against this gene that meet our inclusion criteria. However, *pqsD* is likely to be more highly expressed in PA14 compared to PAO1 based upon its protein abundance.



Supplementary Figure S5. Alternate protein quantification methods show similar trends. (A-B) compare the spectral counting based protein quantification method (APEX; x-axis) to an MS1-intensity based quantification method (LFQ from MaxQuant version 1.4.1.2, with FDR < 0.01 for both peptides and proteins; y-axes). SpR denotes Spearman correlation coefficient. For this analysis, we considered the 485 proteins detected by MaxQuant with FDR < 0.01 that were also present in the set of 702 proteins used for the preceding correlation analyses. All measured LFQ values are available in Supplement Table 8. (C) Correlation between protein abundances from PAO1 and PA14 (similar to Fig 1A) using LFQ (D) Correlation between protein and mRNA

abundances in PAO1 using LFQ instead of APEX (E) Correlation between protein and mRNA abundances in PA14 using LFQ instead of APEX. (F) Correlation of protein-to-mRNA ratios between PAO1 and PA14, using LFQ instead of APEX. As for the spectral counting approach, protein-per-mRNA ratios are more correlated between strains than proteins are correlated with mRNAs within each strain.

Supplementary Table S1. Genes with significant differential mRNA expression. We analyzed 5,890 gene pairs for which we observed mRNA abundances using Affymetrix microarray experiments.

Supplementary Table S2. Genes with significant differential protein expression. We measured protein abundances of 1,730 gene pairs in the shotgun proteomics experiment for at least one strain.

Supplementary Table S3. Top50/Bottom50 genes when sorted by protein-per-mRNA ratio.

Supplementary Table S4. Candidate genes for translational repression or targeted degradation.

Supplementary Table S5. Explanation of differential protein expression by translation efficiency.

Supplementary Table S6. Differential protein expression that cannot be explained by mRNA difference and translation efficiency.

Supplementary Table S7. Raw data for mRNA and protein expression measurements prior to filtering.

Supplementary Table S8. Protein abundance based on MS1-intensities.