Supplemental Figure Captions

Supplemental Fig. S1. **Volcano plots displaying the relationship between significance and log2 fold changes.** The log of the posterior probabilities that each protein fold change is actually in the interval [-.1,.1] are plotted against the log2 fold changes. Probabilities and fold changes for LFQ, RoR and QuantFusion are found in plots A, B and C, respectively.

Supplemental Fig. S2. **Power plots for LFQ, RoR, and unified QuantFusion methods.** Each protein in each model has its own prediction error. These errors are based on the model type, the variability of the peptides and the number of peptides found within the protein. The average prediction variance across proteins (σ^2_{type}) was computed for each model type and used as the true process variation to calculate power as follows. Let Φ be the CDF of a $N(0,1)$ random variable, let X be the prediction of our protein fold change and let Δ be the true log 2 fold change of the protein. Then the test statistic formed under the null hypothesis is distributed as $\frac{X-0}{\sqrt{\sigma^2_{type}}} \sim N(\Delta, 1)$.

Power for a given delta is calculated as the probability of this statistic being greater than 2.326 or less than -2.326. These cutoff points were selected because the FDR corrected p value of 0.05, in these experiments, was close to 0.01 that has associated Z score cutoff values of -2.326 and 2.326. Results show that, on average, true log-scale fold changes of 1.88, 1.31 and 1.46 are needed to have a 0.8 probability of detecting the difference with LFQ, RoR and QuantFusion methods, respectively. RoR is the most powerful here because it had the least lowest prediction variability. However, RoR also provided the fewest total protein estimates.