Supplemental Figure S3

The top panels show stacked barplots of numbers of all true positive identifications (Yeast proteins identified differentially expressed), stacked for all libraries considered, and side by side for each comparison: Comparison 1 - 2% to 5%, Comparison 2 - 2% to 10% and Comparison 3 - 5% to 10%. Each panel represents a scenario for differential expression. The left panels shows a standard criterion of differential expression (Protein p-value < 0.05, Fold Change > 1.5); the middle panel includes multiple testing correction (Benjamini and Hochberg fdr method), and considers BH-adjusted p-values < 0.05 and Fold Change > 1.5. The right panel shows true positives for Peptide-level p-values < 0.05, Fold Change > 1.5, no corrections. The bottom plots show quantitative false discovery rates qFDR (TP/(FP+TP)) for each library and comparison, for each of the three scenarios. Multiple testing corrections restrict the false discovery rate, but dramatically reduce the numbers of true positives, particularly for comparisons 1 and 3, where the effect sizes are small (0.4 and 0.5), hence the statistical power is lower and the test p-values are higher. Peptide level analyses provide a middle ground, with false discovery rates less than 0.2.