

Using peptide-level proteomics data for detecting
differentially expressed proteins.

Supplementary

September 17, 2015

Scatterplots of mean intensity values

Individual points represent mean intensity value of protein or peptide calculated across all of the replicates. Single points are transparent and having multiple points in the same spot makes it gradually darker. Points representing spiked-in UPS proteins are coloured blue.

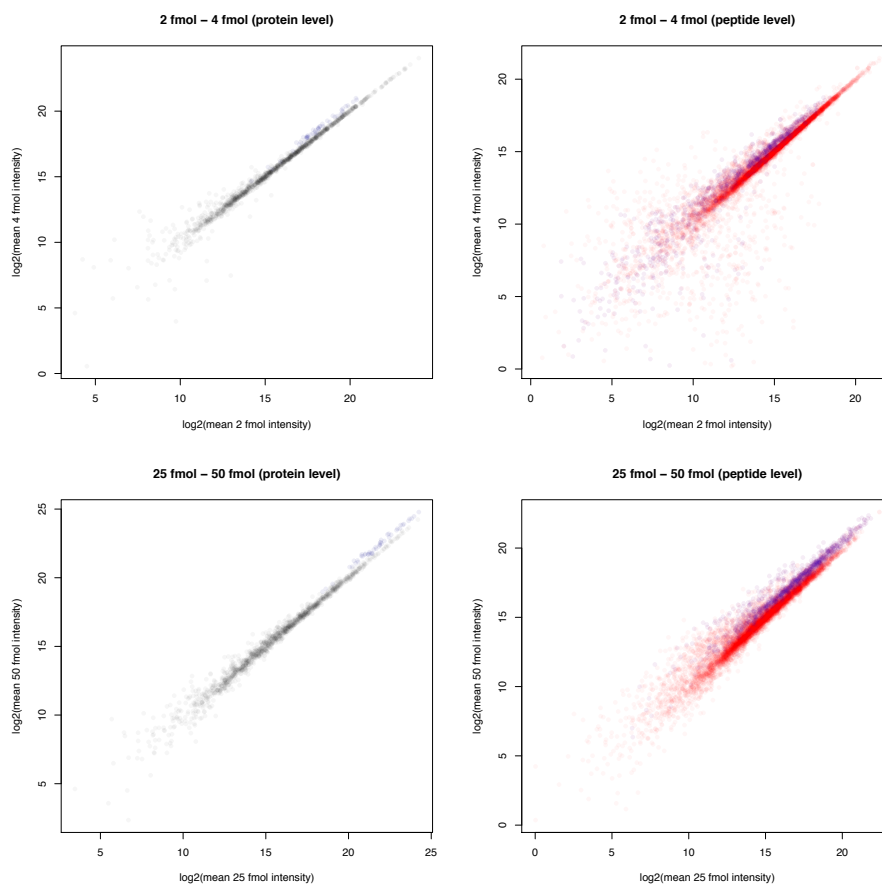


Figure S1: 2-fold scatterplots from UPS spike-in data.

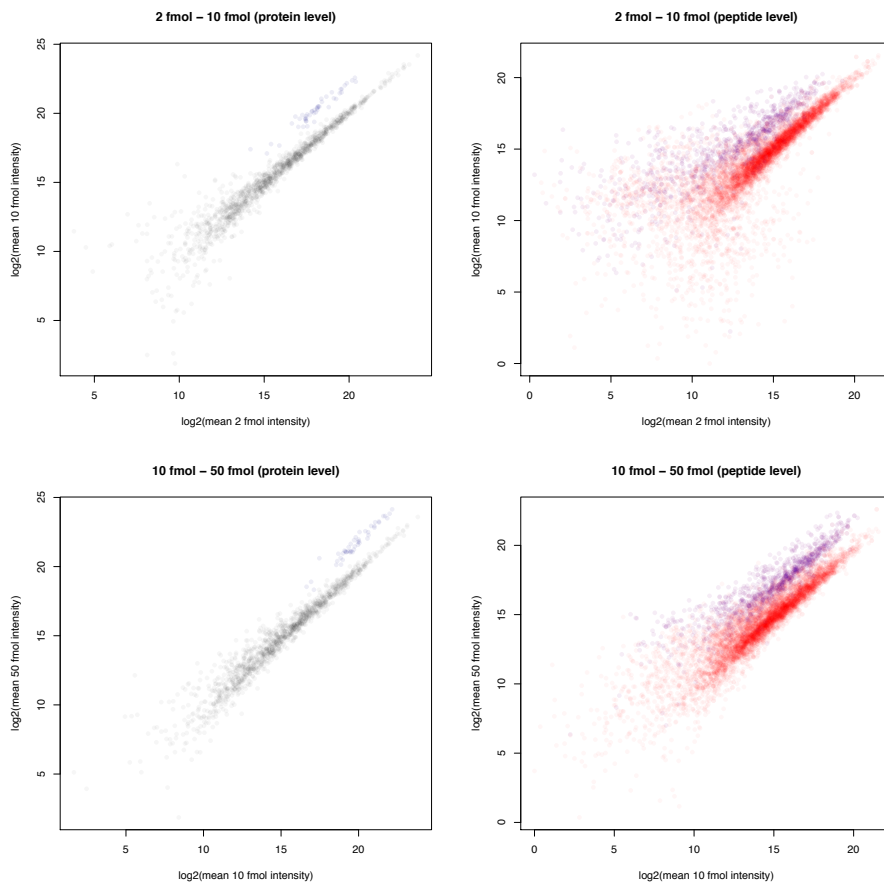


Figure S2: 5-fold scatterplots from UPS spike-in data.

ROC curves of different PECA parameters

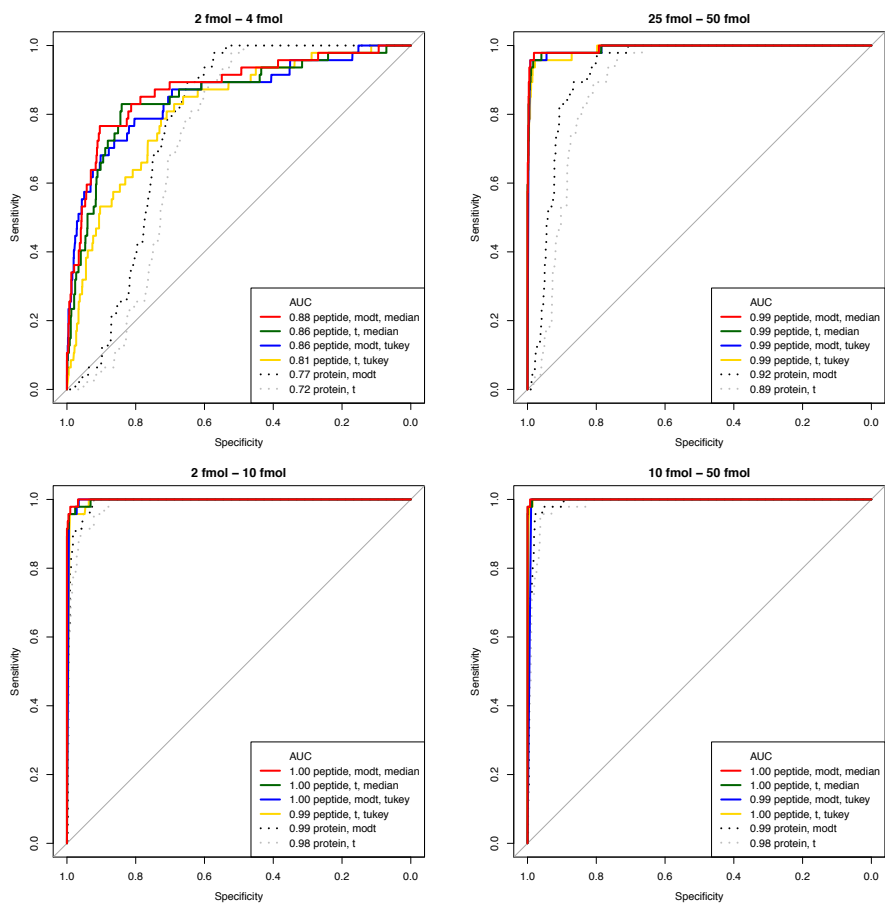


Figure S3: ROC curves using different PECA parameters on UPS spike-in peptide-level data.

Scatterplots of p -values

Single points are transparent and having multiple points in the same spot makes it gradually darker. Points representing spiked-in UPS proteins are coloured blue.

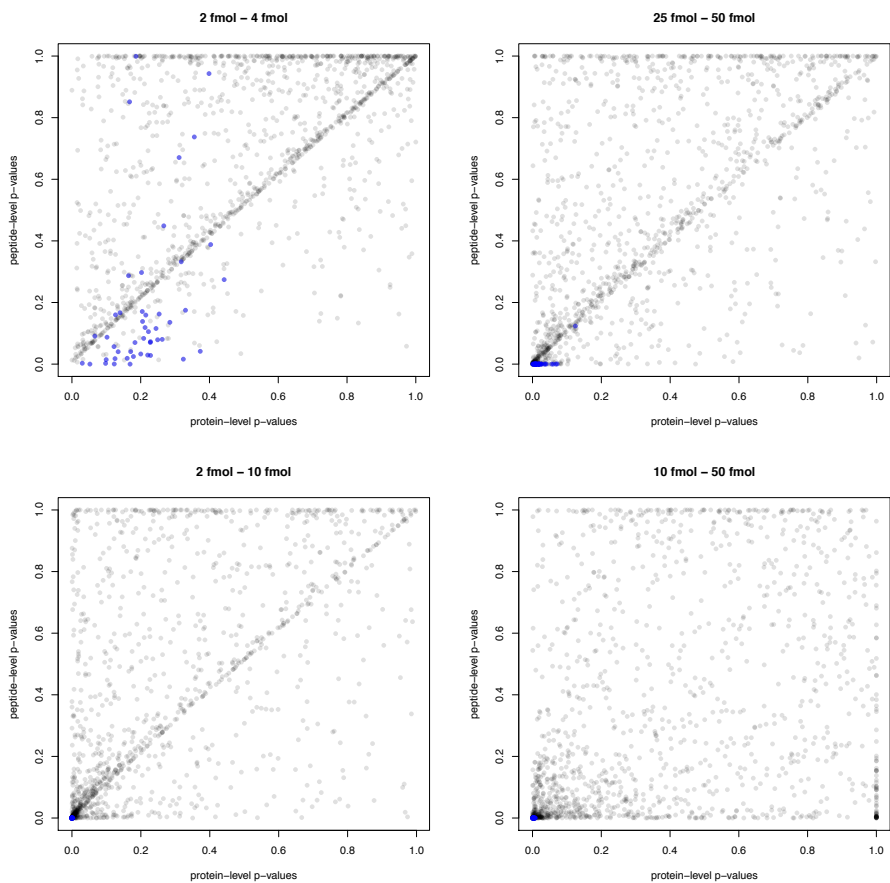


Figure S4: Scatterplots of p -values from UPS spike-in data.

ROC curves of different methods

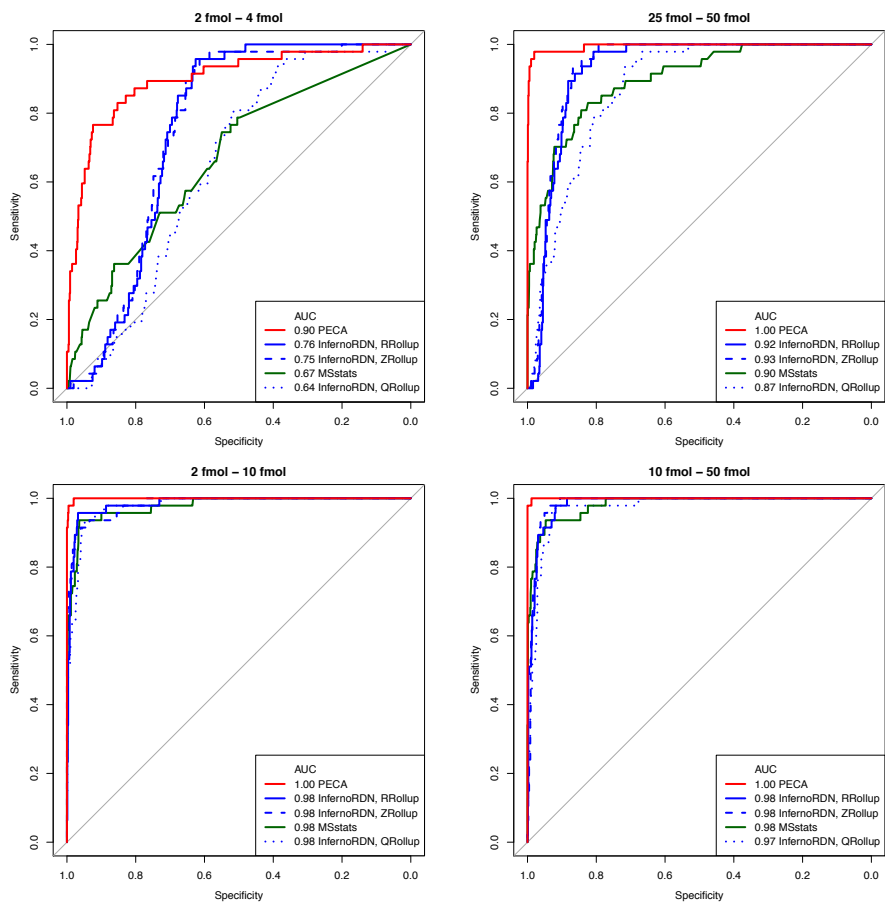


Figure S5: ROC curves comparing different methods on UPS spike-in data.

ROC curves when using different Mascot FDR thresholds

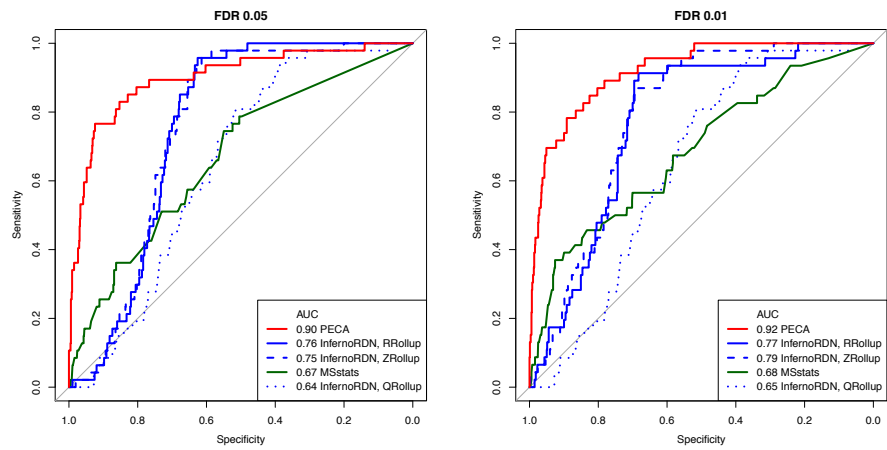


Figure S6: ROC curves comparing different methods on 2 fmol vs. 4 fmol comparison when using Mascot FDR thresholds of 0.05 and 0.01.