

Supporting information.

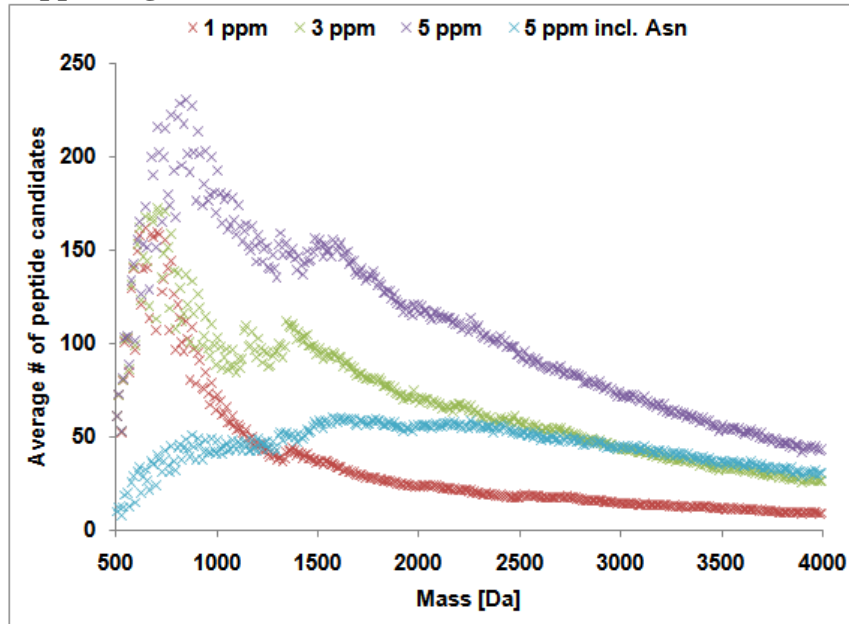


Figure S1. Datapoints originating from masses of all tryptic peptides including those with one missed-cleavage and methionine oxidation from the forward and reversed database (ipi.Human.v3.43). For each peptide, the number of peptide candidates within a specified mass tolerance window was counted. The average number of same mass peptides within bins of 10 Da is plotted. Red crosses: 1 ppm mass tolerance window, green crosses: 3 ppm mass tolerance window, purple crosses: 5 ppm mass tolerance window, blue crosses: 5 ppm mass tolerance window and restriction to include Asn in the peptide sequence.

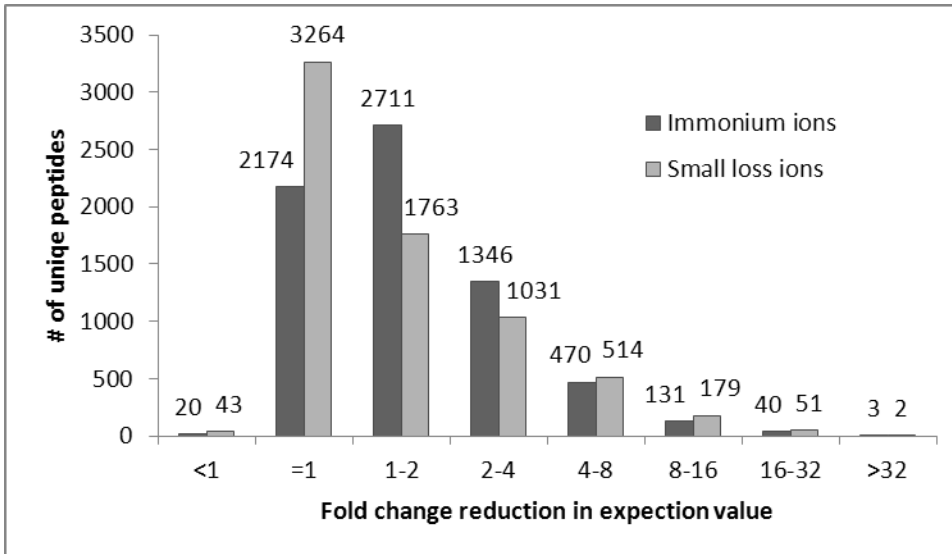


Figure S2. Distribution of peptide fold-changed reduction in expectation value using SNL (light) and immonium ions (dark).