Supplementary Figure 1: Mass accuracy challenge for top-down proteomics. (a) Monoisotopic mass of 20 human proteins were acquired from UniProt Knowledgebase. Each mass was searched against all human proteins in MSDB database with a given peptide mass tolerance (x-axis). The average number of reported proteins (average of 20 protein’s results ± standard deviation) in the results window is shown (y-axis). (b) To test the effect of modification upon search selectivity, UCHL-1 mass was searched adding variable modifications.