

Supporting Information

Targeted Quantification of Peptides using Miniature Mass Spectrometry

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Table of Contents

Figure S1. Miniature MS spectra of selected peptides.

Figure S2. Bruker Q-TOF spectra of selected peptides.

Figure S3. LC-ESI-MS spectra of Met peptide.

Figure S4. Met peptide standard calibration curve.

Figure S5. Trypsin-digested mouse liver peptide spectra.

Figure S6. Effect of background peptides on analyte-to-IS ratio.

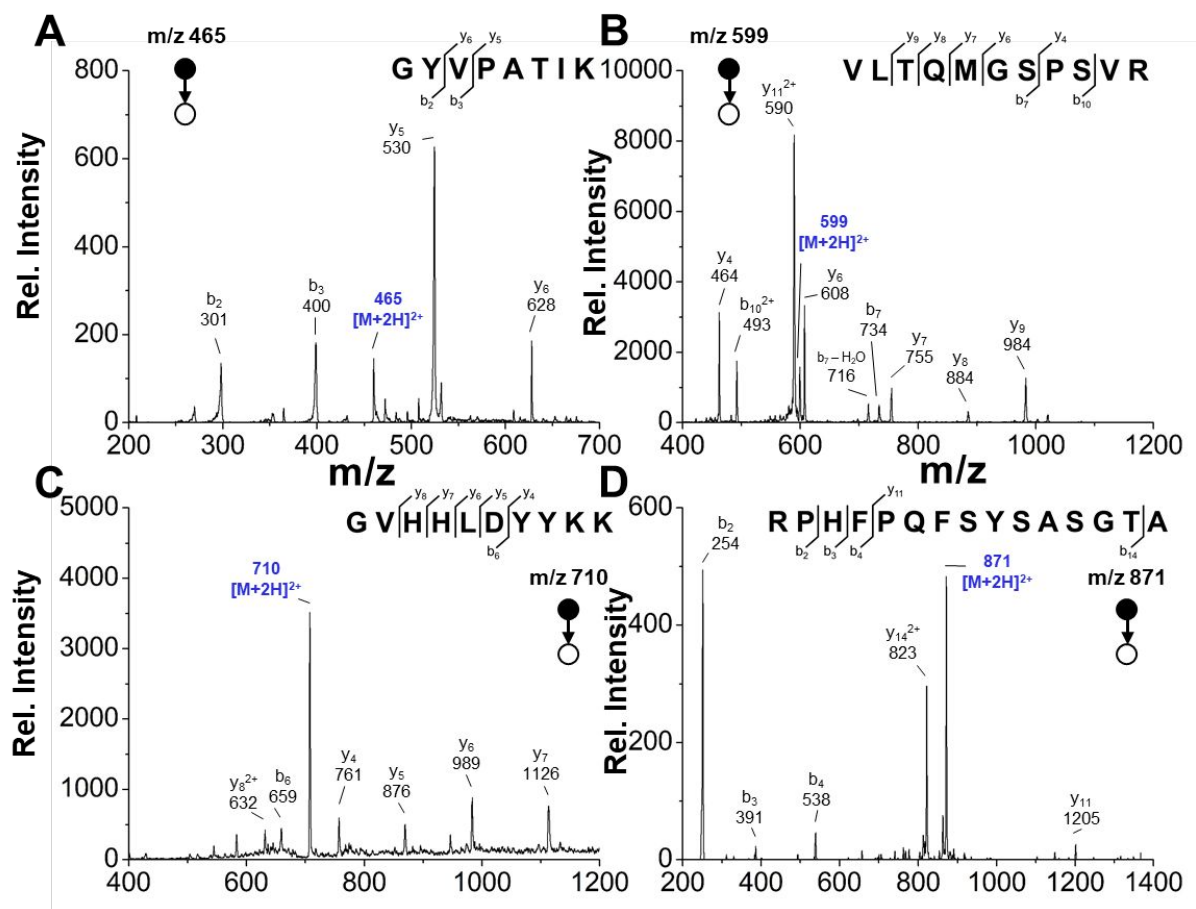


Figure S1. Tandem MS spectra of four different synthetic peptide standards at a concentration of 10 μ M provided by Cell Signaling Technology. All spectra were analyzed in positive ion mode. (A) STAT 6, (B) SMAD 2, (C) FGFR4, and (D) AKT peptide.

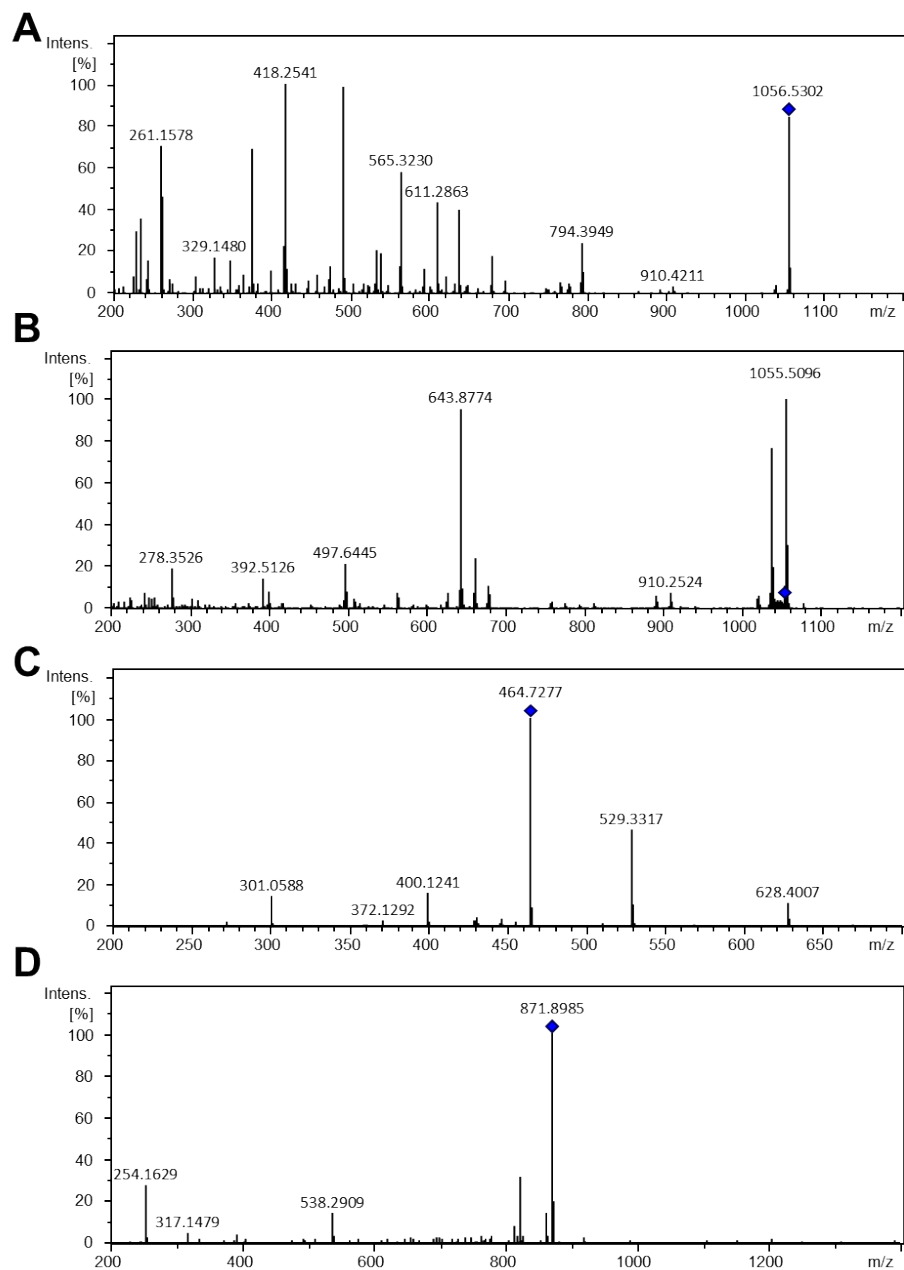


Figure S2. Tandem MS spectra collected from Bruker MaXis Impact Q-TOF of different synthetic peptide standards at a concentration of 10 μ M. (A) *Met* peptide in positive mode, (B) *Met* peptide in negative mode, (C) STAT6 in positive mode, and (D) Akt peptide in positive mode.

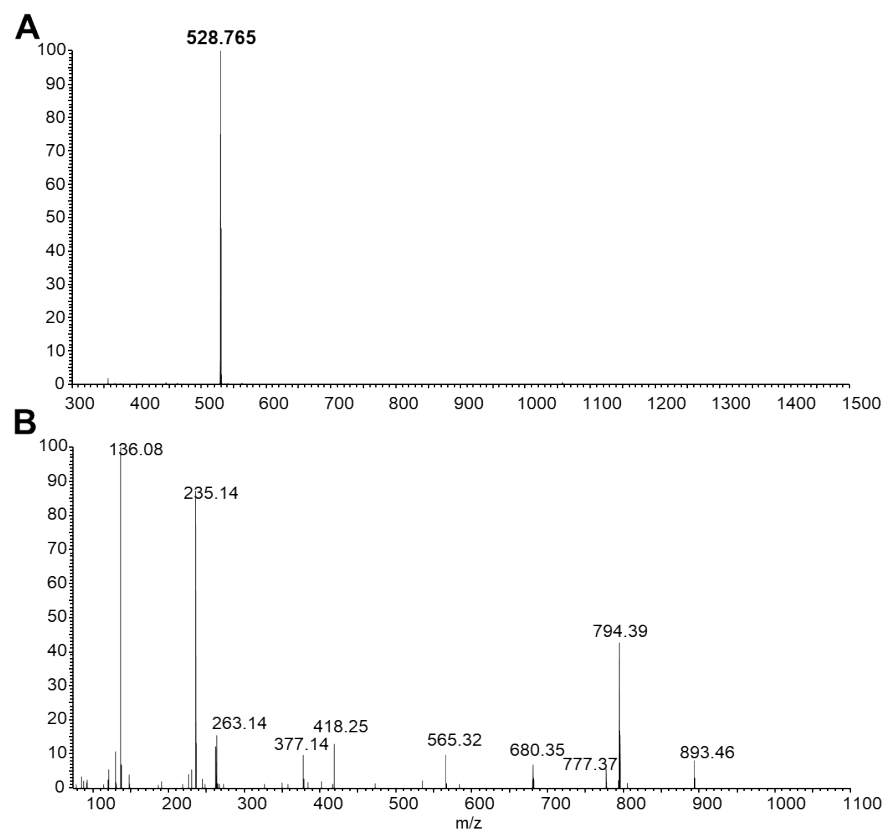


Figure S3. *Met* peptide standard spectra collected by LC-ESI-MS in positive ion mode. (a) Full scan and (b) MS² spectra.

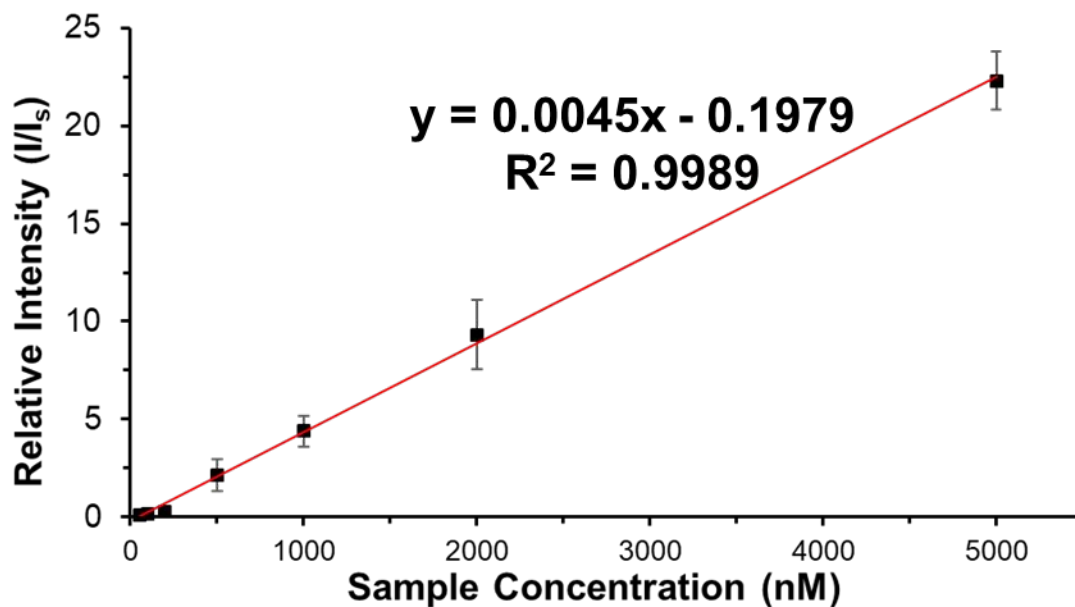


Figure S4. Peptide standard calibration curve drawn using *Met* peptide standard and its internal standard using our miniature mass spectrometer in the negative ion mode. *Met* peptide standards were diluted using 1:1 methanol:water (v/v). Concentration ranges from 50 nM to 5 μ M, spiked with 1 μ M *Met*-IS.

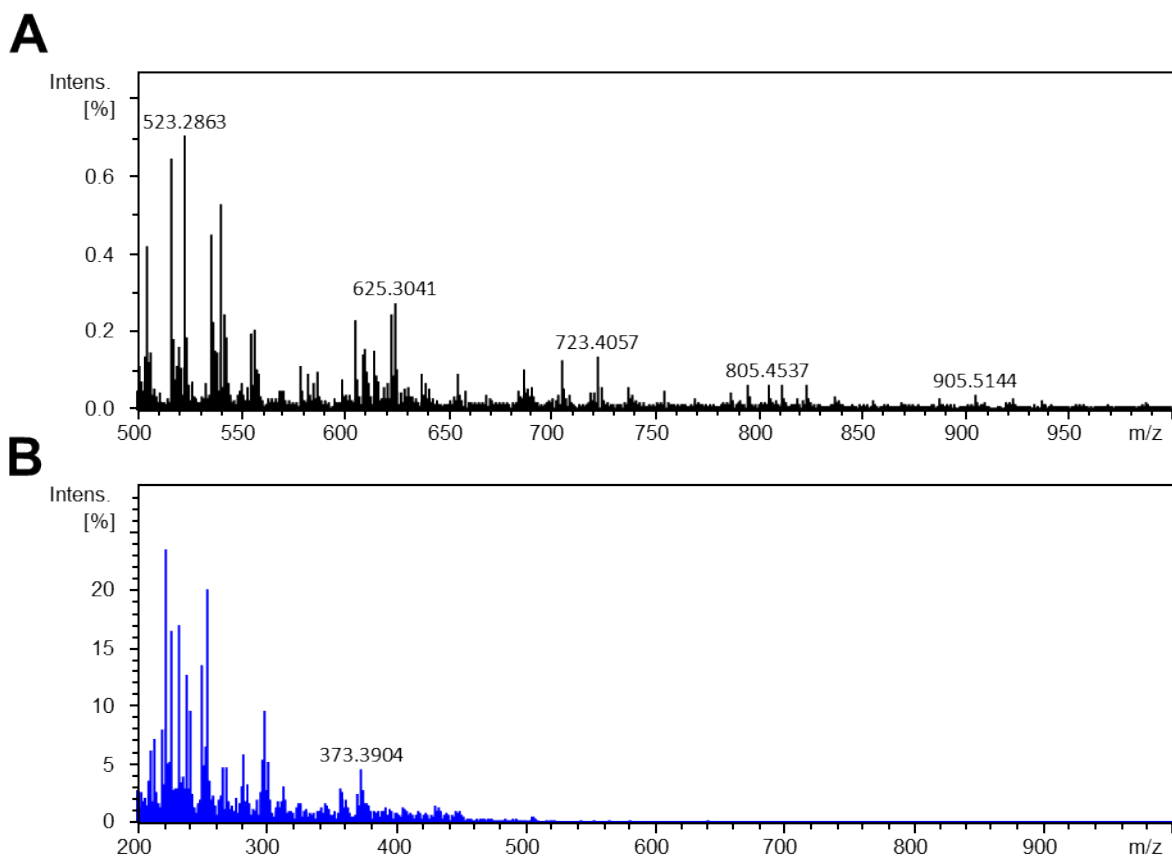


Figure S5. Mass spectra of 100 ppm of trypsin-digested mouse liver peptide samples used as the sample matrix for background peptide studies analyzed in (A) positive and (B) negative mode. Mass spectra were collected by LC-ESI-MS.

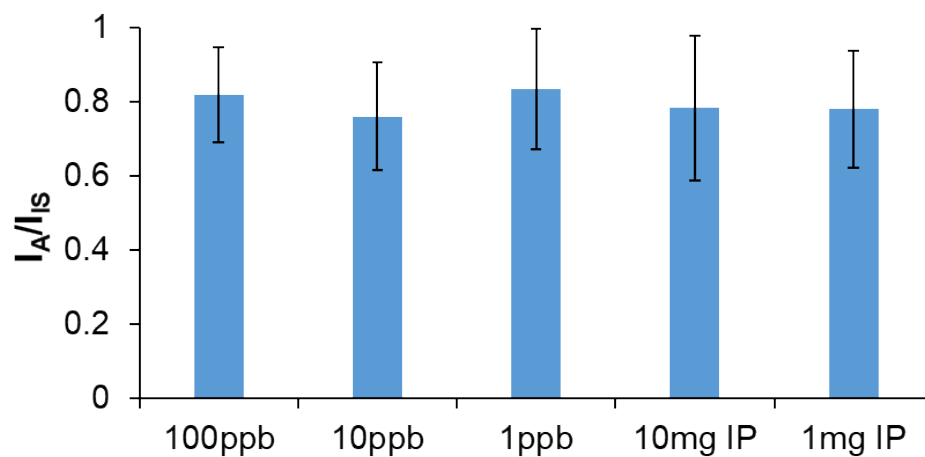


Figure S6. Studies on the effect of background peptides in immuno-enriched samples on analyte-to-IS ratio analyzed in negative ion mode. Trypsin-digested mouse liver peptide samples diluted to concentrations of 1 to 100 ppb were used as a comparison to several non-targeted immuno-enriched samples.