

Supplementary Information for:

Miniprep Assisted Proteomics (MAP) for Rapid Spin-Binding Proteomics Sample Preparation

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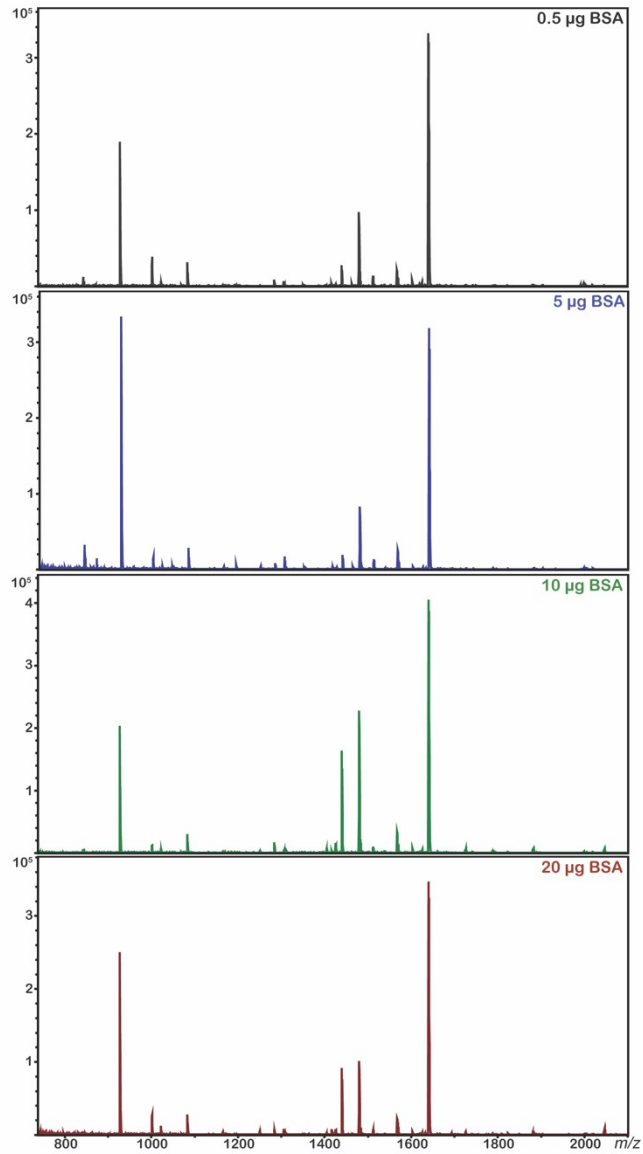
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SI Figure 1



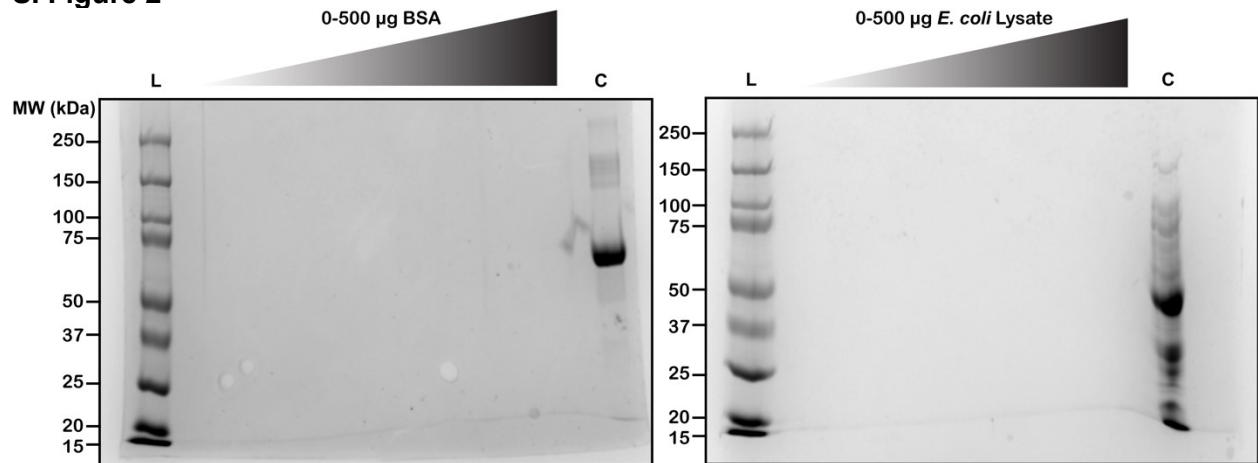
SI Figure 1. MALDI spectra from digests performed using MAP for 0.5-20 µg BSA. The table above includes peptide matches, sequence coverage, and MASCOT scores derived from the MALDI spectra above x axis is m/z ratio, y-axis is intensity [a.u.].

SI Table 1:

<u>Sample (MAP Digest)</u>	<u>Peptides</u>	<u>Sequence Coverage (%)</u>	<u>MASCOT Score</u>
0.5 µg BSA	28	46	132
5 µg BSA	29	45	139
10 µg BSA	30	56	154
20 µg BSA	29	45	180

SI Table 1. Relevant data from a PMF search using Mascot

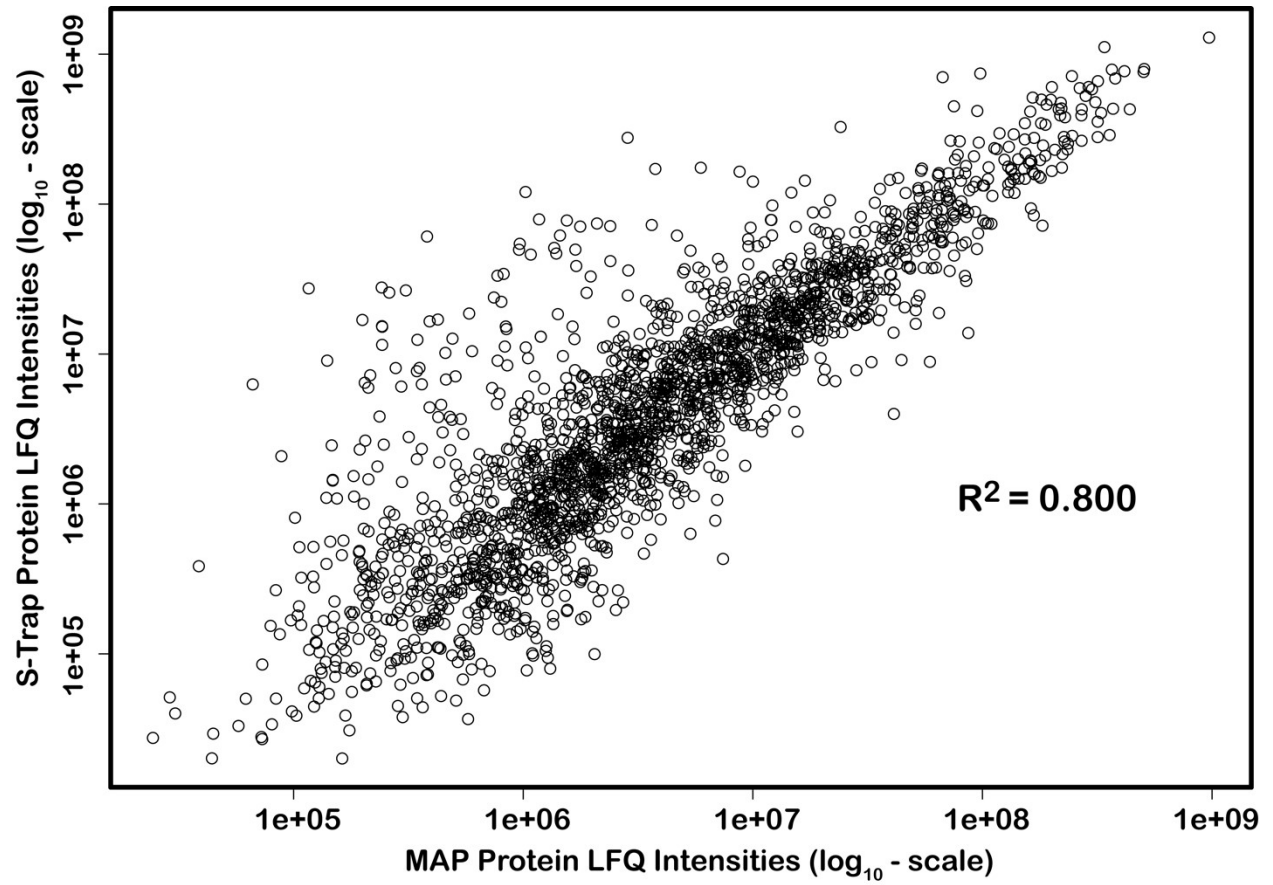
SI Figure 2



SI Figure 2: SDS-PAGE protein capacity experiments with DNA miniprep filters.

Loading increasing amounts of protein on the filters demonstrates if flow-through contains protein due to over-capacity. Shown here, the filters demonstrate a capacity of at least 500 µg of BSA (left) and *E. coli* lysate (right). "L" lane is molecular weight ladder, "C" lane is a control sample of 25µg unfiltered protein.

SI Figure 3:



SI Figure 5: Log-scale LFQ intensities of proteins identified by both preparations. The data are linear ($R^2 = 0.800$) between the two filter-based approaches.