Supporting Information

Robust Analysis of the Yeast Proteome under 50 kDa by Molecular Weight-Based Fractionation and Top-Down Mass Spectrometry

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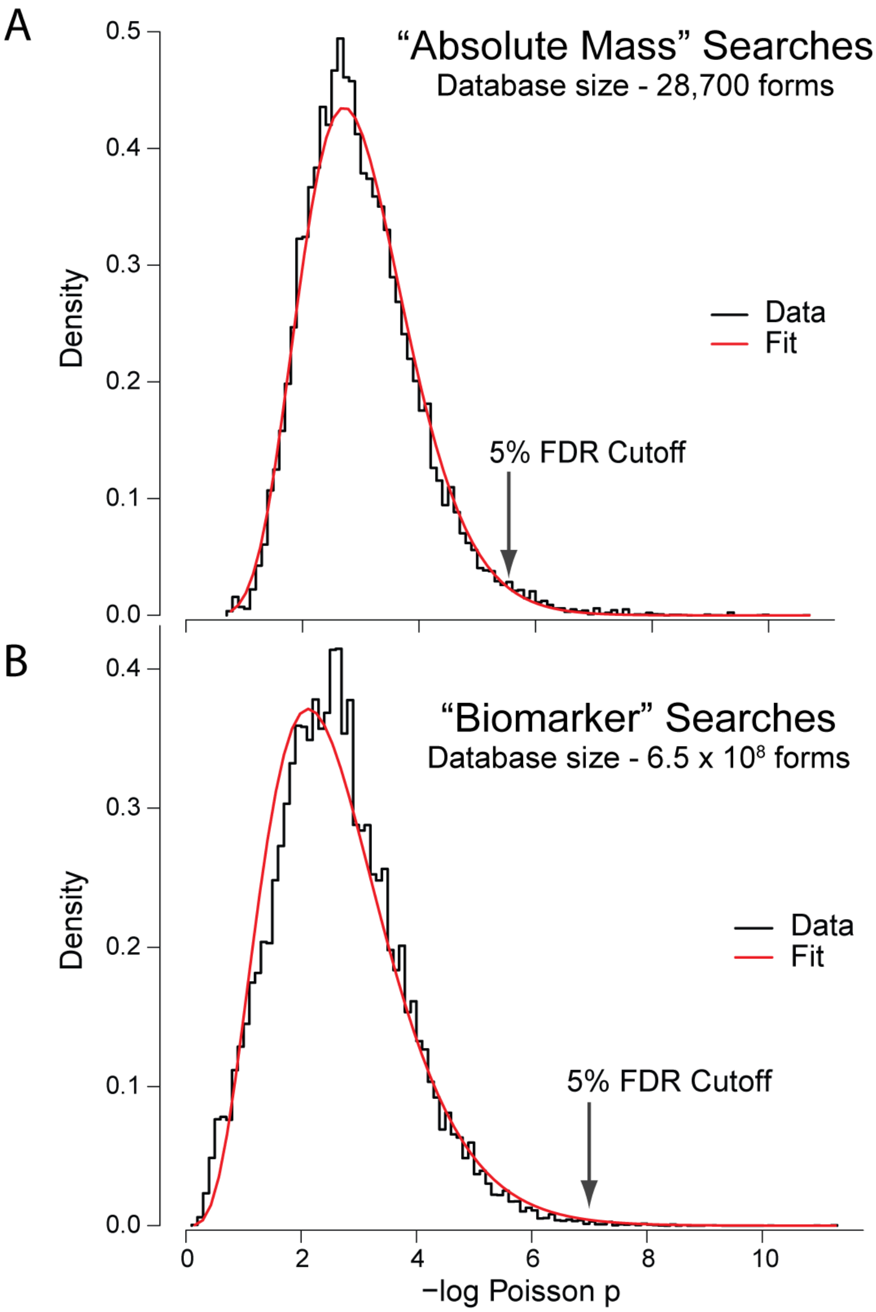

Supplementary Figure 1. Results from decoy searches against a scrambled database. Results are fit to a gamma distribution (an estimate of the distribution of scores under H_0 that the match was due to chance). P-score cutoffs of 2 x 10^{-6} for "absolute mass" mode (**A)** and 9 x 10^{-8} for "biomarker" mode (**B**) each give a cutoff for 5% FDR.