



**Figure S3, Intersection Of Proteins and Peptides Between Experimental Designs of Training Sets and Predictions**

Four large-scale proteomic data sets, representing different common experimental workflows were used in the studies presented here. In total, the data here represents 61% of the proteins in yeast. These datasets are detailed in tables S1-S6. Details of intersections are given in tables S7-S10. As illustrated in the top two panels, there was significant overlap in the proteins identified amongst the experiments, but the overlap in proteotypic peptides was much smaller suggesting experimental variants are important to consider when determining proteotypic peptides. In the bottom panel, we describe the set of high-confidence predicted yeast proteotypic peptides as generated by each of our predictors. Notably, 2,394 proteins have a proteotypic peptide in all experimental designs. By combining all experimental workflows it is possible to cover 95% of all proteins in yeast. The set of peptides (not shown) that are universally proteotypic is quite small; instead the majority of peptides are uniquely proteotypic to a particular experimental design.