Comparing the FDR Curves of Target-Decoy and Decoy Fusion Methods

In addition to the experiment performed for Figure 5, the actual FDR curves of target-decoy and decoy fusion methods were compared with each other. For each searching method (Mascot, SEQUEST, Mascot+Percolator, and PEAKS DB), the CID dataset was searched against the Yeast database using the parameters described in the result section. Target-decoy and decoy fusion were used to estimate the FDR curves, respectively. The FDR curves are plotted in Figure S1. Clearly the two types of FDR curves are identical or almost identical for Mascot, SEQUEST, and Mascot+Percolator, but show a large difference for PEAKS DB.

However, such an experiment does not reveal which of the two FDR estimation methods is better. First, the difference on PEAKS DB’s result does not indicate which curve is more accurate. Secondly, since the database generated by target-decoy has twice as many protein entries than the database by decoy fusion, a search engine that uses protein shortlisting (such as PEAKS DB) may have different performances on the two databases. This may also contribute to or cancel out the difference of the two FDR curves. A better experiment for comparing the FDR estimation methods is the experiment for Figure 5 described in the result section.

Figure S1. The FDR curves of different search methods on the CID dataset, estimated by target-decoy and decoy fusion, respectively.

![FDR Curves](image-url)