Supplemental Figure 1 - Hierarchical clustering of consensus results.

A. All 7840 consensus peptide spectrum matches.

B. 605 consensus PSM's identified by only 3 participants.
The 5 categories for each consensus peptide spectrum match in Supplemental Table 3 were assigned an integer value of 1 thru 5 to partition the categories’ relative significance (bad to good). Clustering was done with GENE-E configured to use a Pearson correlation distance metric and average linkage for both rows and columns. The participants are further annotated according to the number of tryptic termini (NTT) search parameter, the peptide identification program used, and the peaklist used. Coloring corresponds to equivalent features in Figure 1. The clustering row order (A) has been incorporated into Supplemental Table 3 to enable inspection of PSM characteristics based on clustering adjacencies. The identification categories and their integer values are: 5: YS - Yes Id, Same as consensus, 4: NS – No Id, Same as consensus, 3: ND - No Id, Different from consensus, 2: --- No result reported, 1: YD - Yes Id, Different from consensus.