

S4 Cluster GO enrichment analysis

GO term enrichment analysis as described in the main manuscript was used to gain additional insight into the biological relationships between molecule profiles belonging to the same cluster. We calculated p-values using the hypergeometric distribution based on the number of molecules in the domain of interest. S4 File shows the overlap of enriched GO terms identified by clustering the different modelling approaches on the iTraQ breast cancer dataset (mean, SME, LMMS and DLMMS) before and after removing GO terms that contained only one molecule. Table S1 lists the common enriched GO terms in at least two of the mean, SME and LMMS and DLMMS clusters, while Table S2 lists the enriched GO terms uniquely identified by each set of clusters.

