

Figure S1. Scatterplots of the retention time (RT) vs. the deconvoluted experimental mass (m) by proteoform ID. The sequential color scale highlights the proteoform IDs assigned to each PrSM according to a) PS or b) TP.

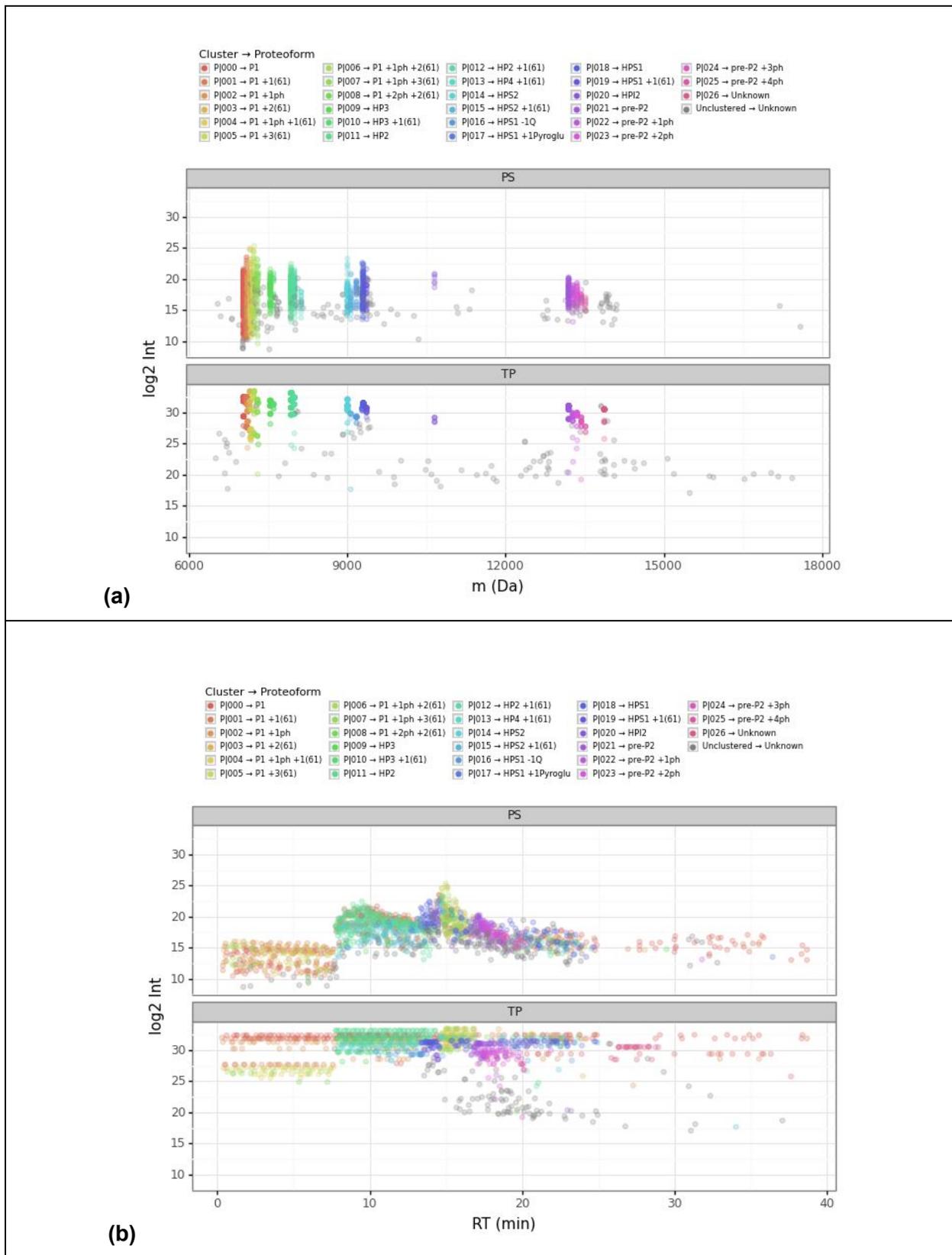


Figure S2. Scatterplots of the intensity ($\log_2 Int$) vs. the deconvoluted experimental mass (m) and the retention time (RT) for PS and TP by cluster. The sequential color scale highlights the clusters obtained sorted by increasing experimental mass, while unclustered PrSMs appear in grey. a) $\log_2 Int$ vs. m projection. b) $\log_2 Int$ vs. RT projection. (ph = phosphorylation, Q = glutamine, pyroGlu = pyroglutamic acid).

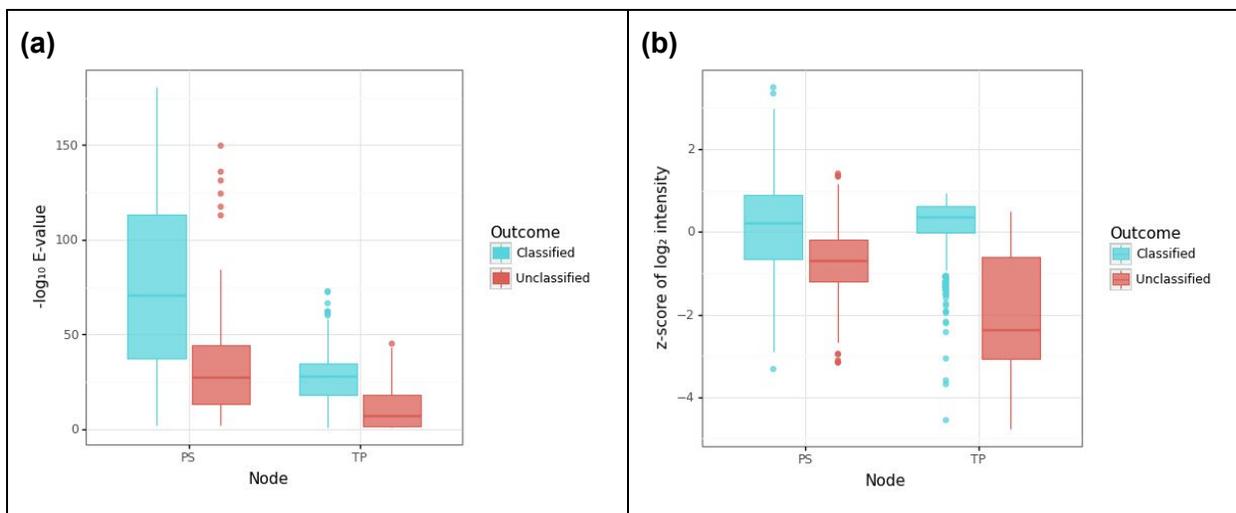


Figure S3. Boxplot of $-\log_{10}$ E-value and z-score of \log_2 intensity vs. Node by outcome (classified and unclassified PrSMs).