Supplemental Figure 5: Correlations between measured RT and the predicted RT calculated by Spectronaut (\( RT = f(iRT) \)) of peptides identified in OD5P samples applying the BigLib library in the DDA-to-DIA approach (A) and with the Prosit-predicted BigLib library in the DDA-to-Prosit-to-DIA approach (B). The difference between the predicted RT = \( f(iRT) \) and the mean measured RT in the DIA data calculated for peptides identified in the DDA-to-DIA (C) and in the DDA-to-Prosit-to-DIA (D). The overlap between peptides identified in the two approaches is represented in a venn diagram (E). The fraction of peptides predicted as HLA binders is provided for unique and common peptide groups. Common 9 mer peptides were clustered to reveal the binding motifs. Frequency plot of the delta apex, which is the difference between the measured peptide apex obtained in the DDA-to-DIA and the DDA-to-Prosit-to-DIA (F). The same analyses as above are provided for JY samples (G-L).