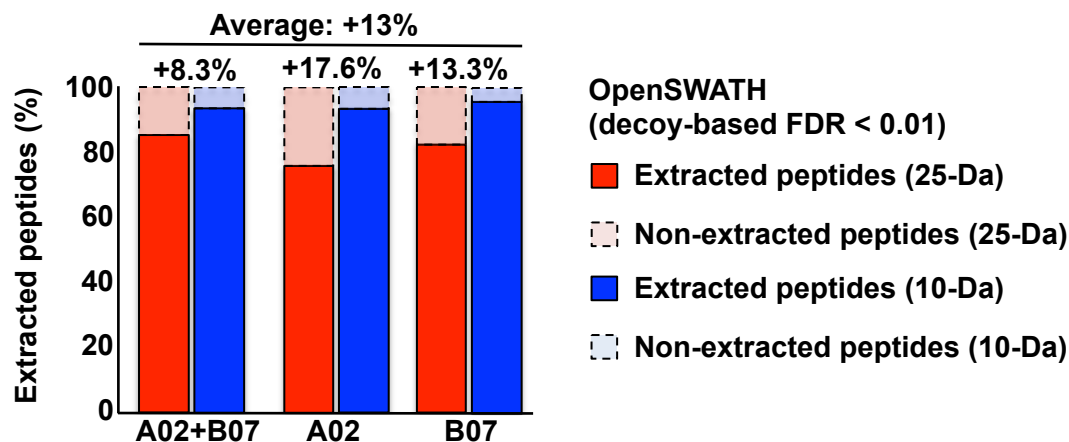
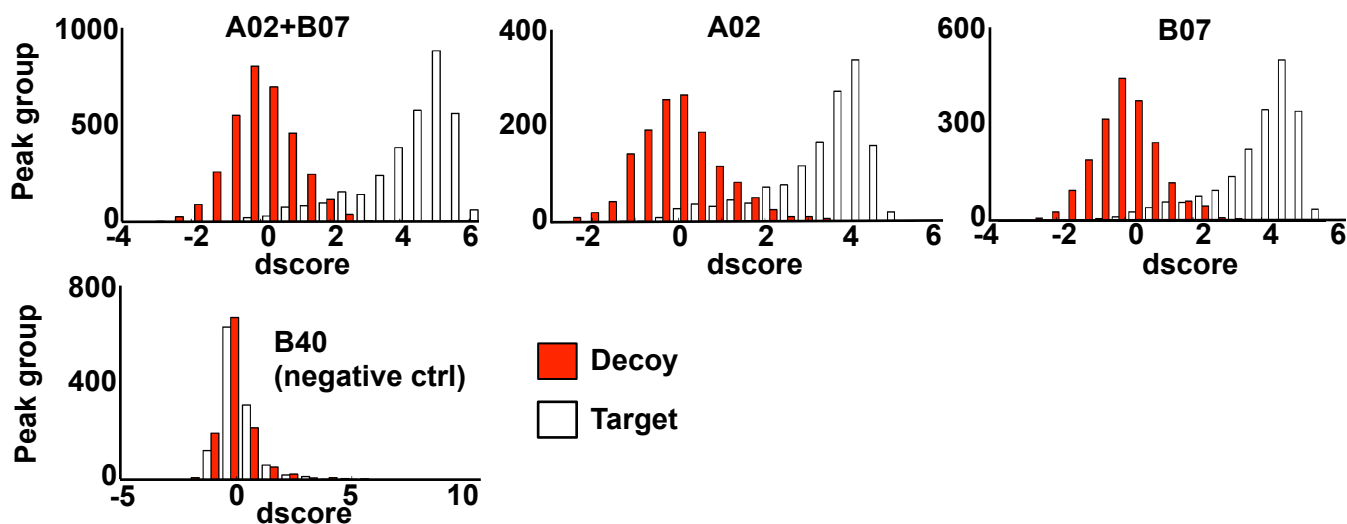


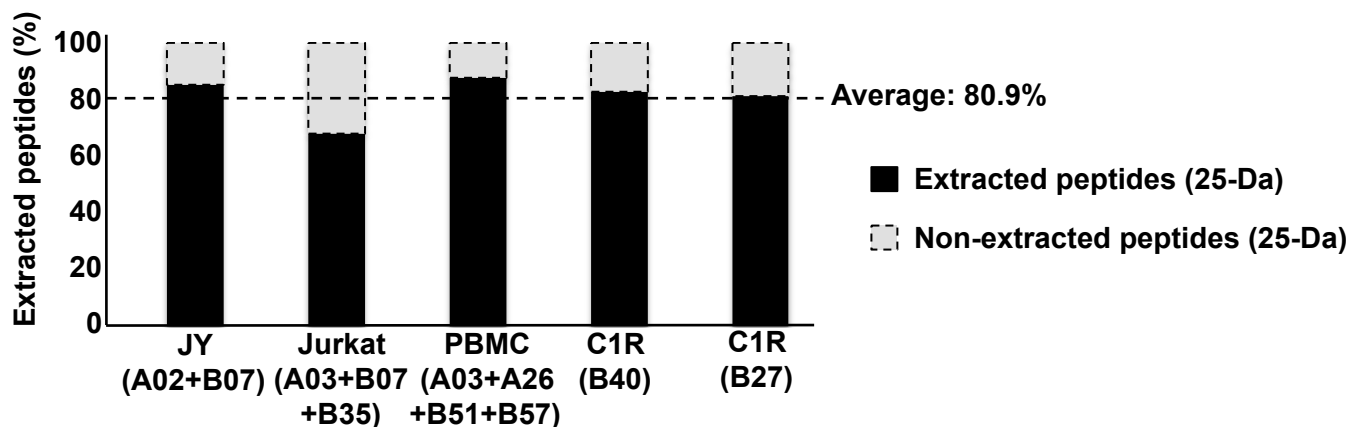
**A**



**B**



**C**



**Figure 3—figure supplement 1. OpenSWATH analysis of HLA peptidomic data.** (A) HLA class I peptides isolated from JY cells were acquired in SWATH/DIA mode using windows of 10 Da (blue) or 25 Da (red) width each. The graph shows the proportion of peptides that were confidently extracted (FDR < 0.01) using OpenSWATH from a merged (A02+B07) or unmerged (A02 or B07) HLA allele-specific assay library. (B) pyProphet statistical analysis from a JY HLA class I peptide extract. The histogram plots show the distribution of decoy and target transition groups according to their discriminant score (dscore) determined by the pyProphet software. (C) HLA class I peptides were isolated from various cell types and analyzed by SWATH-MS using windows of 25 Da width each. The histogram shows the number of HLA peptides that were confidently extracted (FDR < 0.01) using OpenSWATH from different HLA allele-specific assay library.