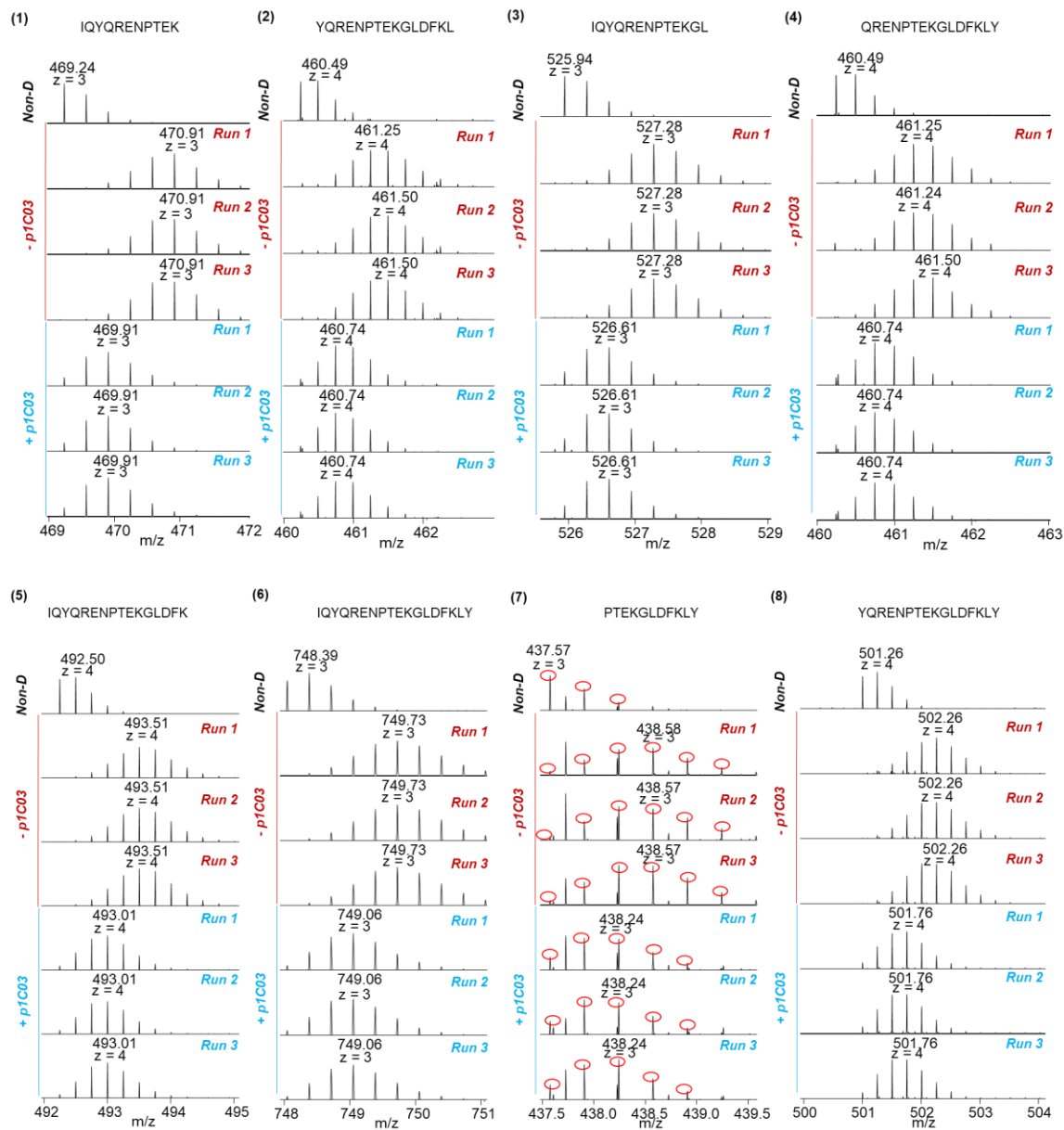


Supplementary Materials: Hydrogen–Deuterium Exchange Mass Spectrometry Reveals a Novel Binding Region of a Neutralizing Fully Human Monoclonal Antibody to Anthrax Protective Antigen

Mulin Fang, Zhe Wang, Kathleen Norris, Judith A. James, Si Wu and Kenneth Smith*

(A)



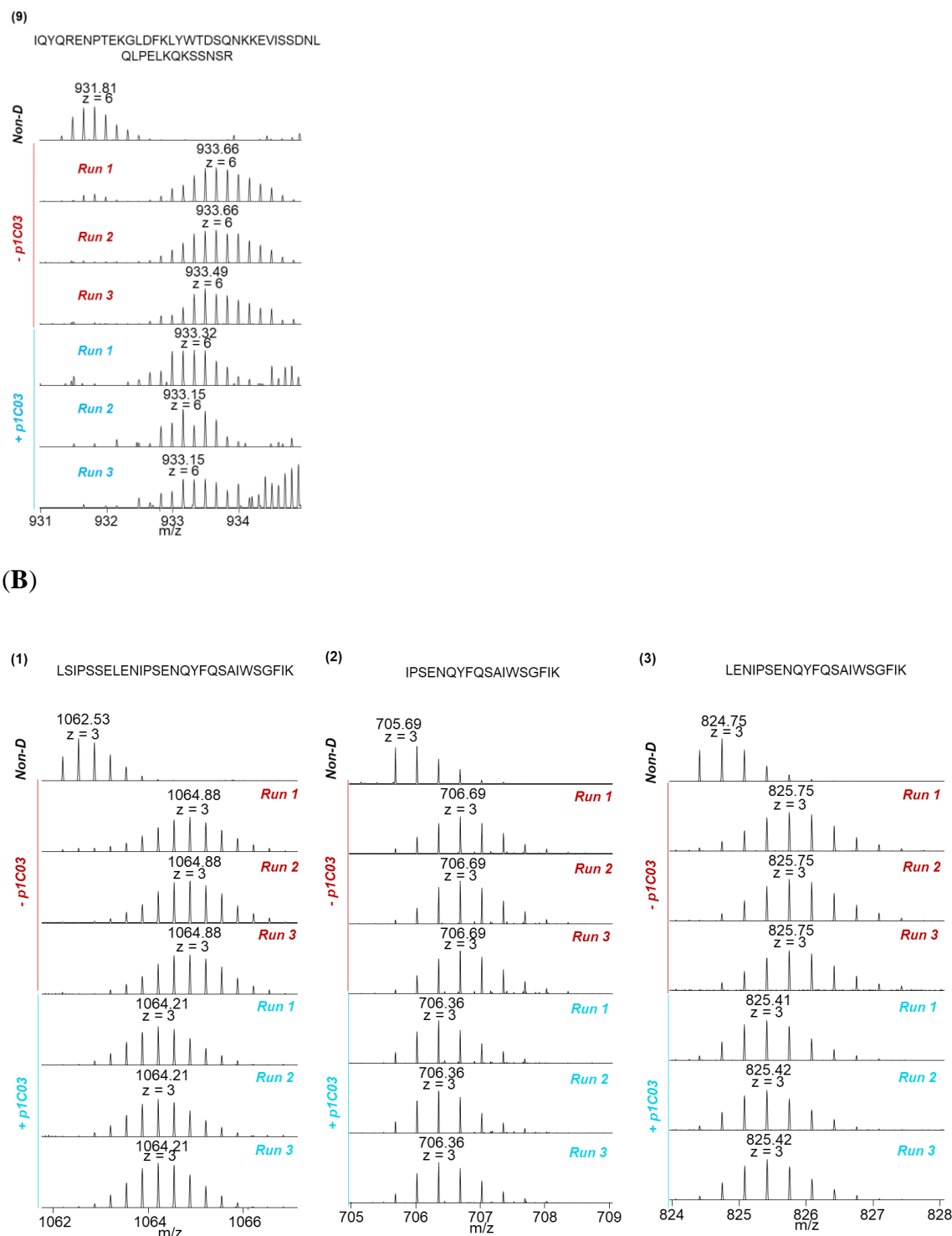
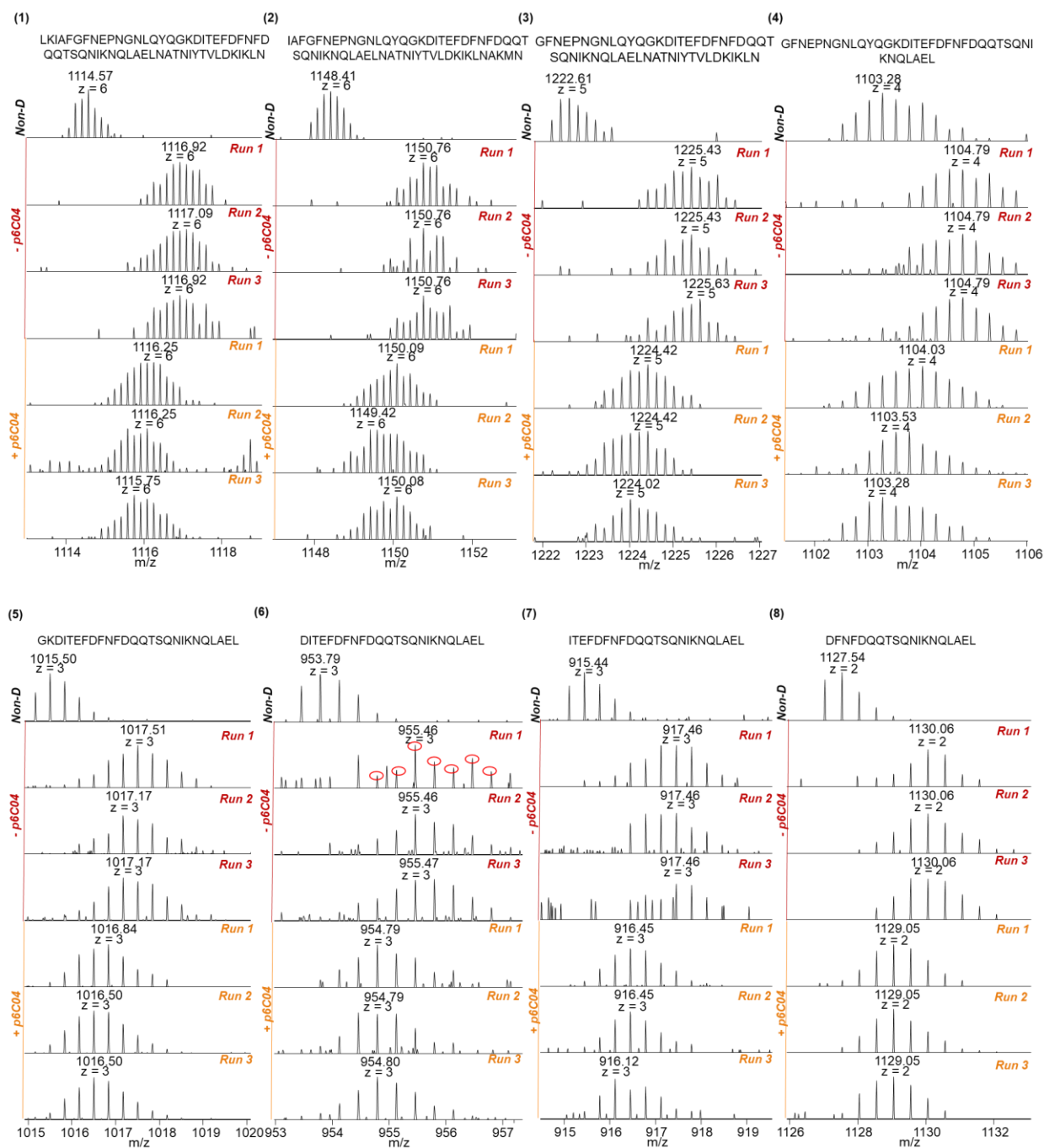


Figure S1. MS spectra of 12 identified peptides for p1C03 binding. (A) MS spectra of 9 identified peptides in primary epitope. (B) MS spectra of 3 identified peptides in secondary epitope. Red ovals highlight the correct peak distribution for peptide 7.



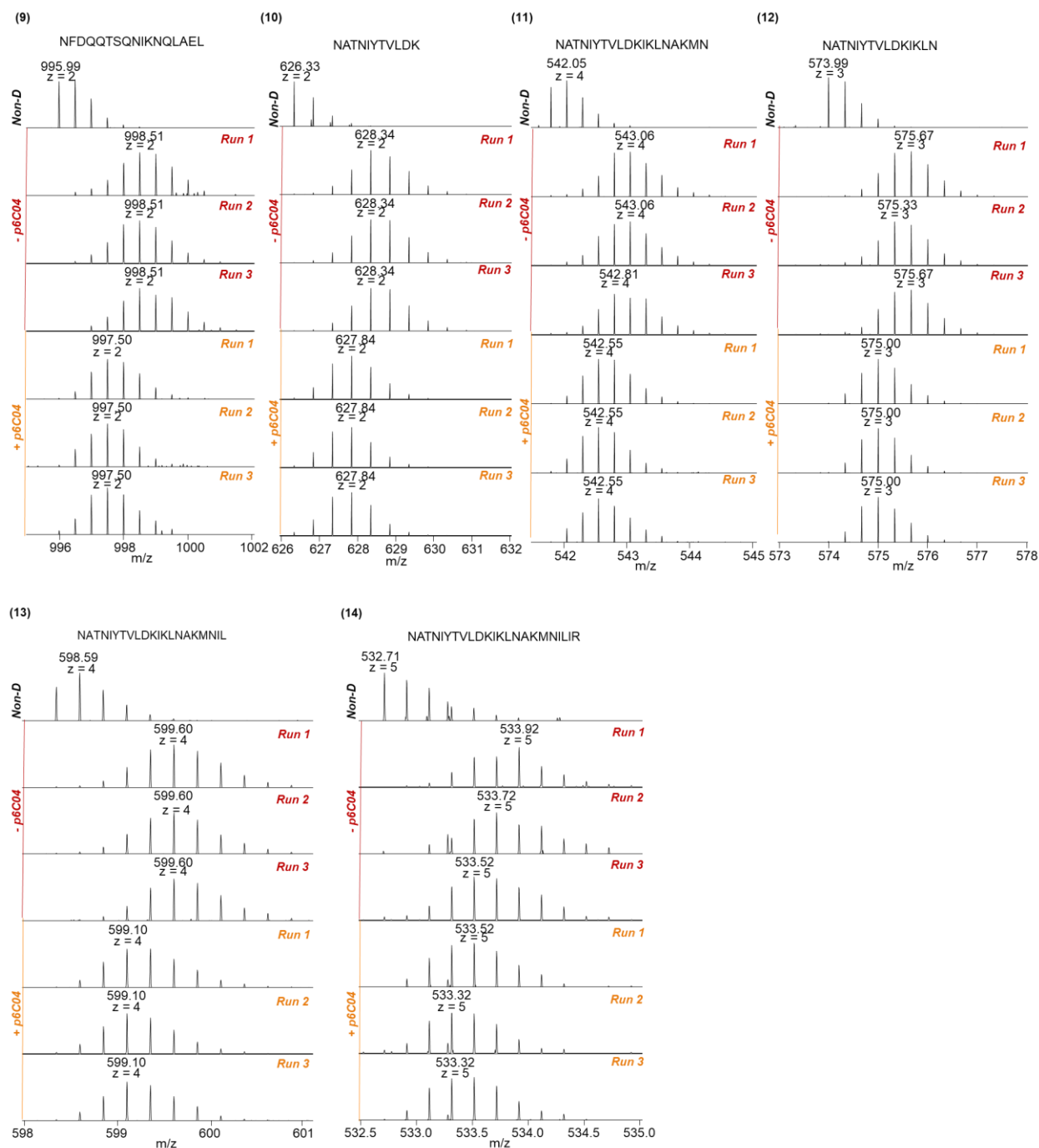
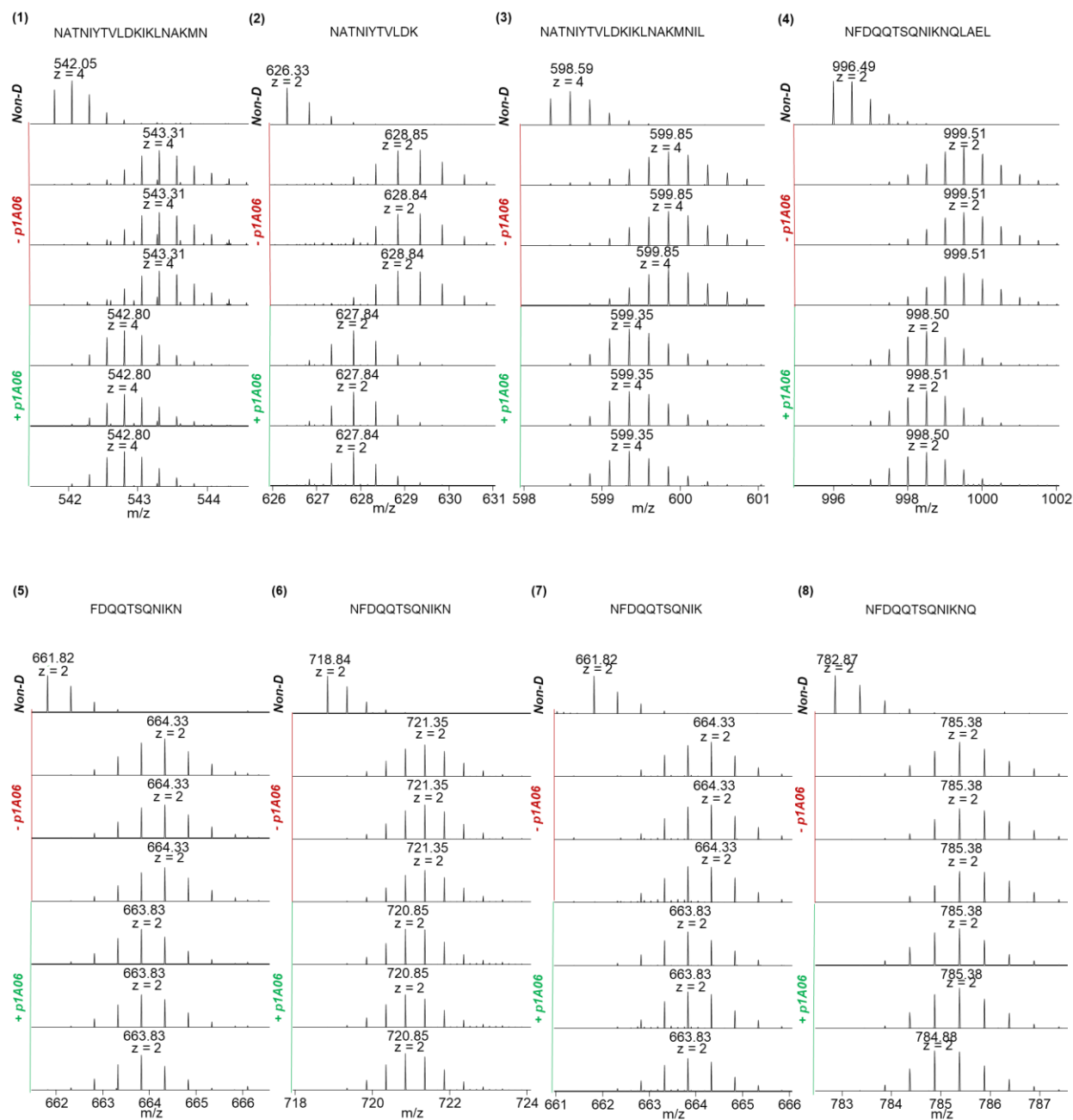


Figure S2. MS spectra of 14 identified peptides in primary epitope for p6C04 binding.



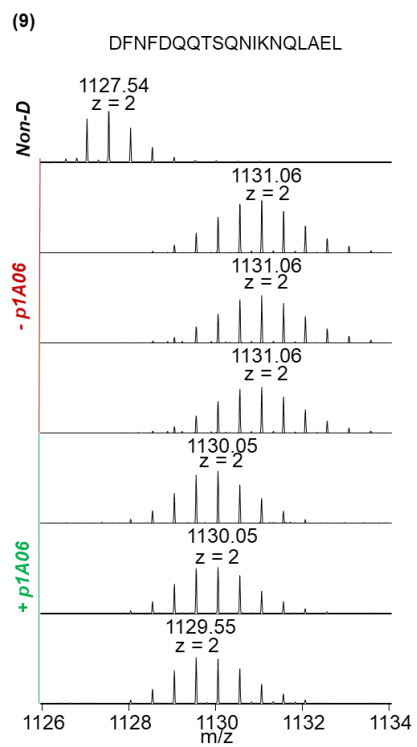
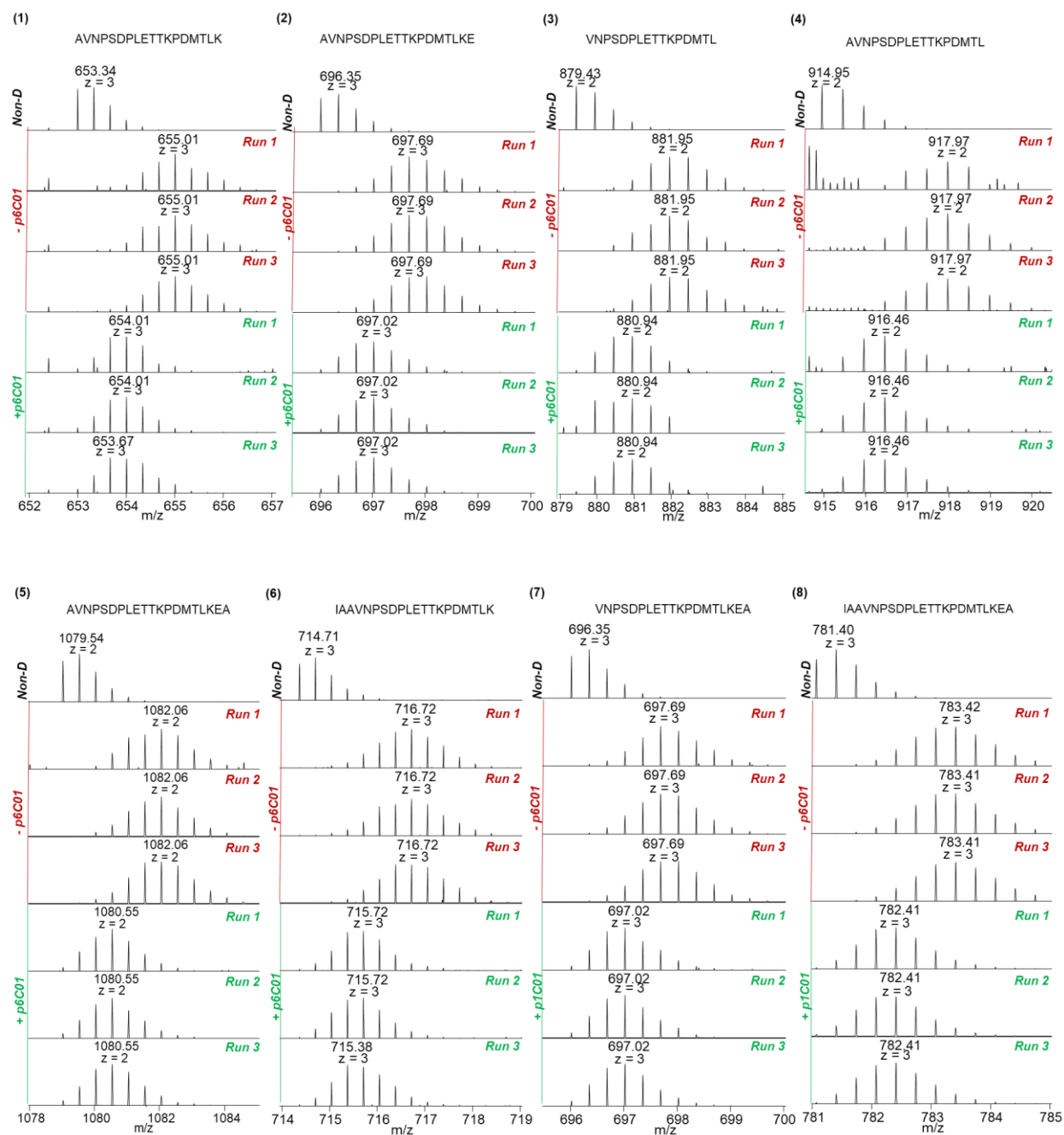
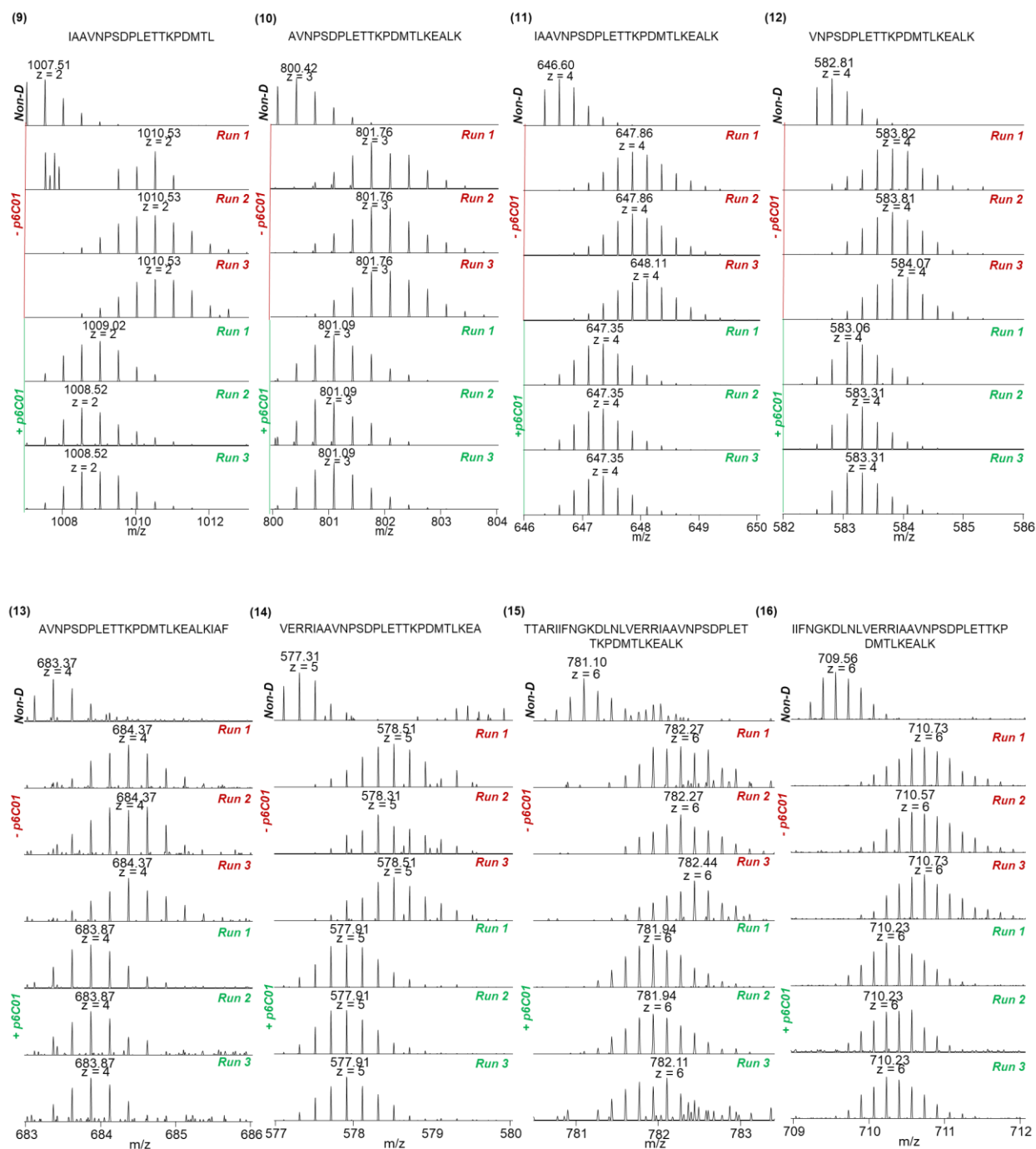
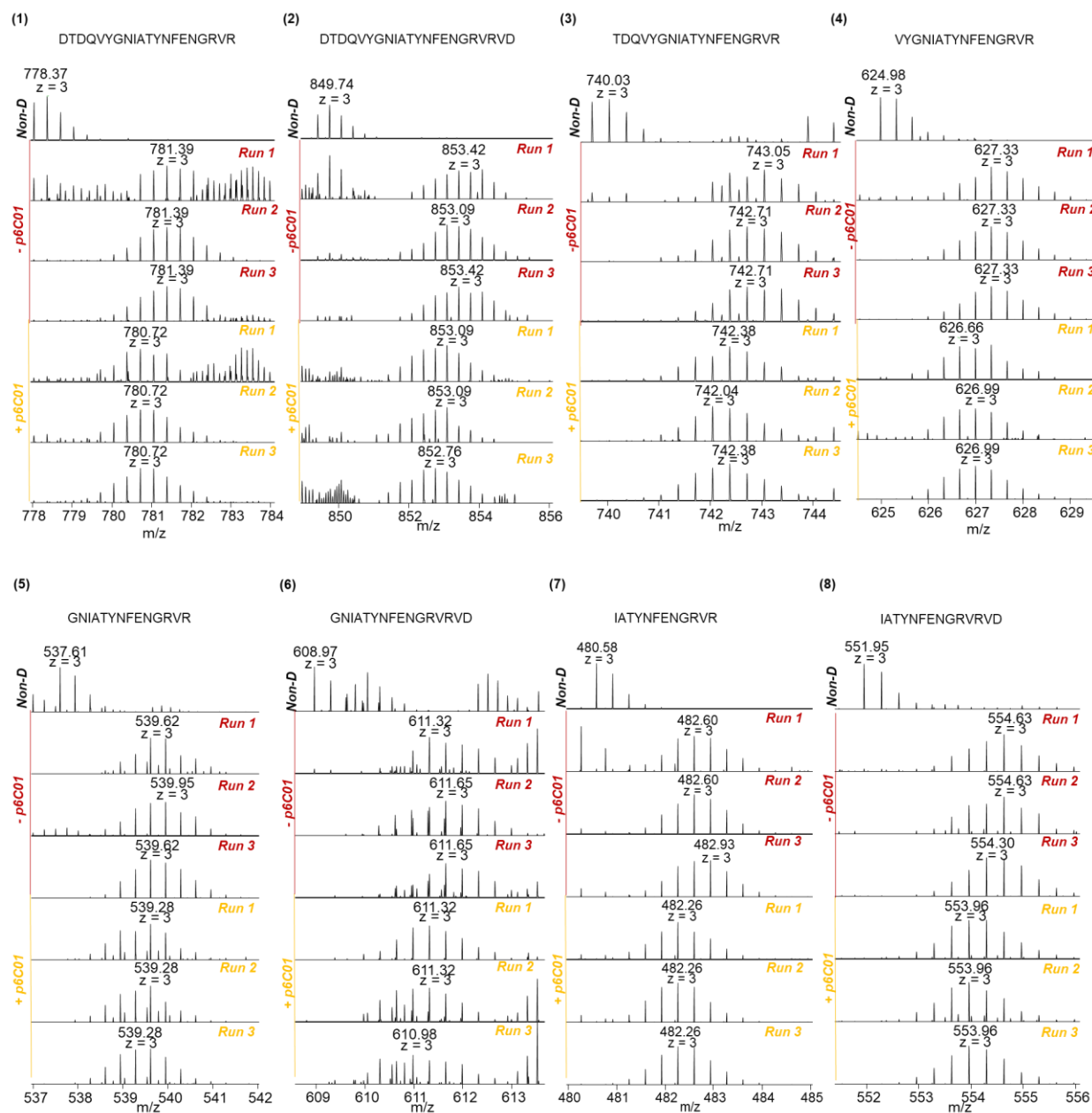


Figure S3. MS spectra of 9 identified peptides in primary epitope for p1A06 binding.

(A)





(B)

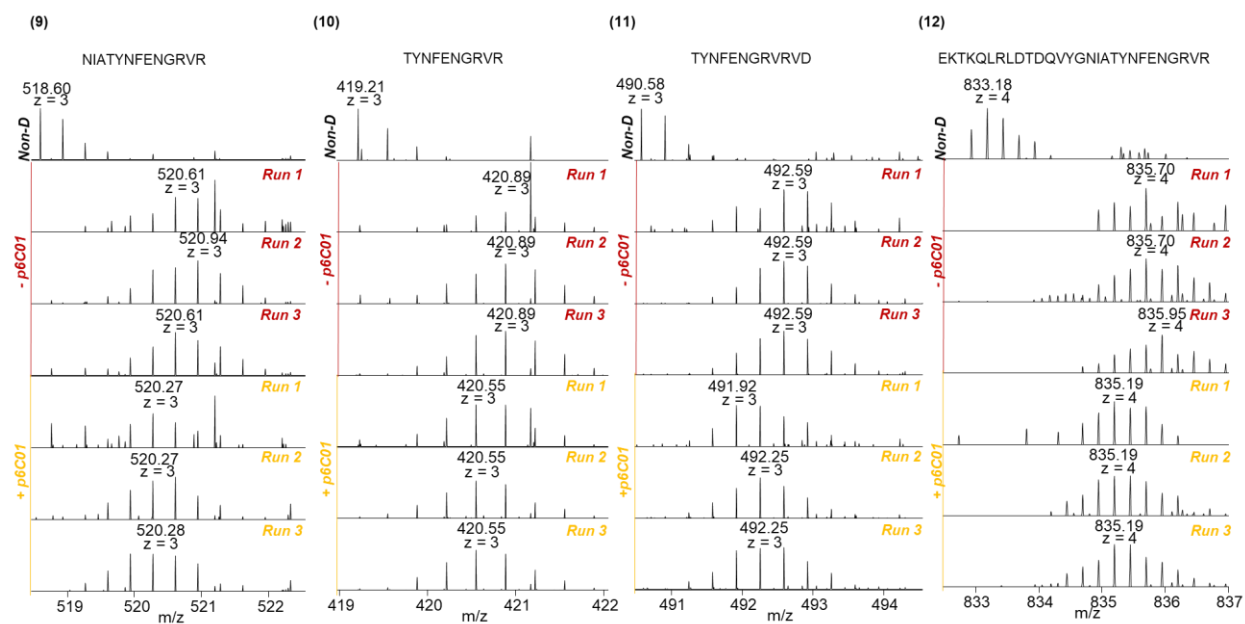


Figure S4. MS spectra of 28 identified peptides for p6C01 binding. (A) MS spectra of 16 identified peptides in primary epitope. (B) MS spectra of 12 identified peptides in secondary epitope.

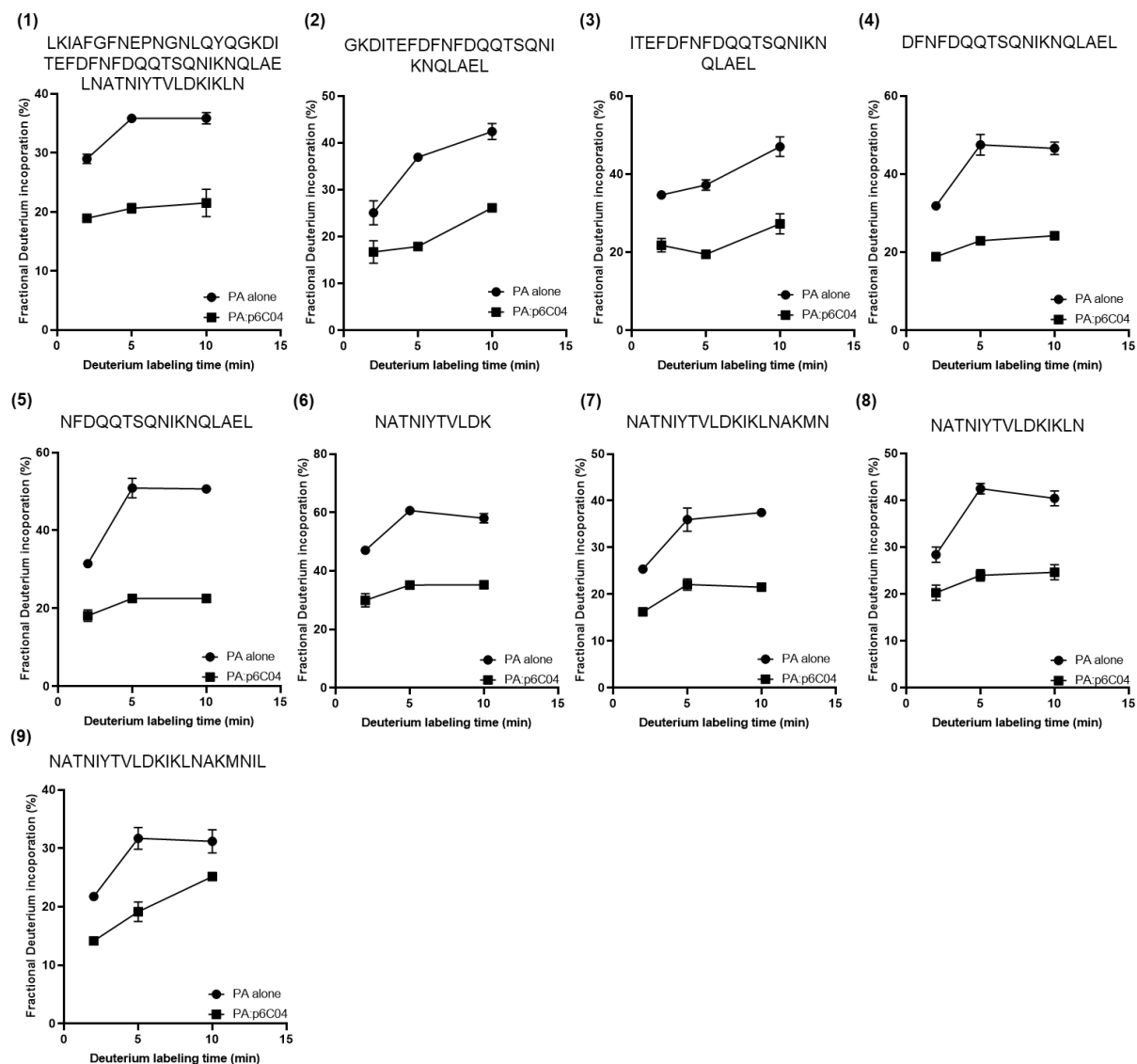


Figure S5. HDX time-course study for PA upon p6C04 binding. Relative fractional deuterium incorporation for 9 peptides in binding region were compared in the absence (Free PA) and presence of p6C04 (PA:p6C04) under 2 minutes, 5 minutes, and 10 minutes deuterium labeling conditions. Experiments were performed in triplicate.