Supplementary Material for

On the Feasibility of Mapping Protein-Binding Motifs in Heparin Chains using a Combination of Ion-Mobility and Top-Down Mass Spectrometry

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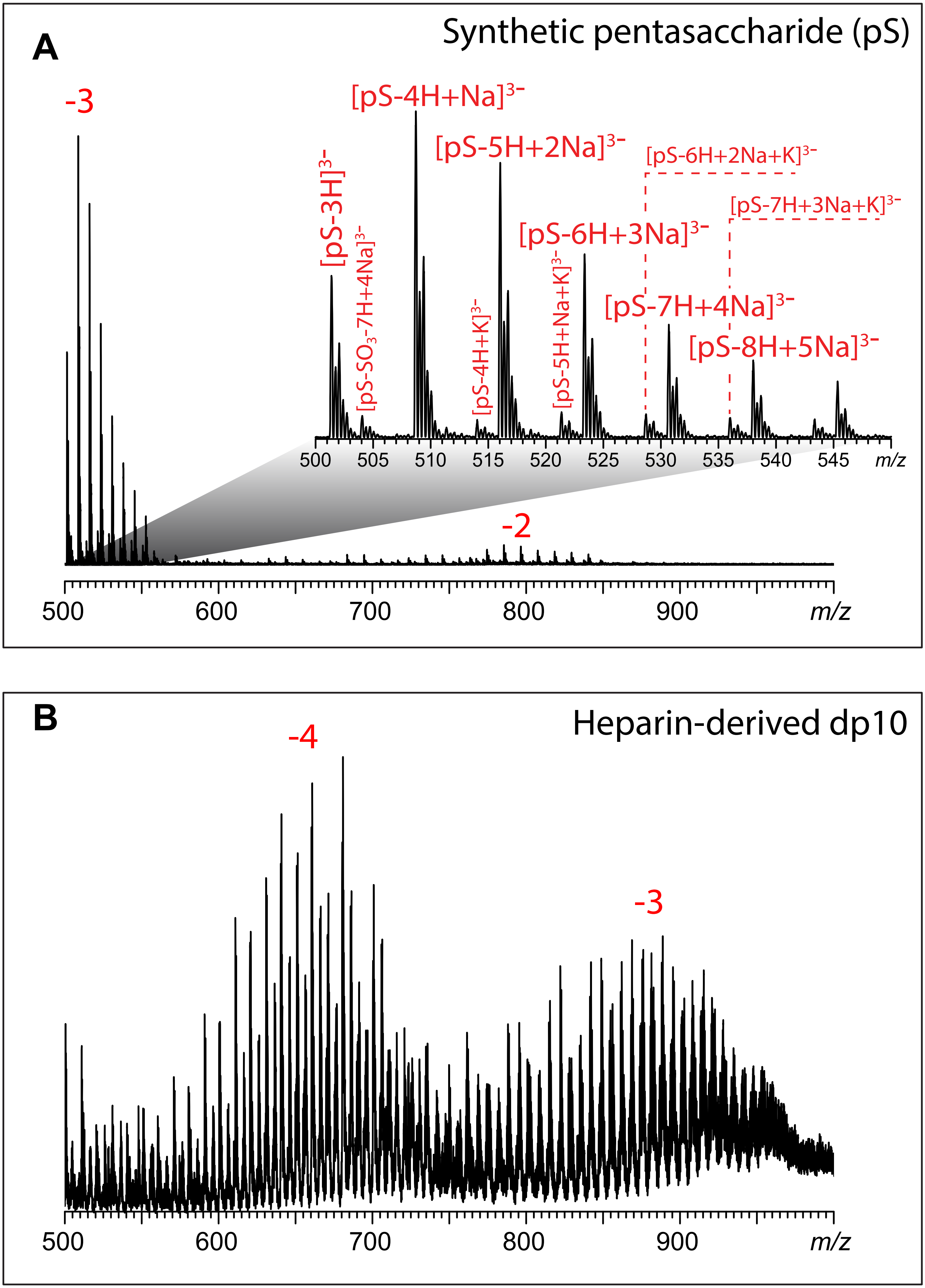
Figure S1. Negative ion ESI MS of the synthetic pentasaccharide (**A**) and dp10 (**B**).

Figure S2. Zoomed views of the precursor regions in CID fragment ion mass spectra of $(FGF\cdot pS)^{+7}$ acquired at different collision voltages.

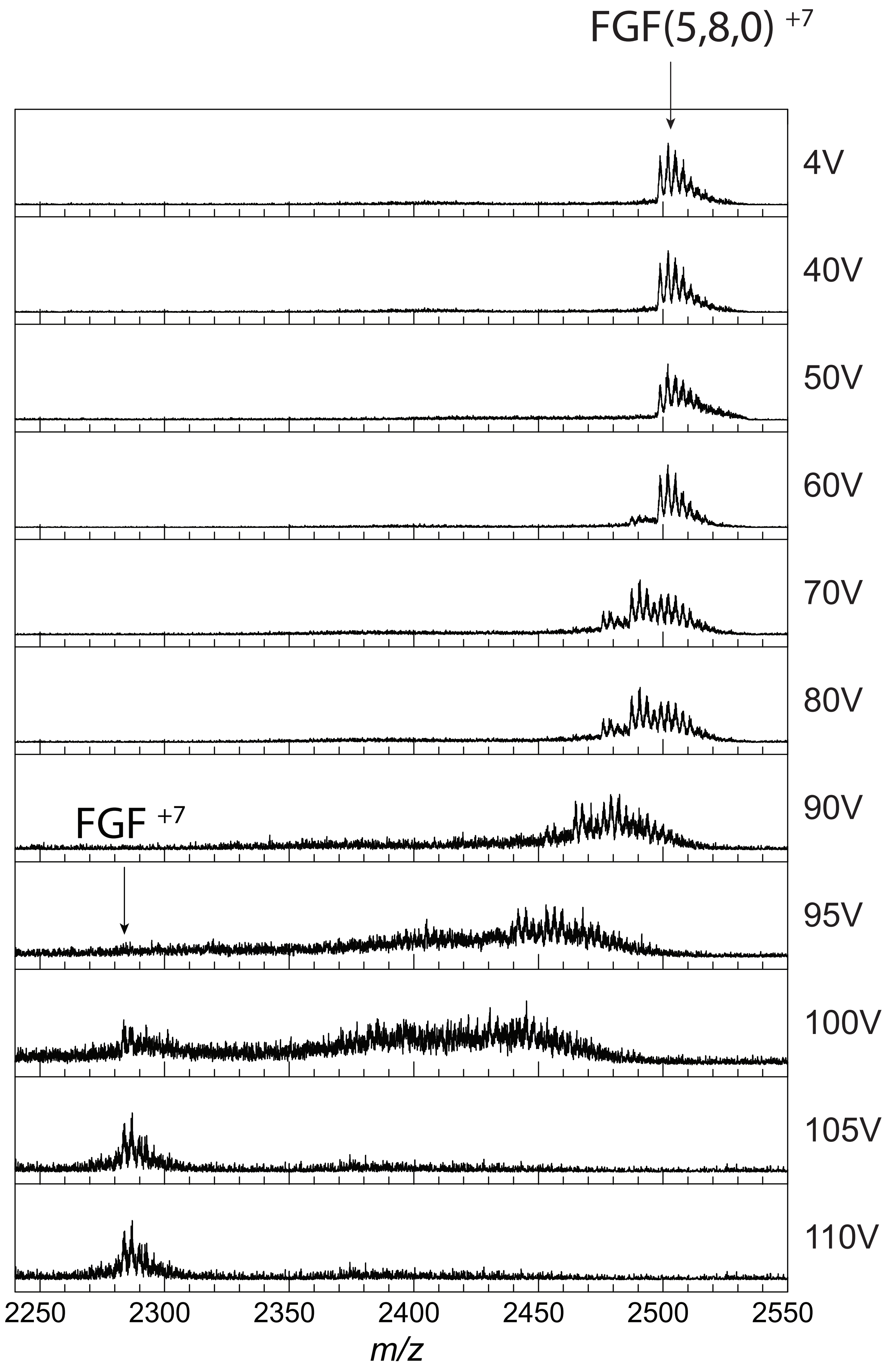
Figure S3. CIU fingerprint graphs of FGF^{+7} (**A**), $(FGF\cdot pS)^{+7}$ (**B**) and FGF^{+8} (**C**).

Figure S4. Two-dimensional IMS/MS plots for fragments ions derived from FGF^{+8} (**A**), $(FGF\cdot pS)^{+8}$ (**B**) and FGF^{+7} (**C**) at several representative collisional voltages. Labels on the graphs highlight critical mass and conformation changes.

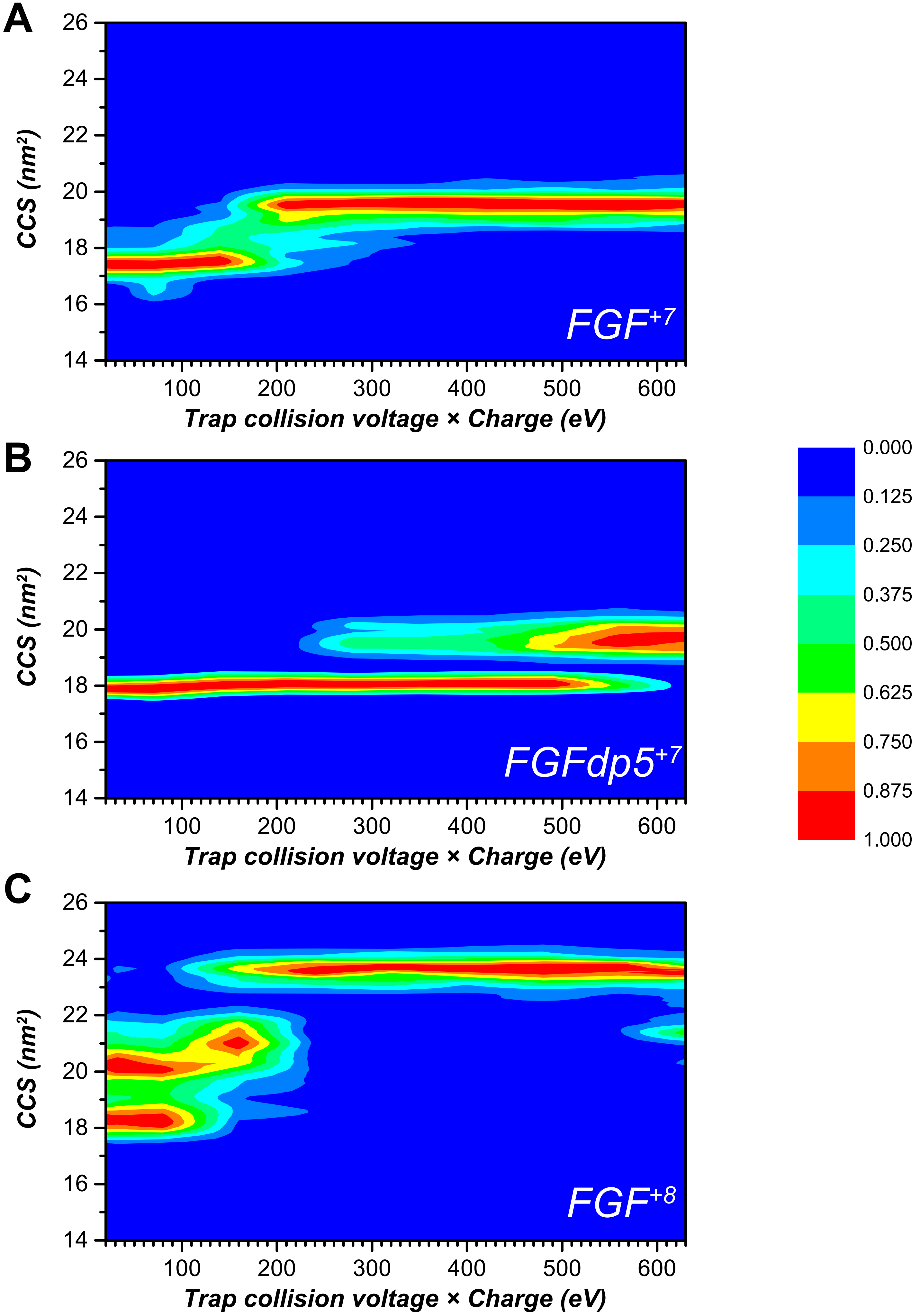
Figure S5. CIU fingerprints of $(FGF\cdot dp10)^{+8}$ and $(FGF\cdot dp10)^{+7}$ representing binary protein/heparin oligomer complexes in the FGF/dp10 mixture.



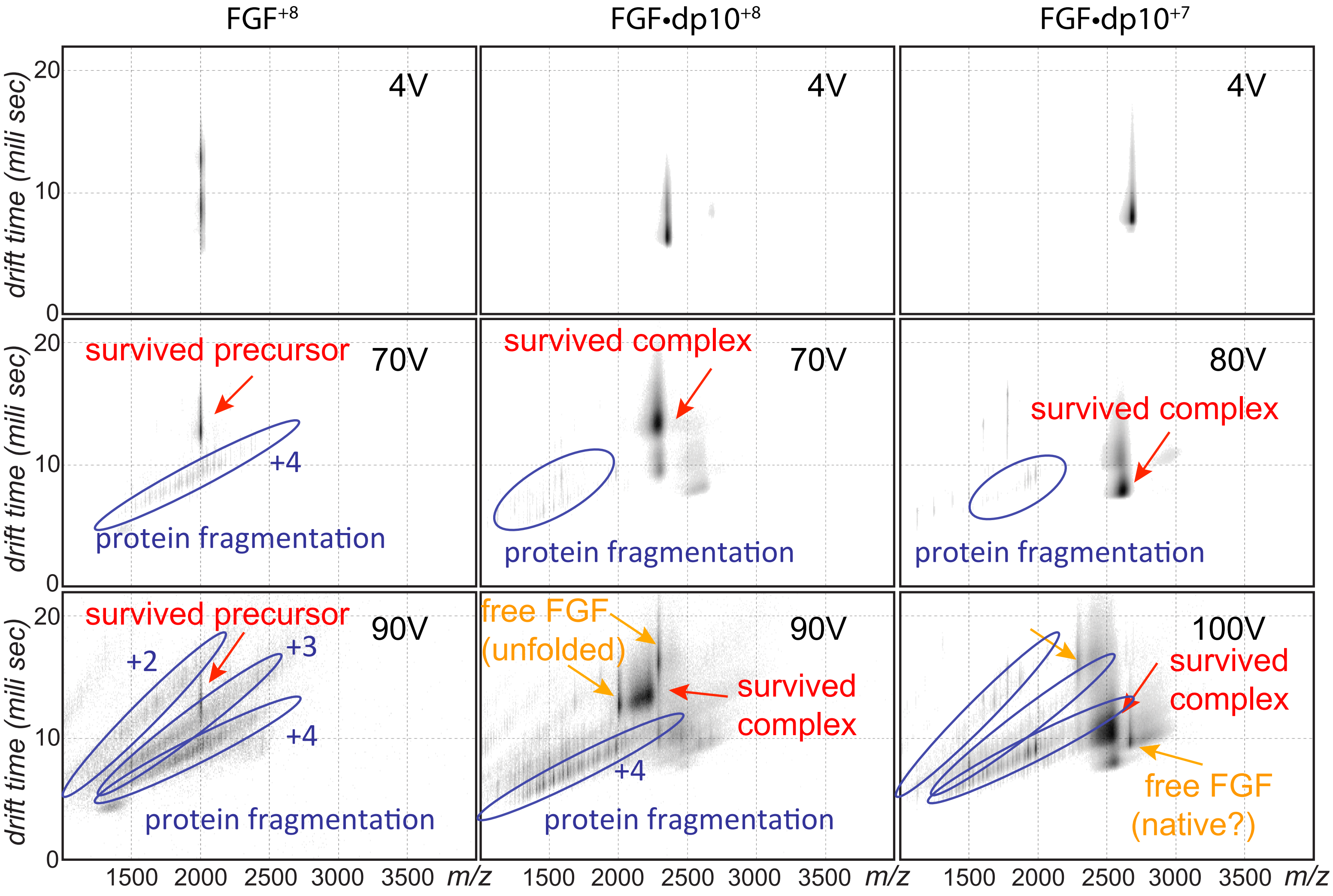
Zhao & Kaltashov, **Figure S1**



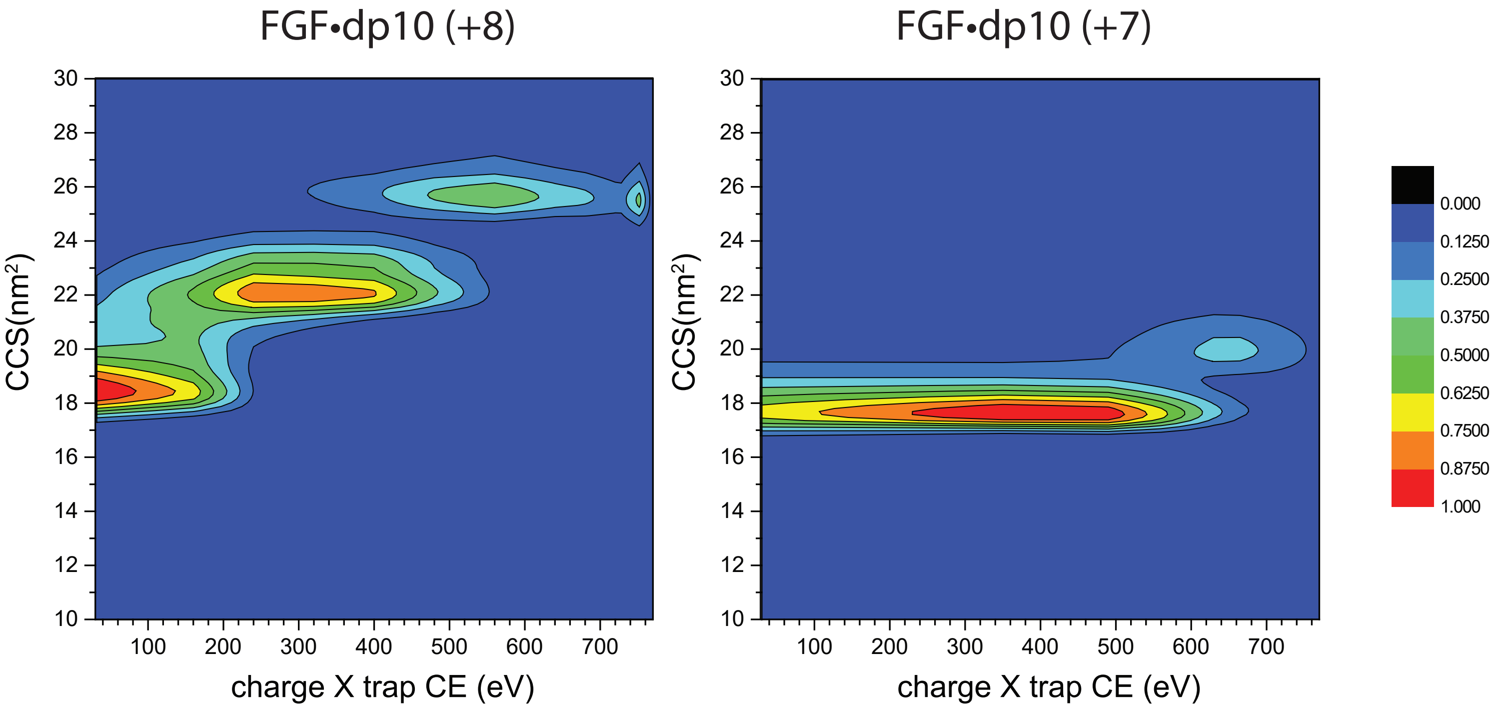
Zhao & Kaltashov, **Figure S2**



Zhao & Kaltashov, **Figure S3**



Zhao & Kaltashov, **Figure S4**



Zhao & Kaltashov, **Figure S5**