

Supporting Information

Exploring the Conformational and Binding Dynamics of HMGA2•DNA Complexes Using Trapped Ion Mobility Spectrometry – Mass Spectrometry

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Trapped Ion Mobility Spectrometry (TIMS)

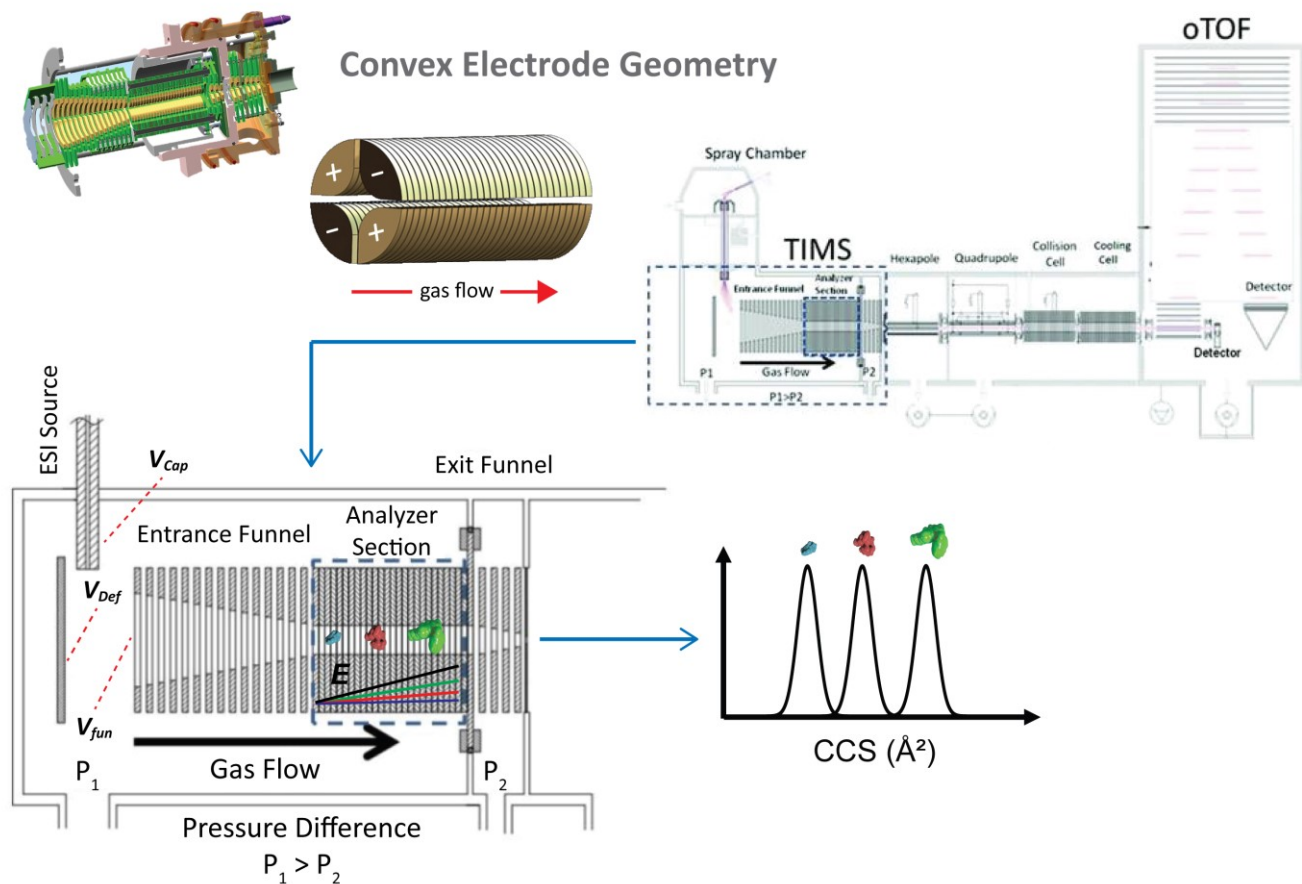


Figure S1. TIMS-MS instrument showing the convex electrode TIMS geometry and TIMS operation.

Collisional Activation (ΔV)

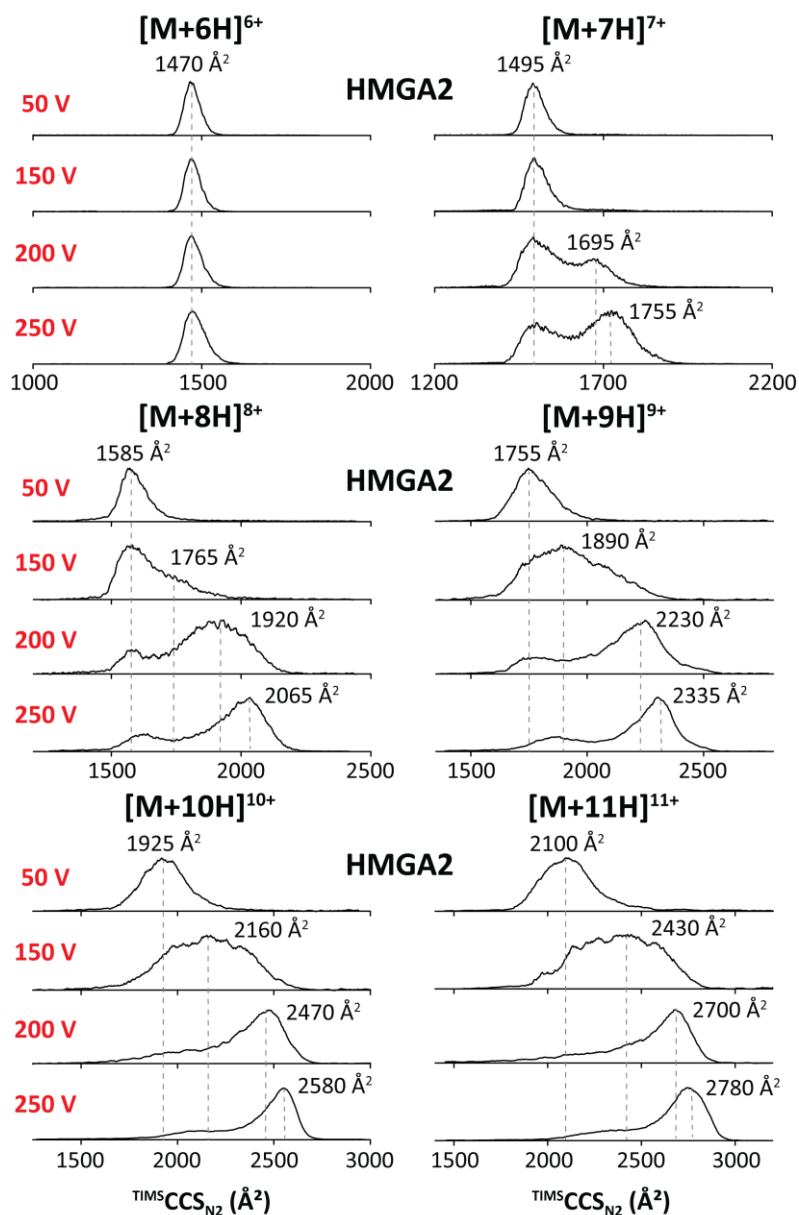


Figure S2. TMS profiles as a function of the collisional activation for the multiply protonated species of the free HMGA₂ protein (black traces).

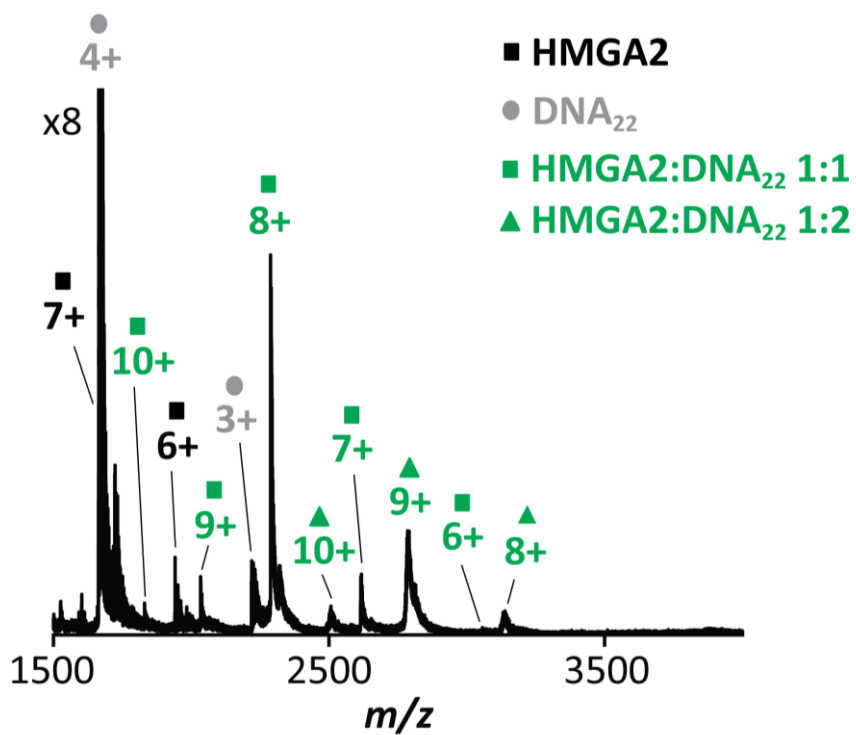


Figure S3. Typical native nESI MS profile of the HMGA₂·DNA₂₂ complexes with 1:3 excess DNA₂₂ in solution. Notice the absence of the 1:3 stoichiometry when DNA is in excess.

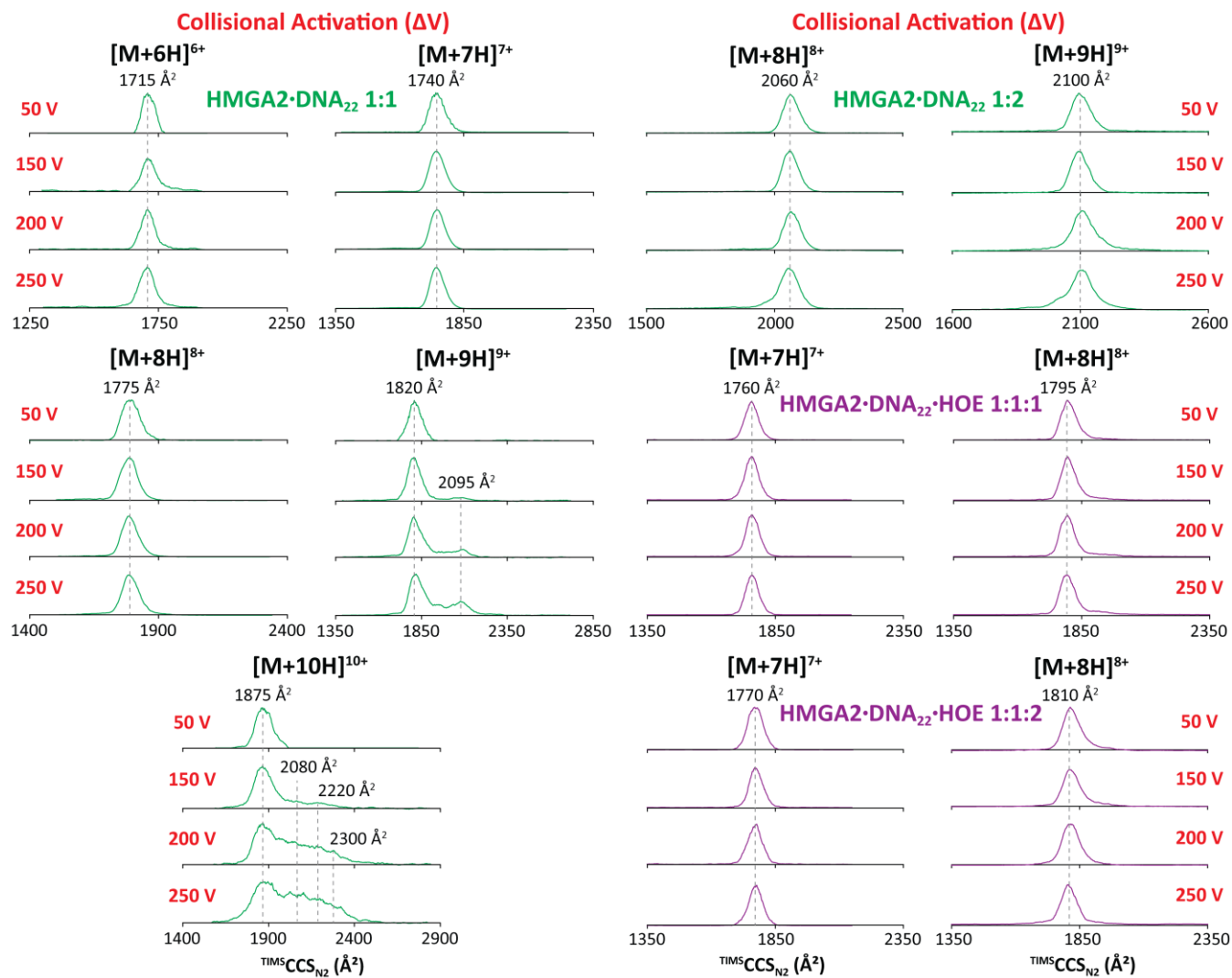


Figure S4. TMS profiles as a function of the collision activation for the multiply protonated species of the HMGA2•DNA₂₂ (green traces) and HMGA2•DNA₂₂•HOE (purple traces) complexes.

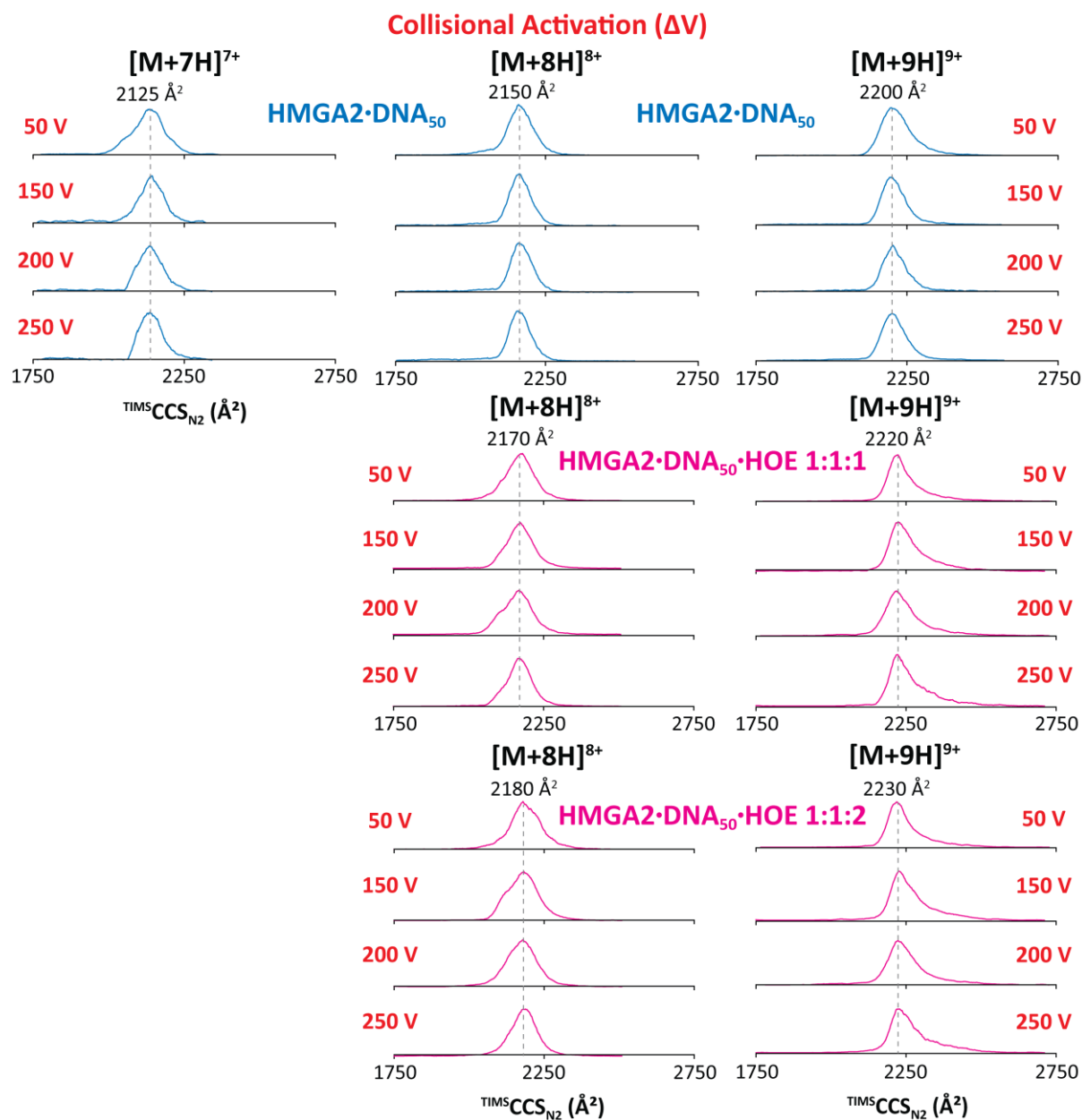


Figure S5. TMS profiles as a function of the collisional activation for the multiply protonated species of the HMGA2·DNA₅₀ (blue traces) and HMGA2·DNA₅₀·HOE (magenta traces) complexes.