

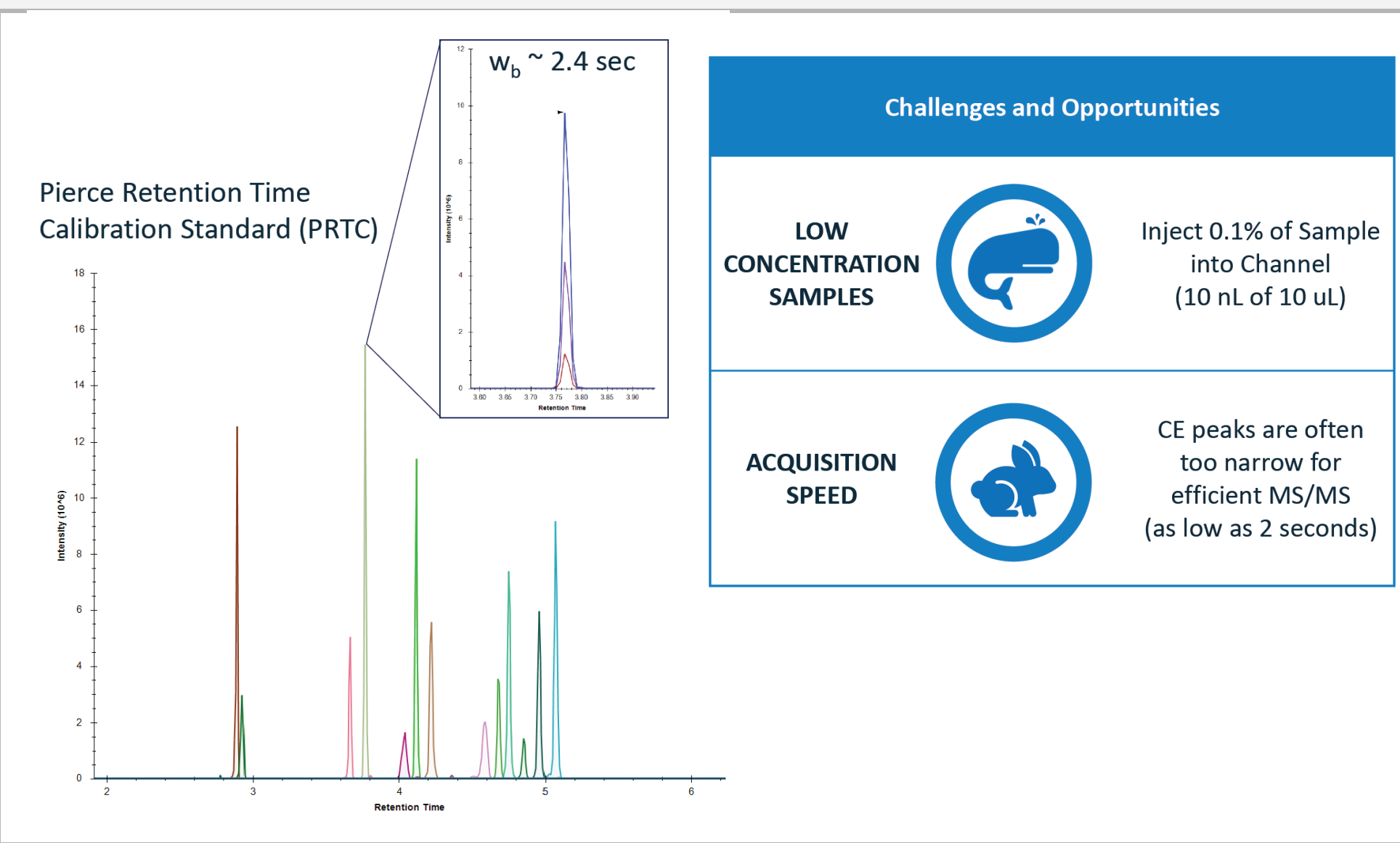
Pushing the Boundaries of Speed and Sensitivity in Proteomics: Coupling SPE-Enabled Microfluidic Capillary Electrophoresis with Ultrafast Tandem Mass Spectrometry

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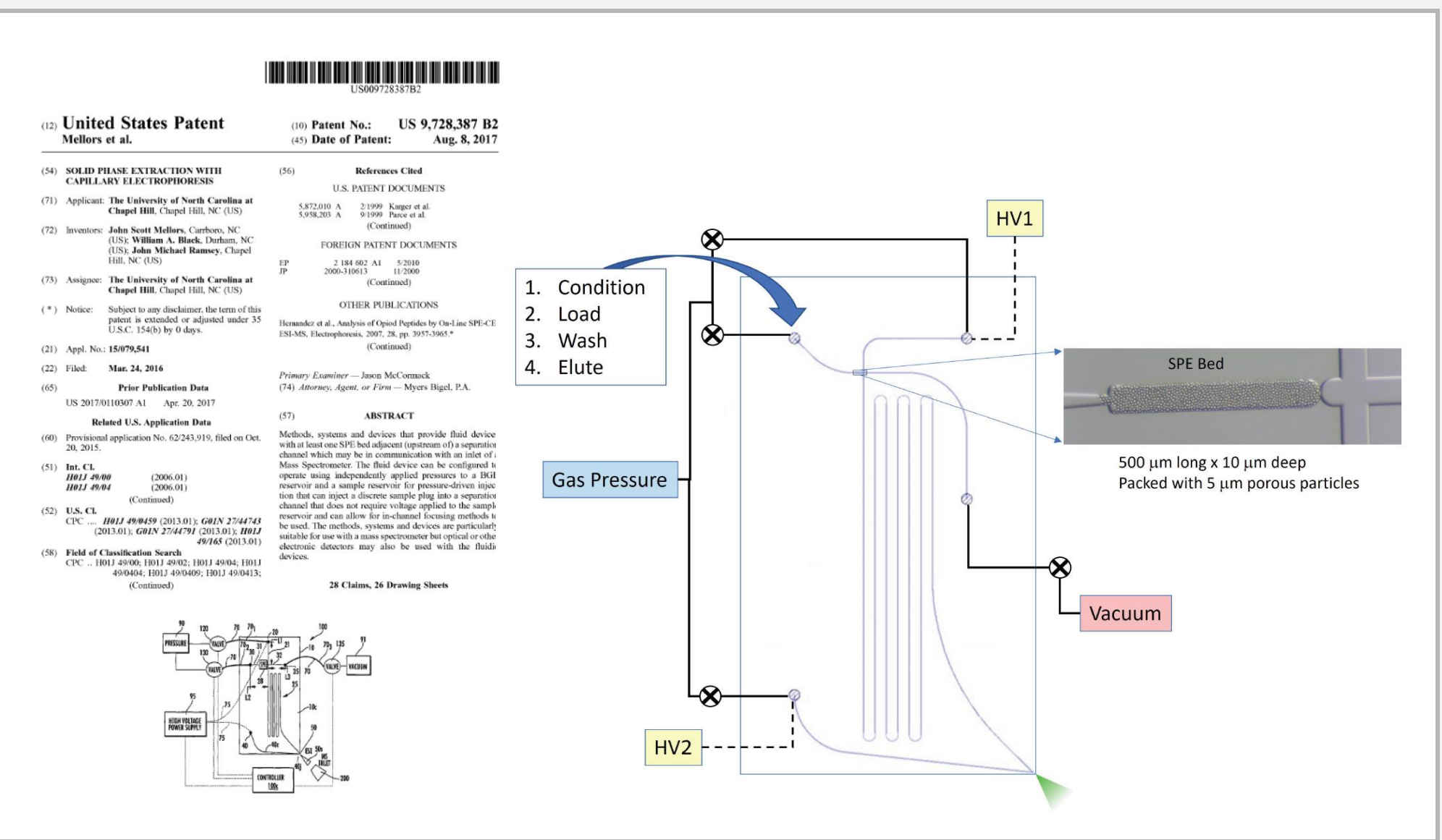


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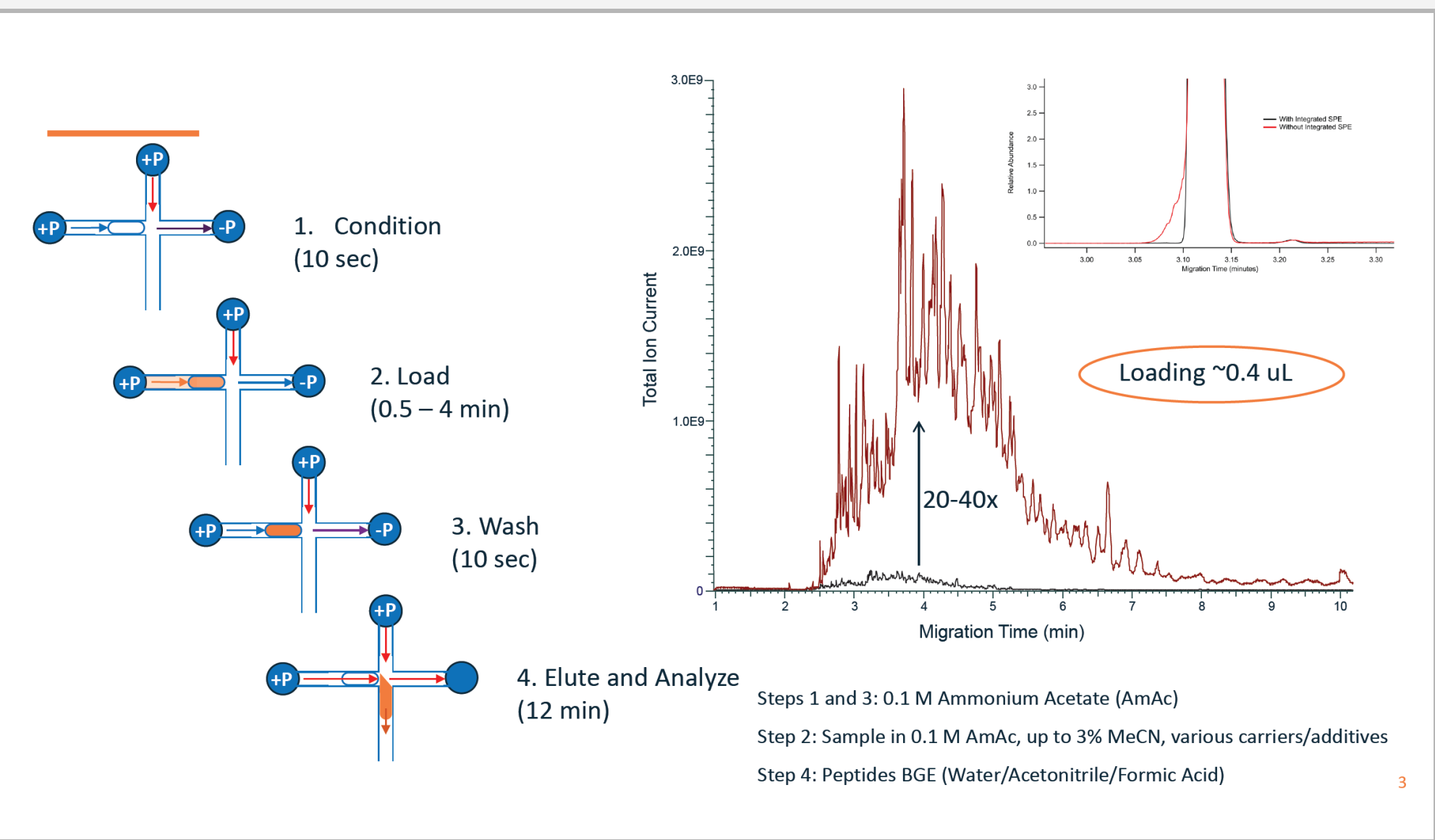
PATsmart™ ZipChip® System: High Speed and Low Sample Volume



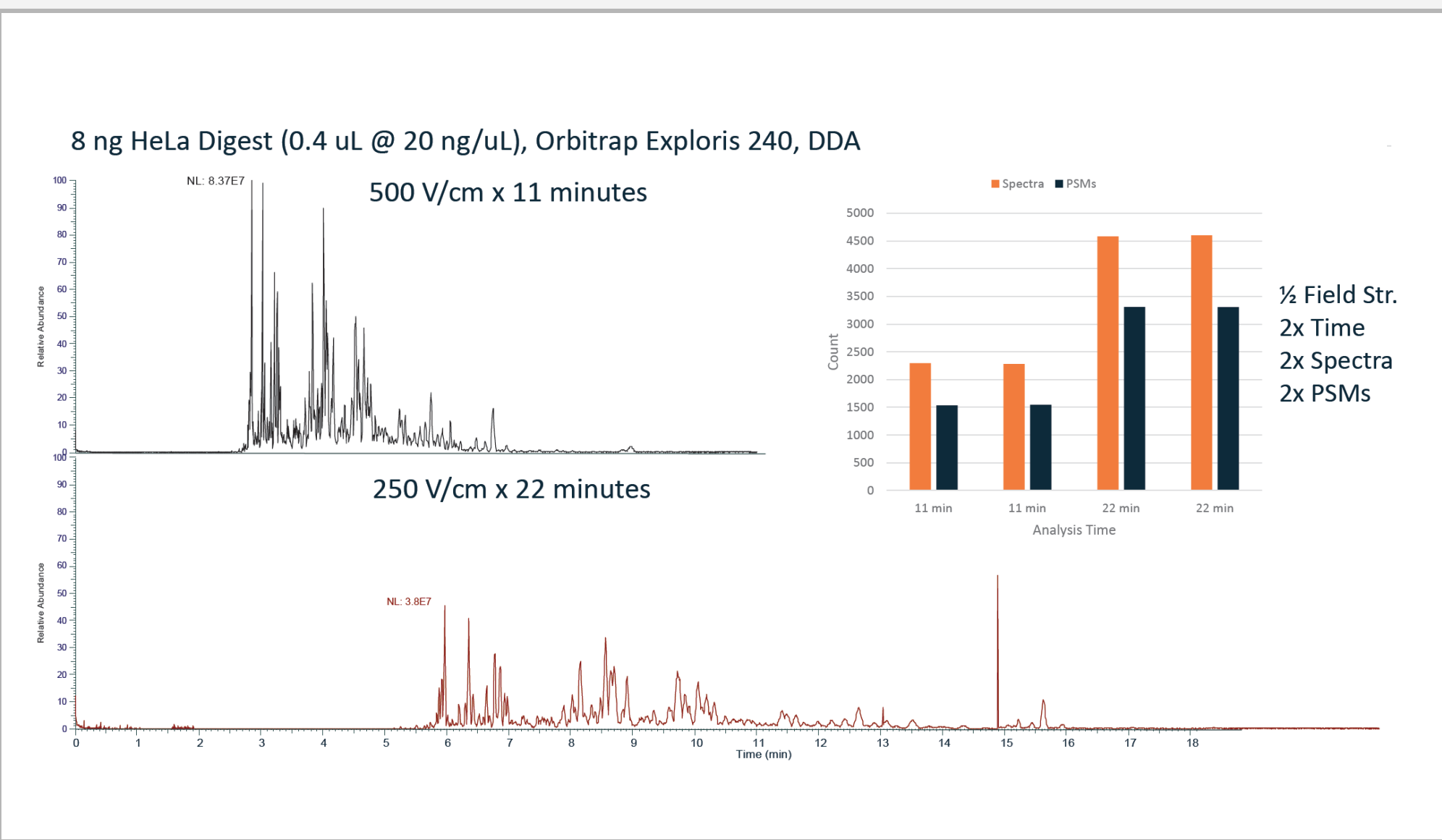
Solving the Sample Volume Problem using On-Chip Preconcentration



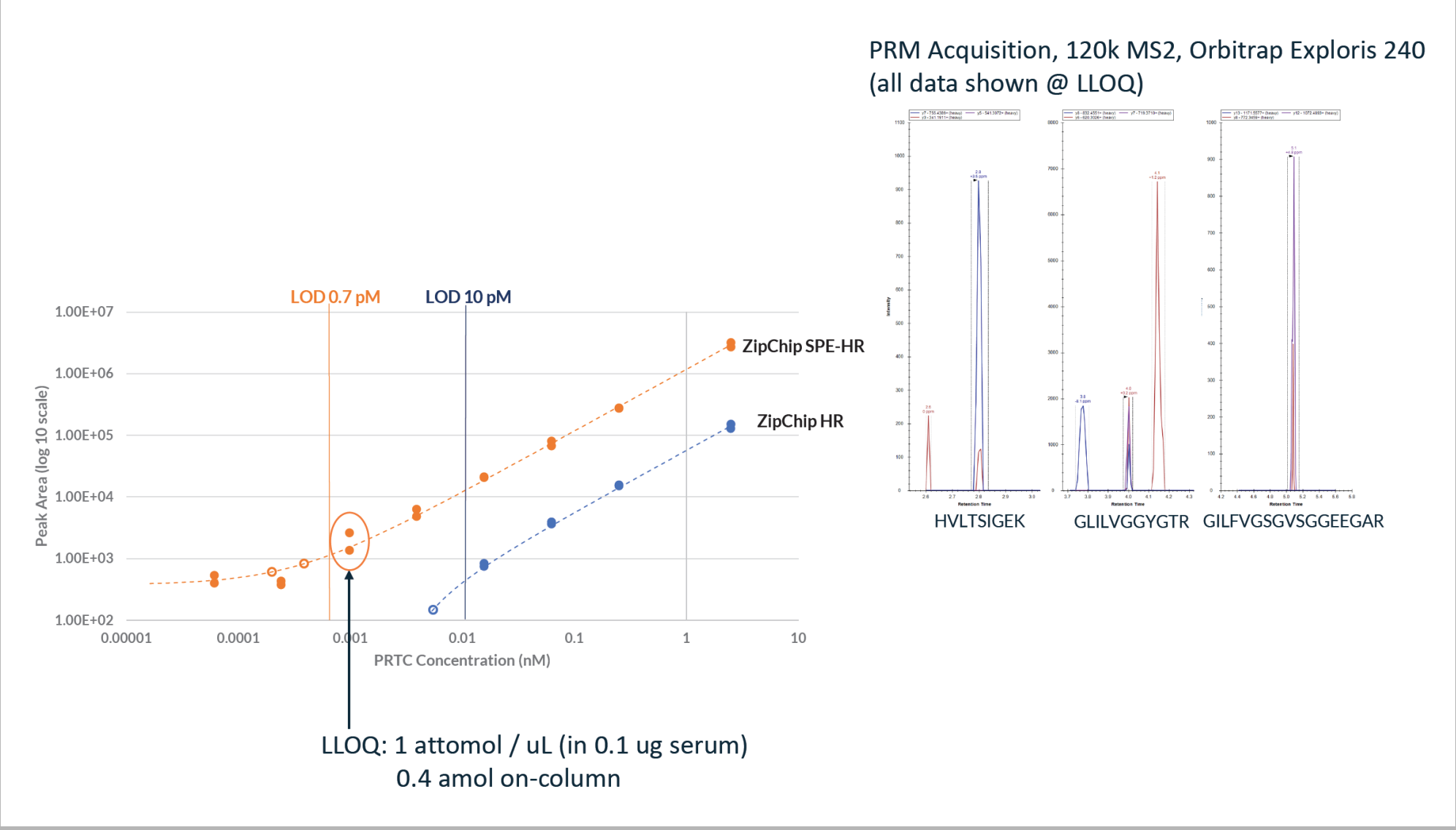
SPE-ZipChip Operation



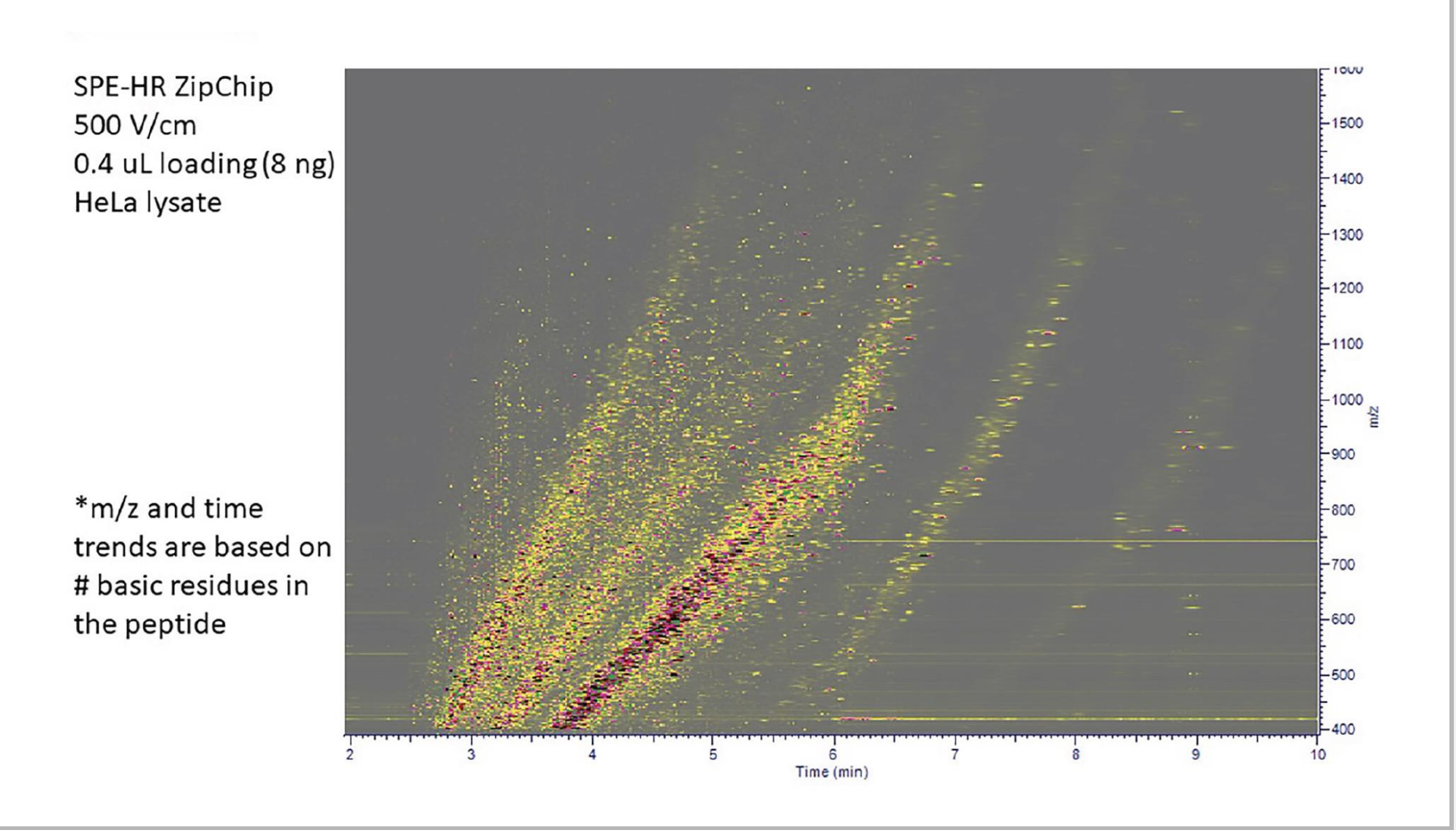
Number of IDs Dependent on Time, not Sensitivity or Efficiency



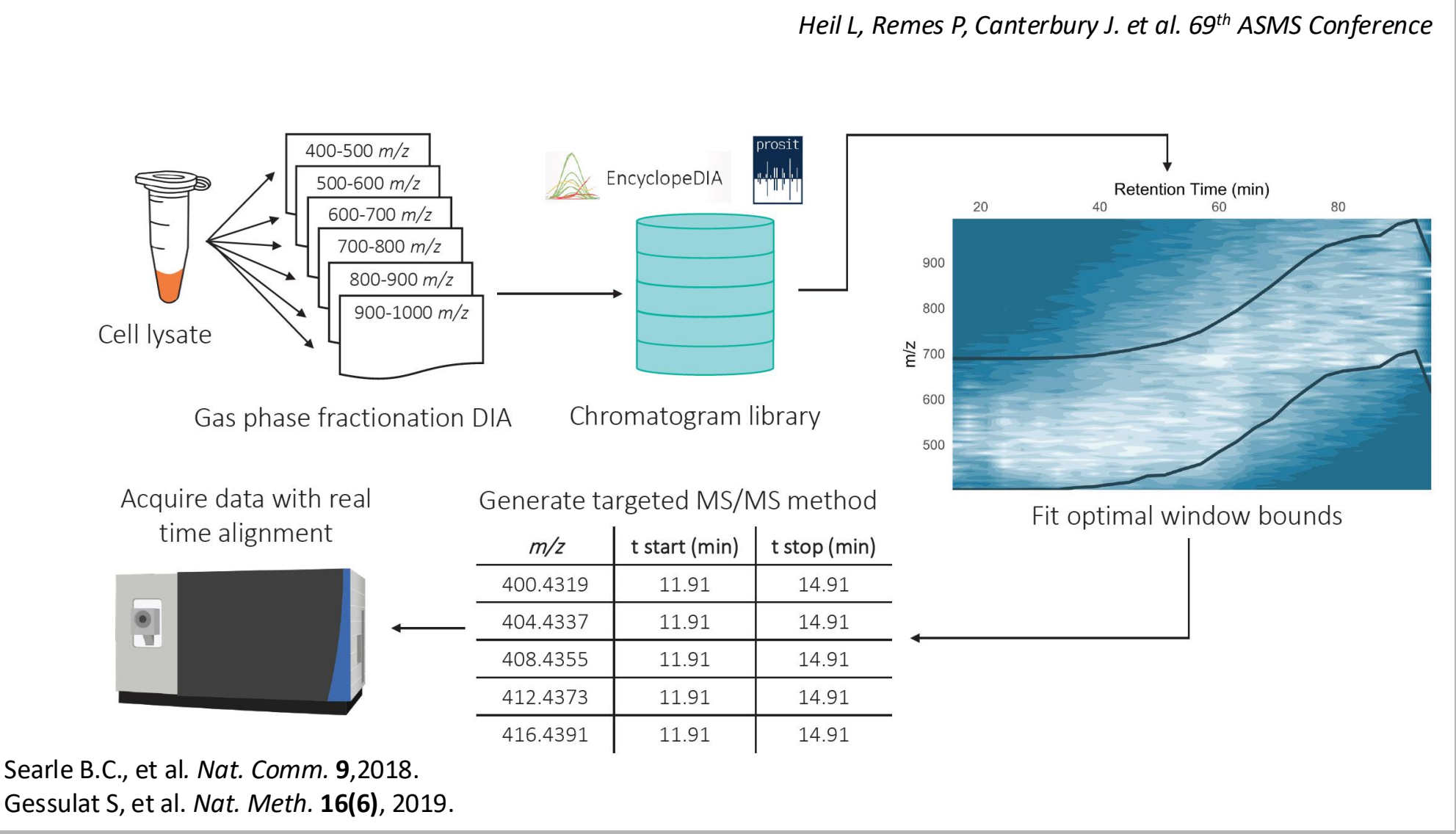
Serial Dilution in Serum using PRM to Evaluate Ionization Efficiency



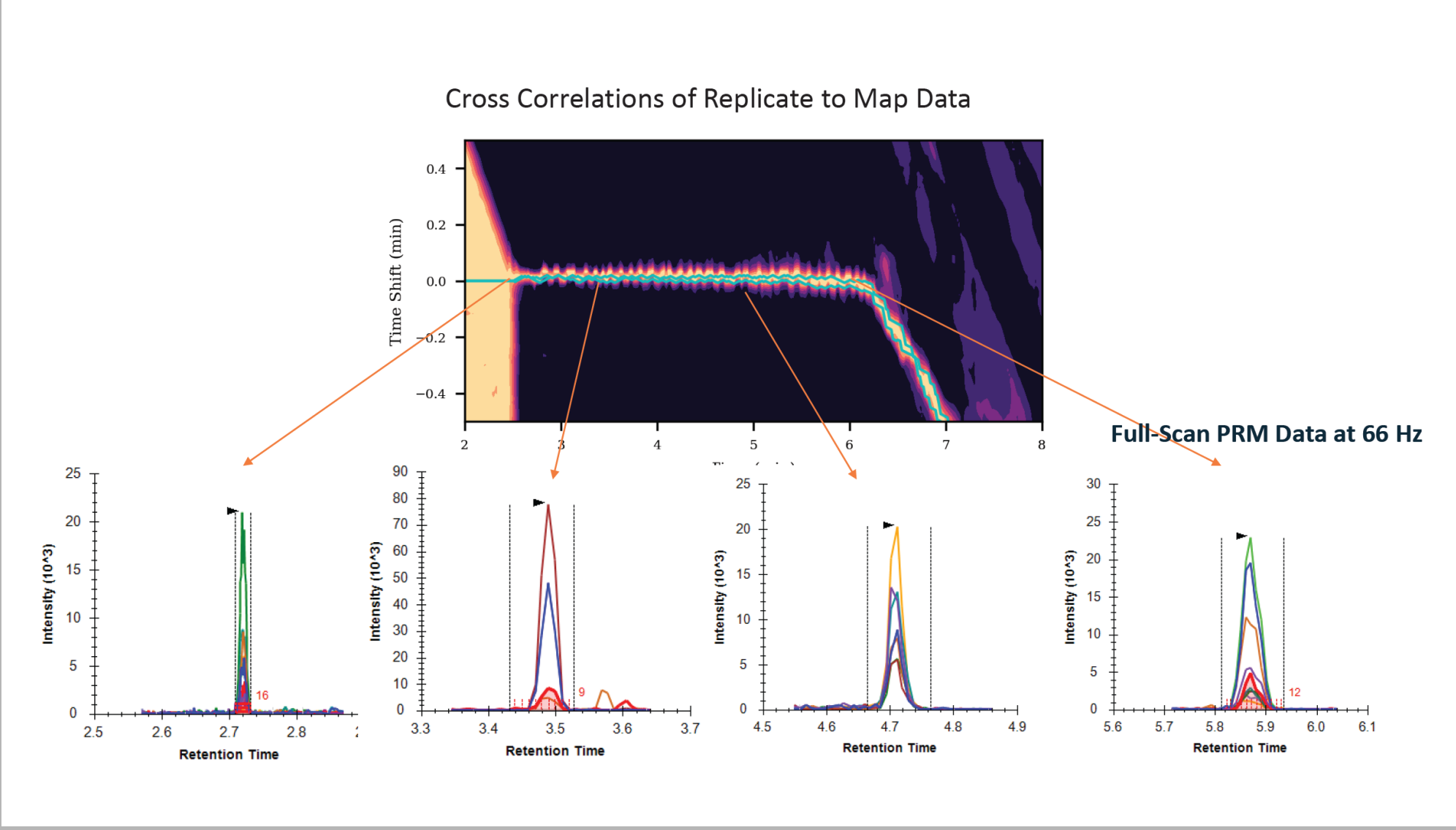
Migration Time in CE is Based on Analyte Size and Charge



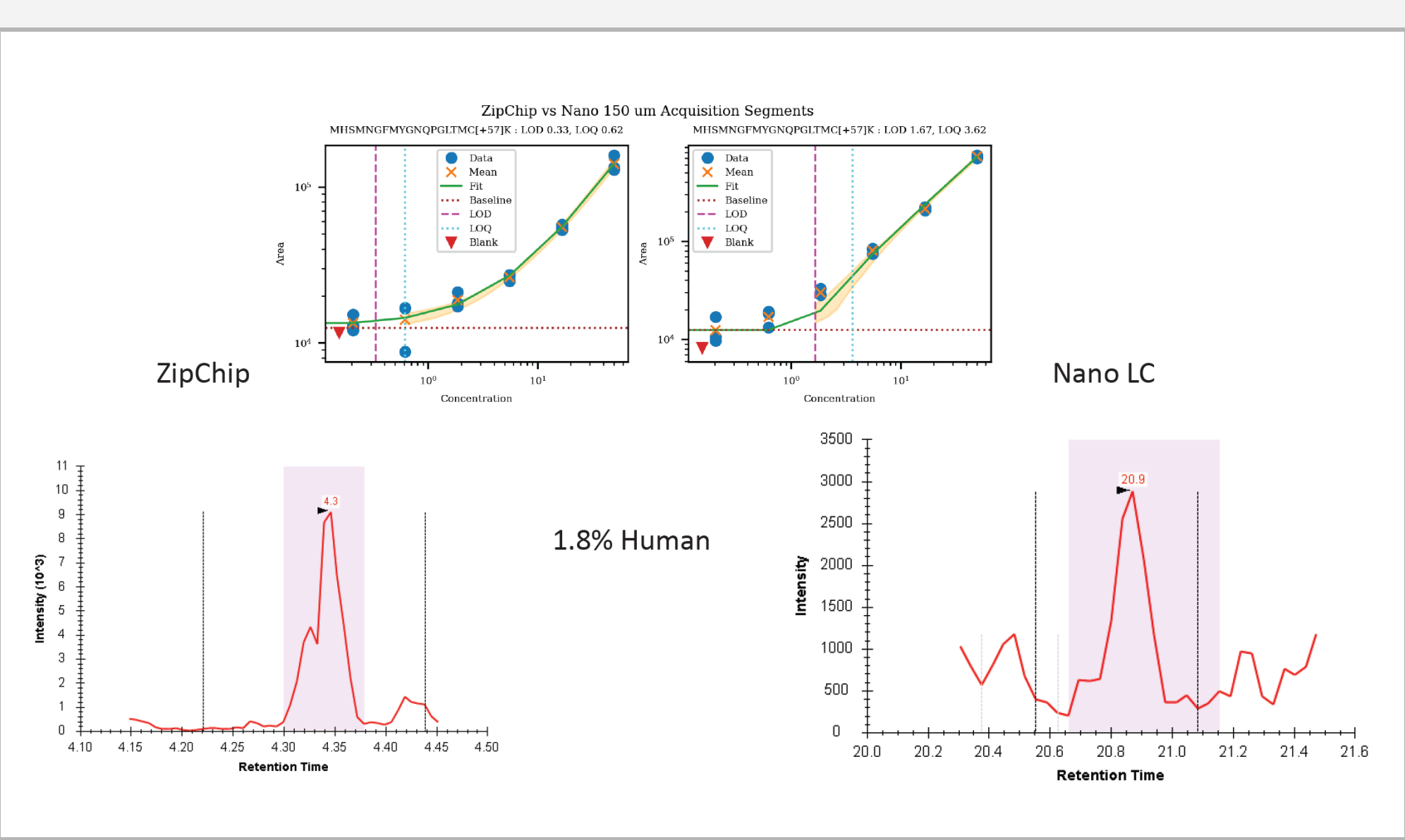
Creating a dynamic DIA method



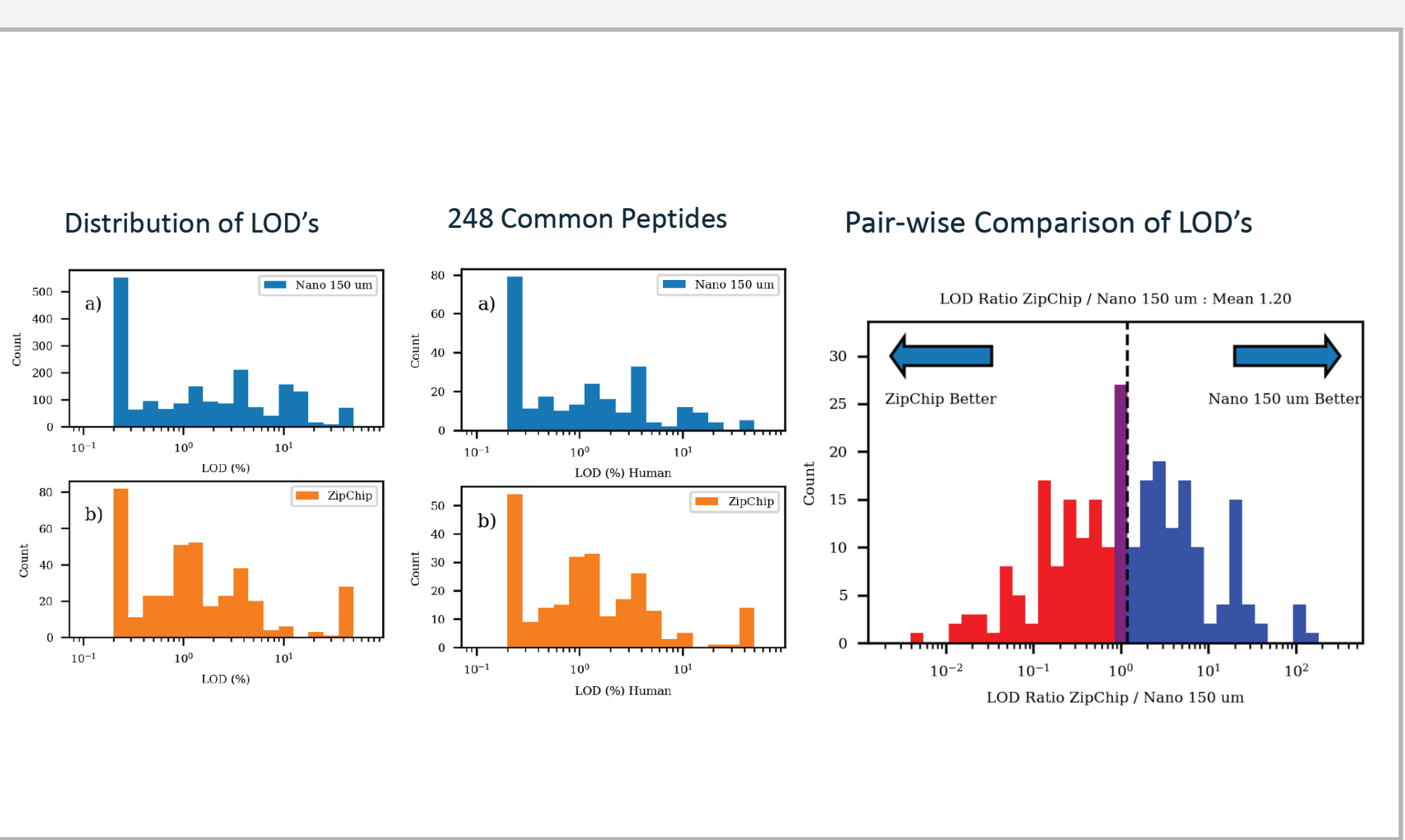
Real-time Alignment Allows Very Narrow Target Windows



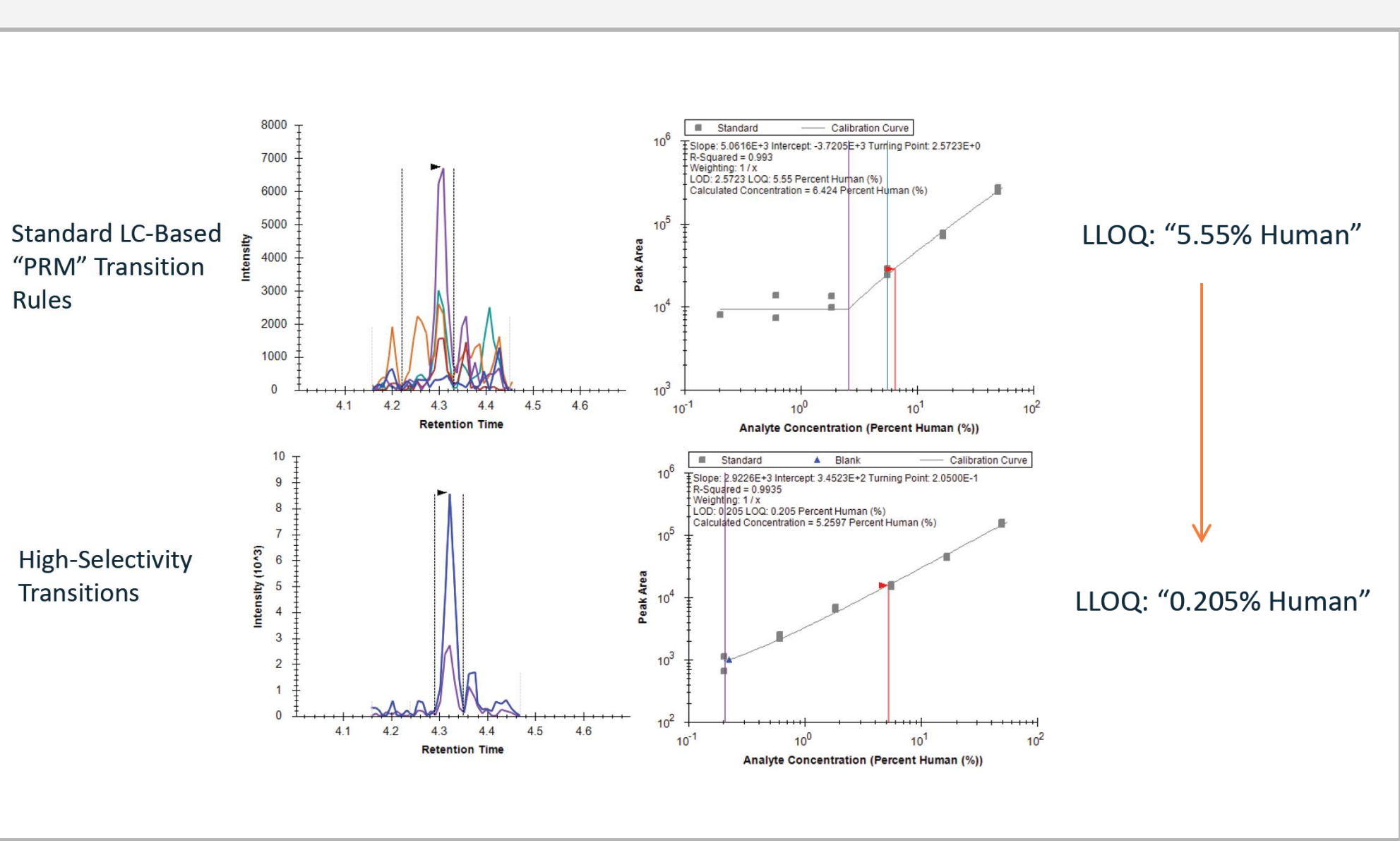
LOD and LOQ Comparison Based on Plasma Matrix Dilutions



LOD Dilution Results



Product Ion Selectivity is more Critical for Faster Separations



Conclusions and Future Directions

- Where is SPE-ZipChip potentially most useful?
- Applications requiring fast total analysis time with minimum sample input
 - Exciting data from Marto lab on Enriched Sub-proteomes
- Lots of potential avenues for exploration
- DIA for complex proteomes
 - Simplified proteomes with pre-enrichment
 - Online preconcentration for top-down proteomics
 - Low-input (low/single cell) proteomics



Learn more at repligen.com/zipchip