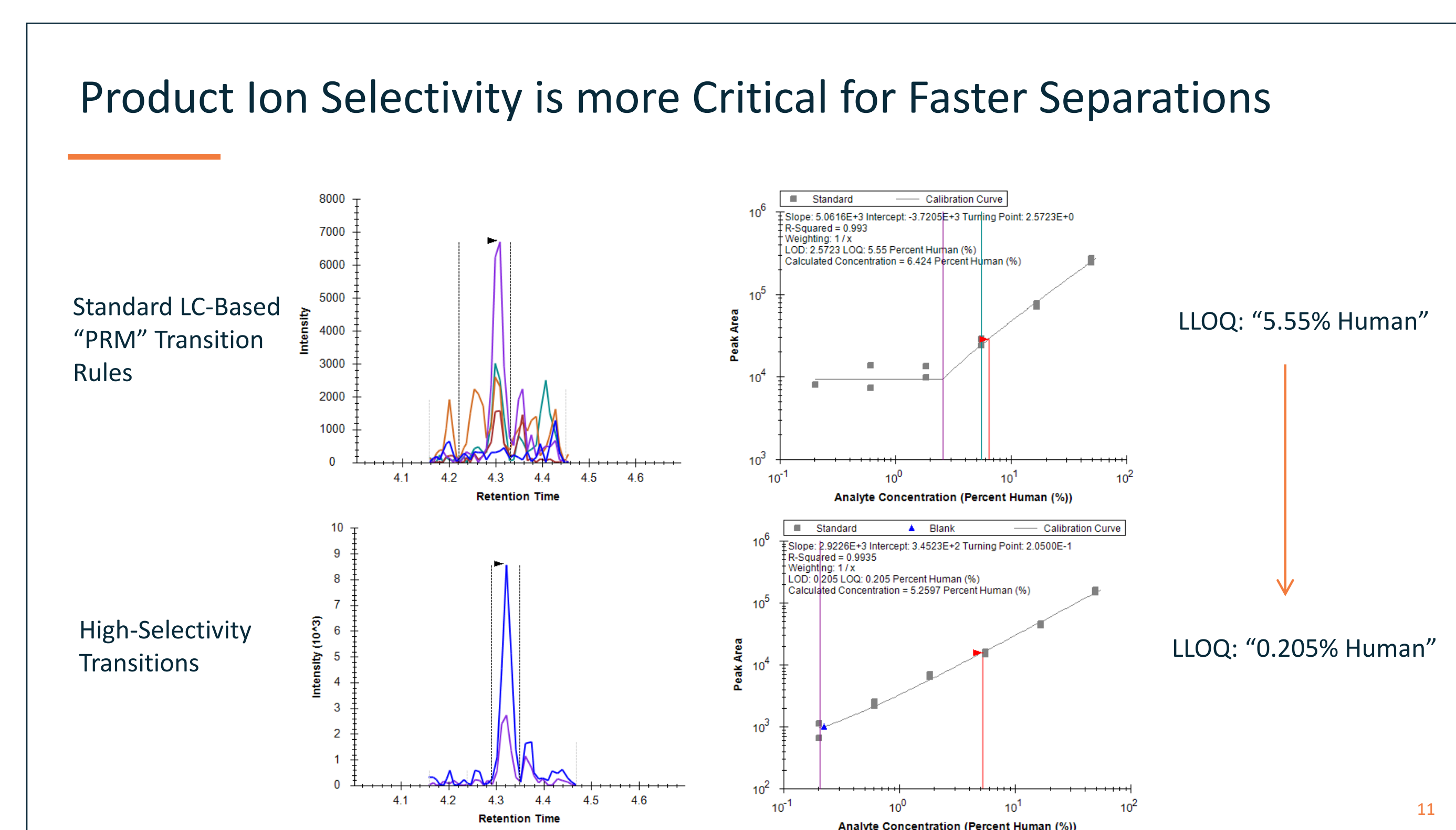
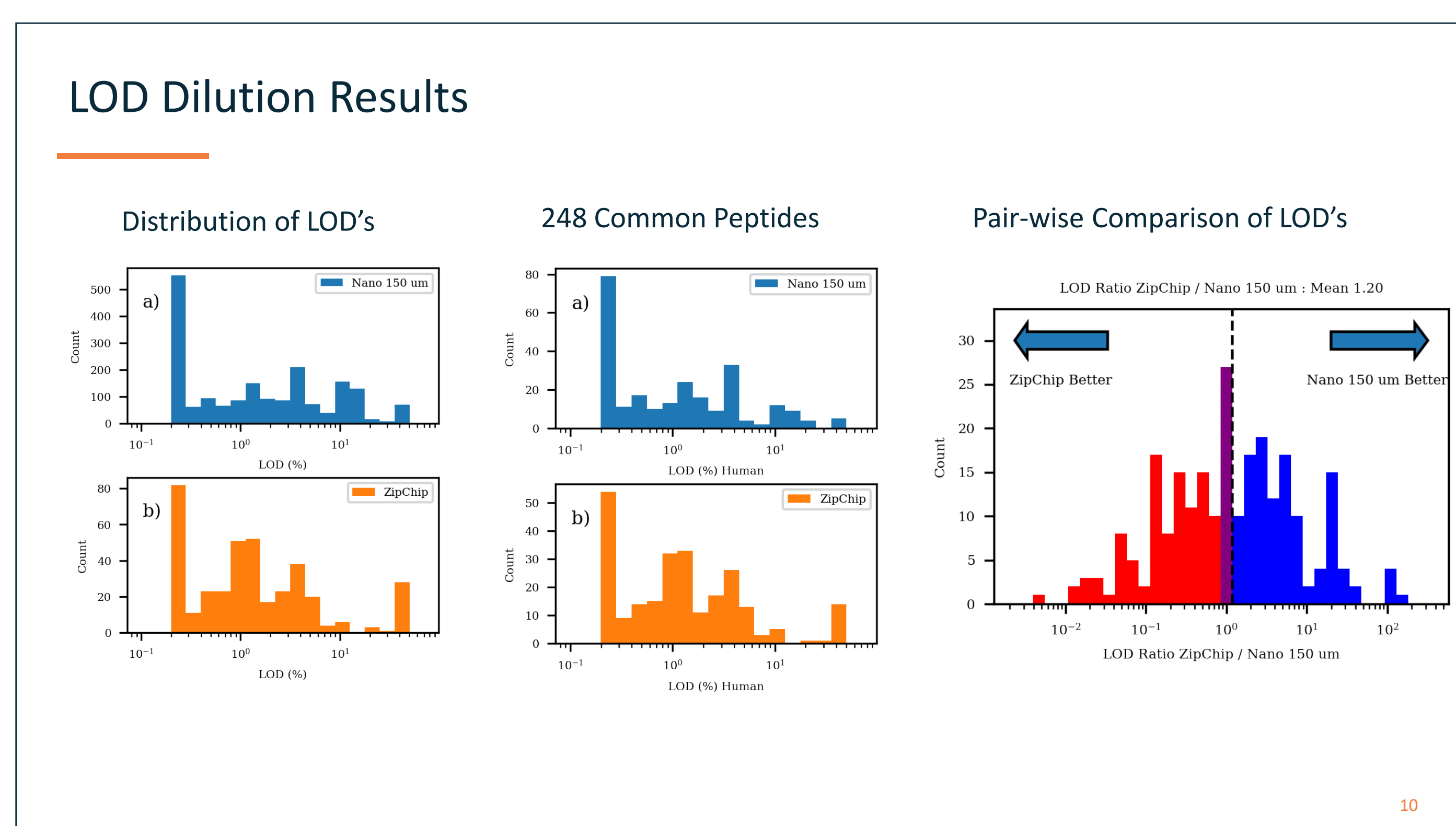
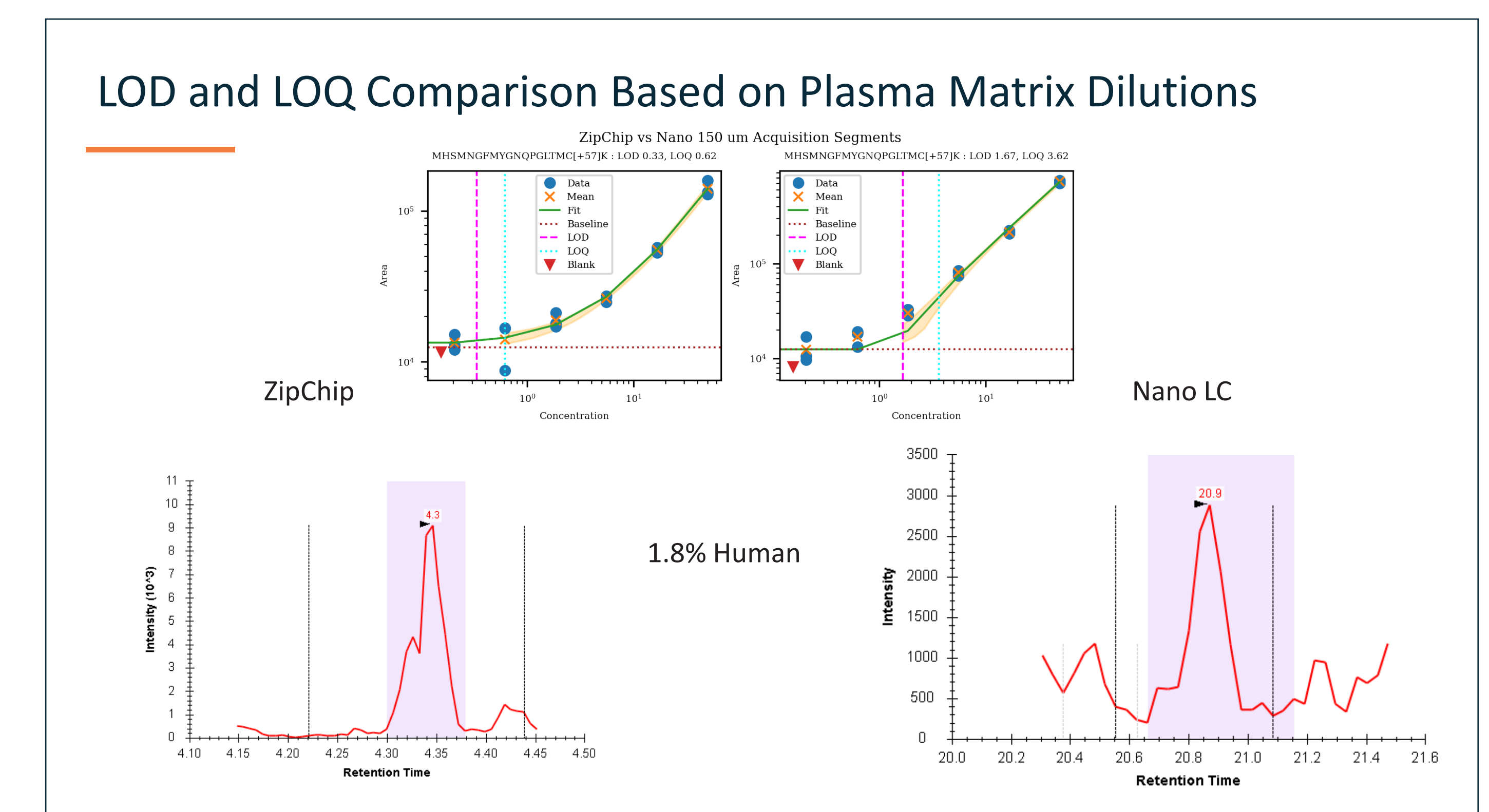
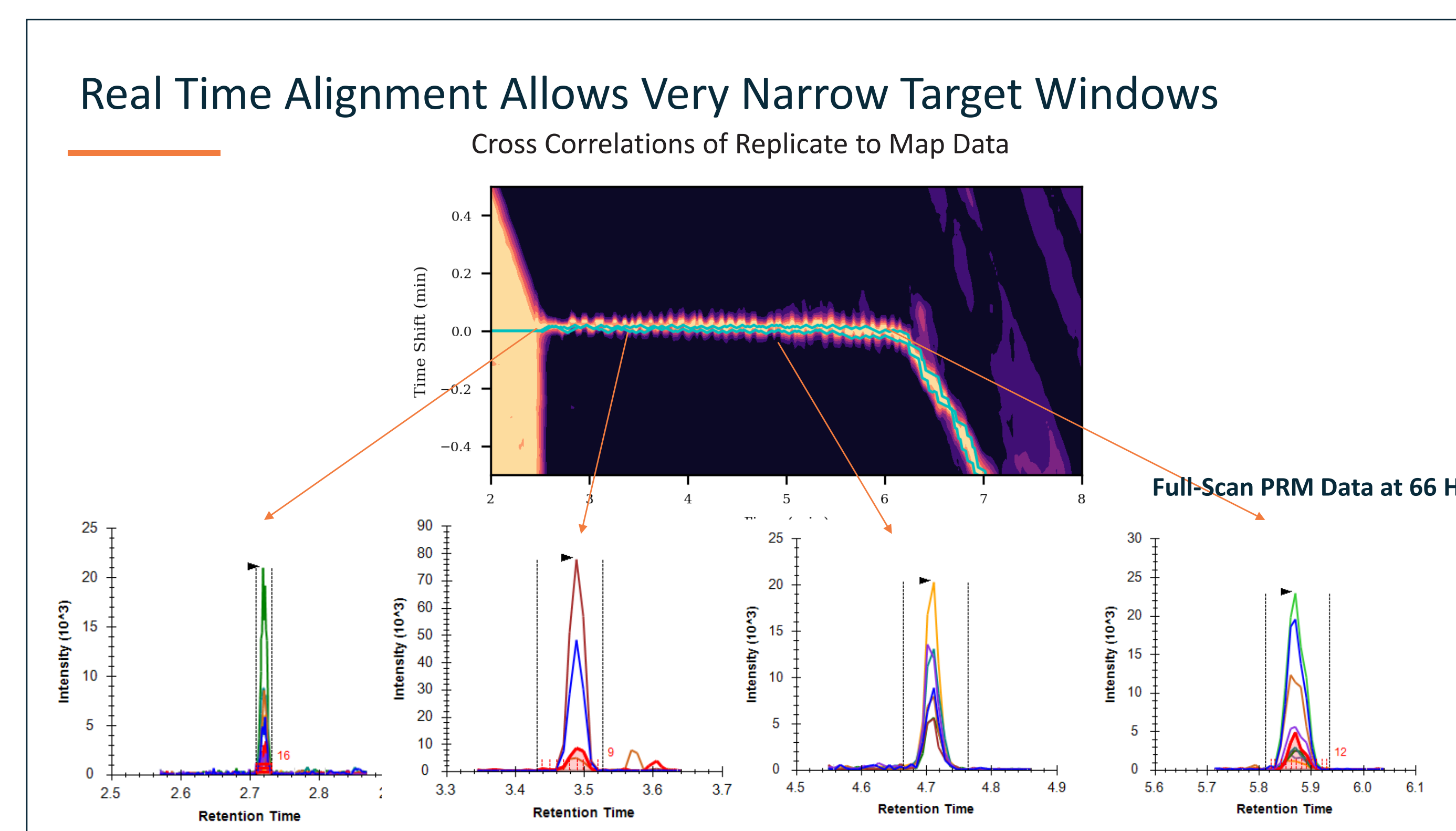
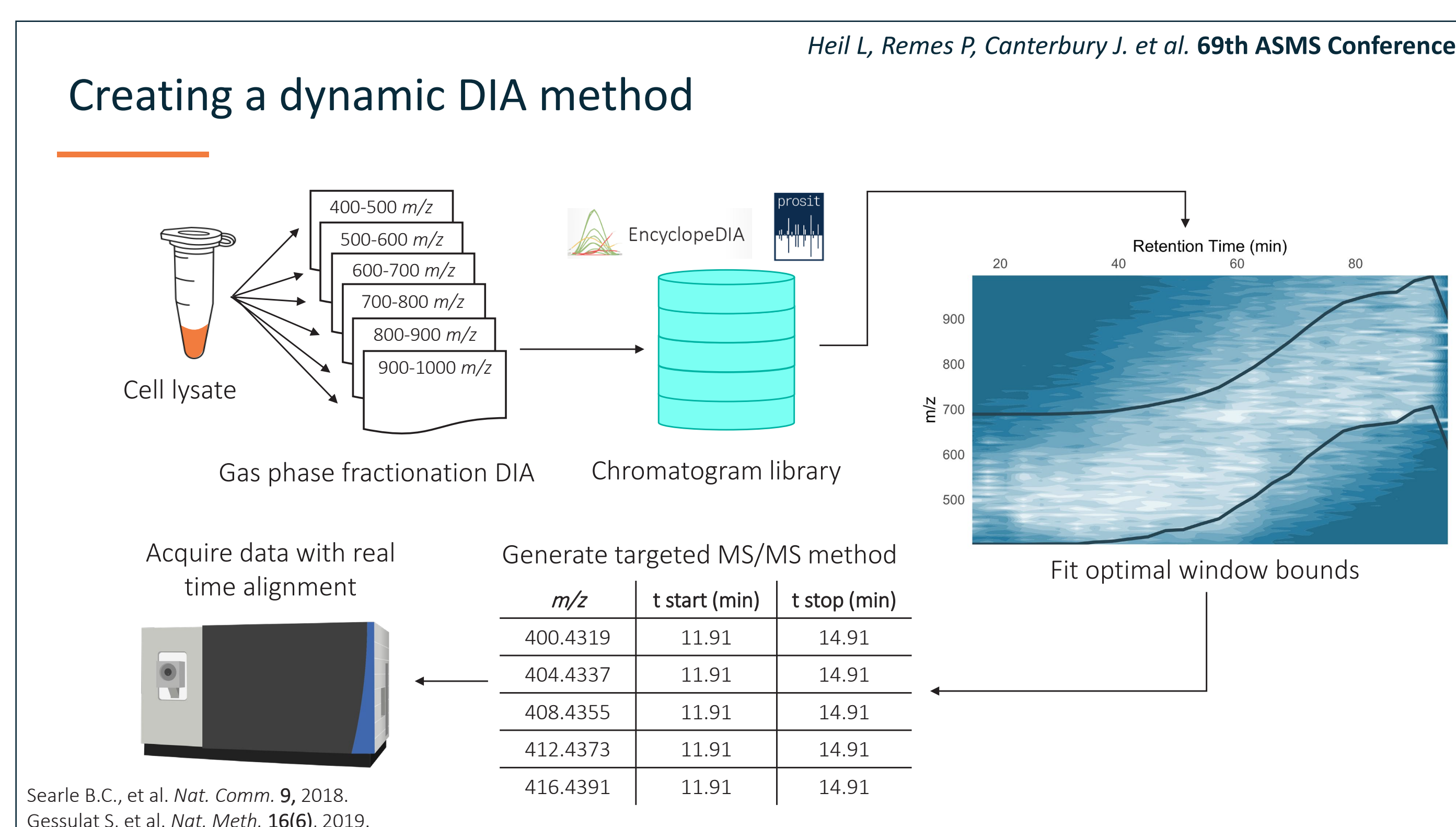
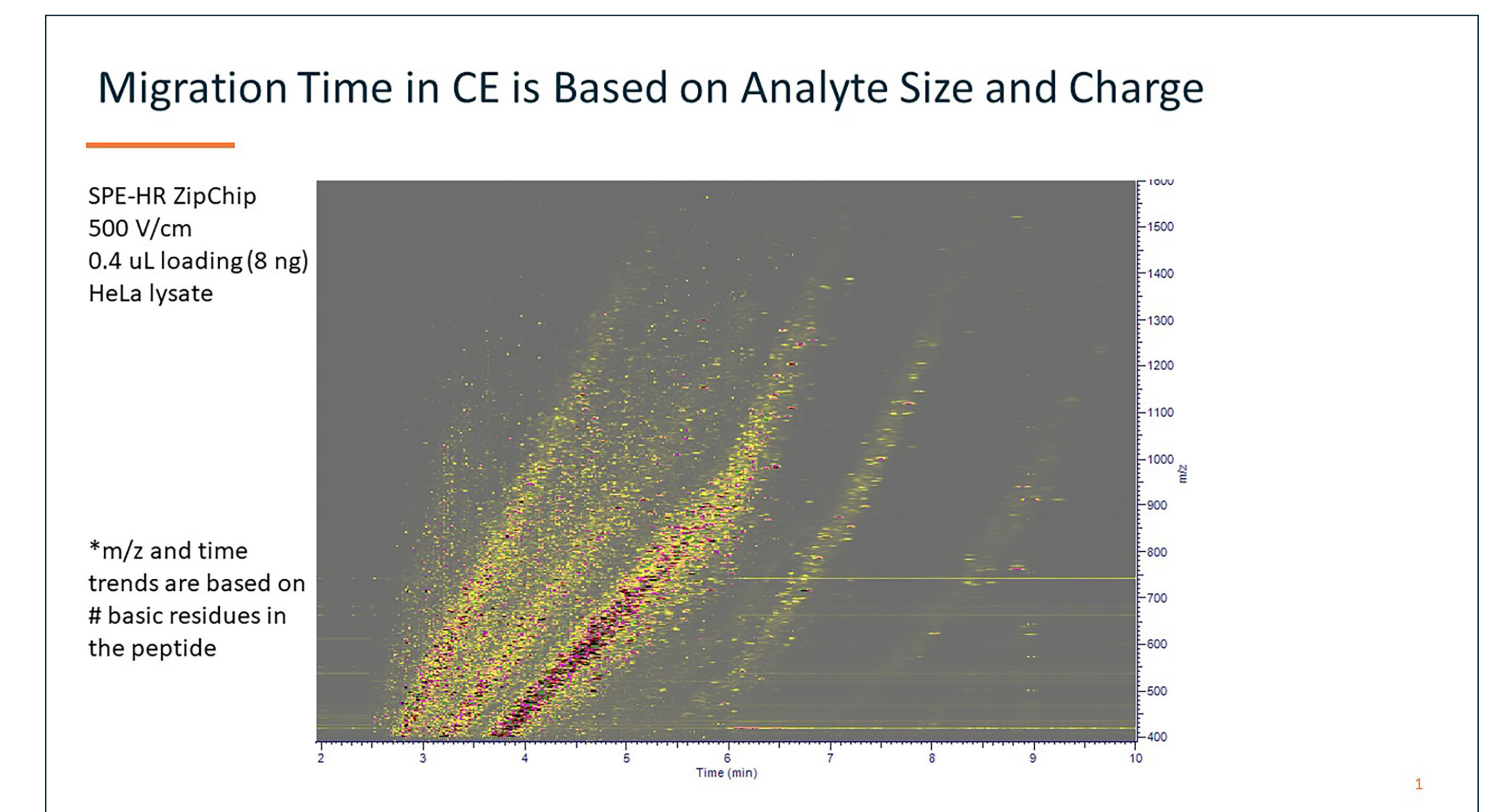
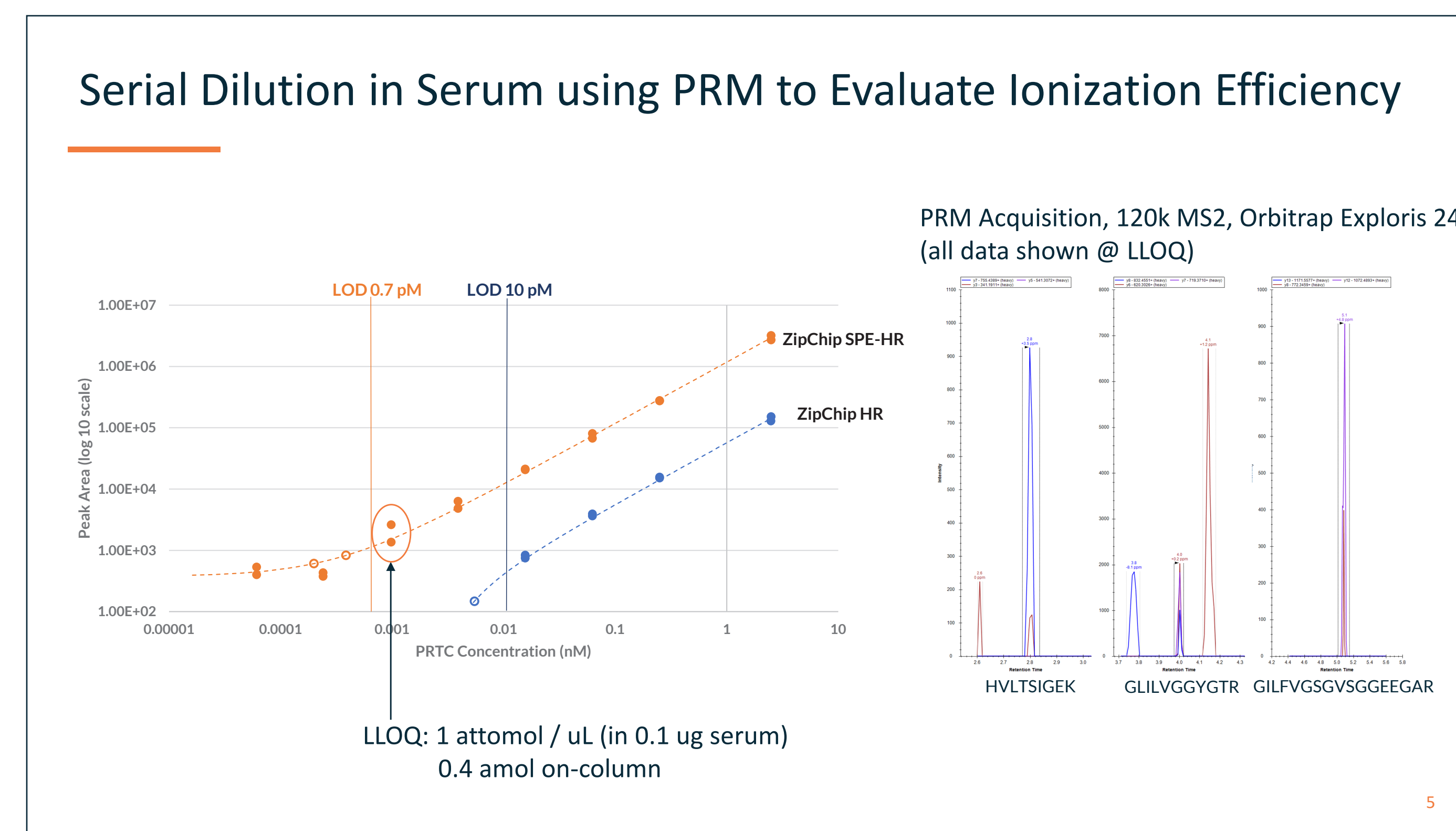
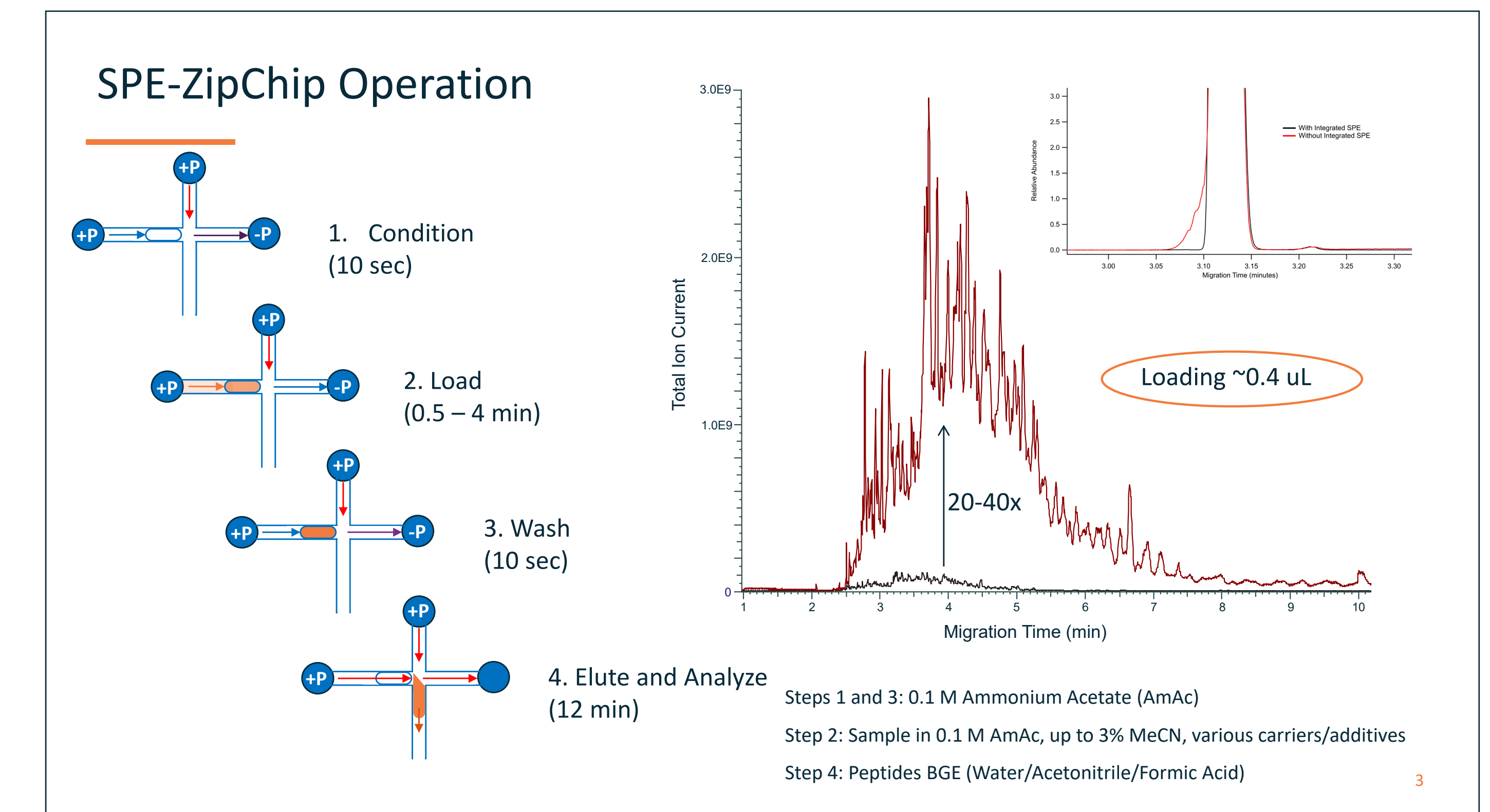
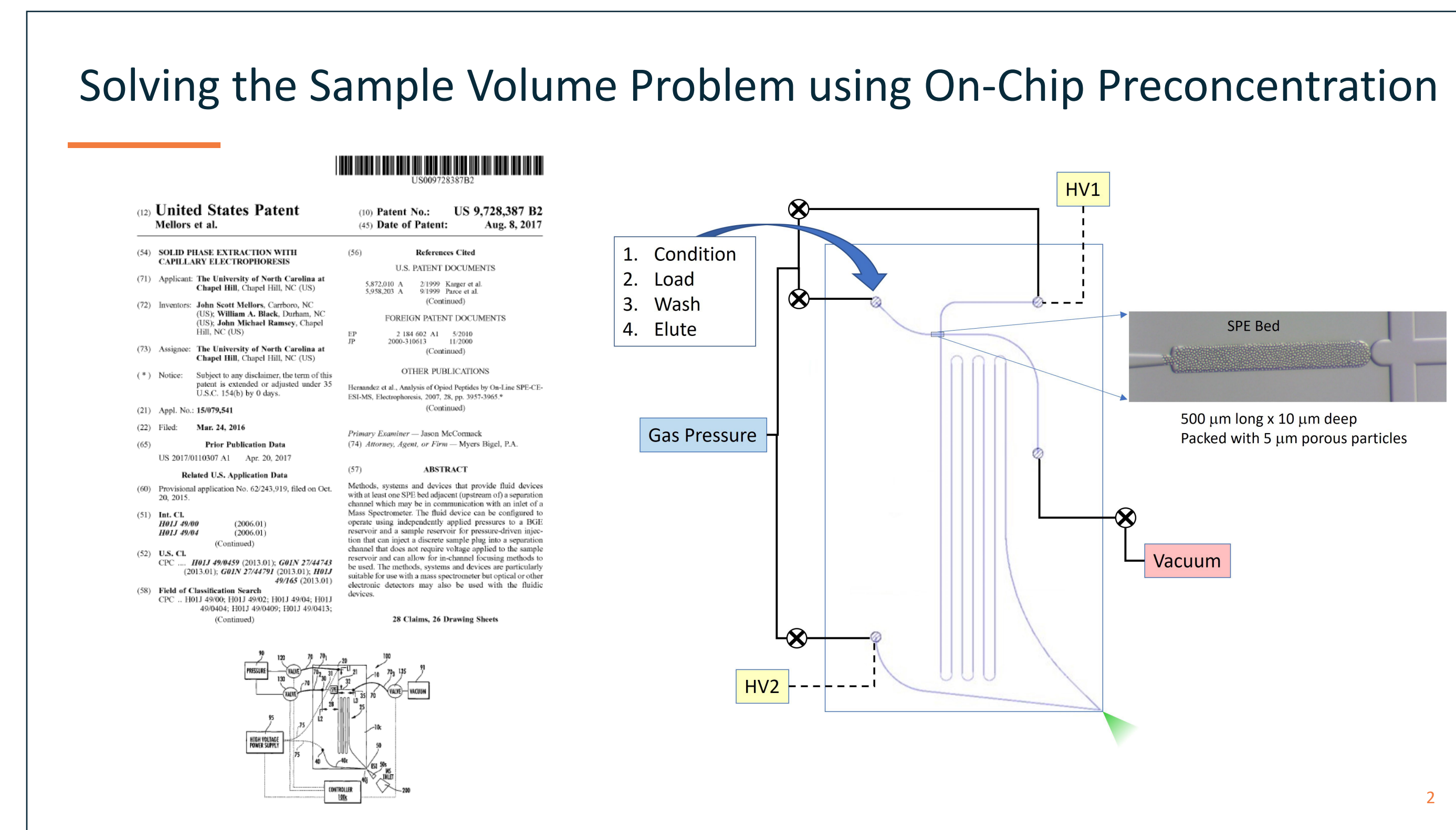
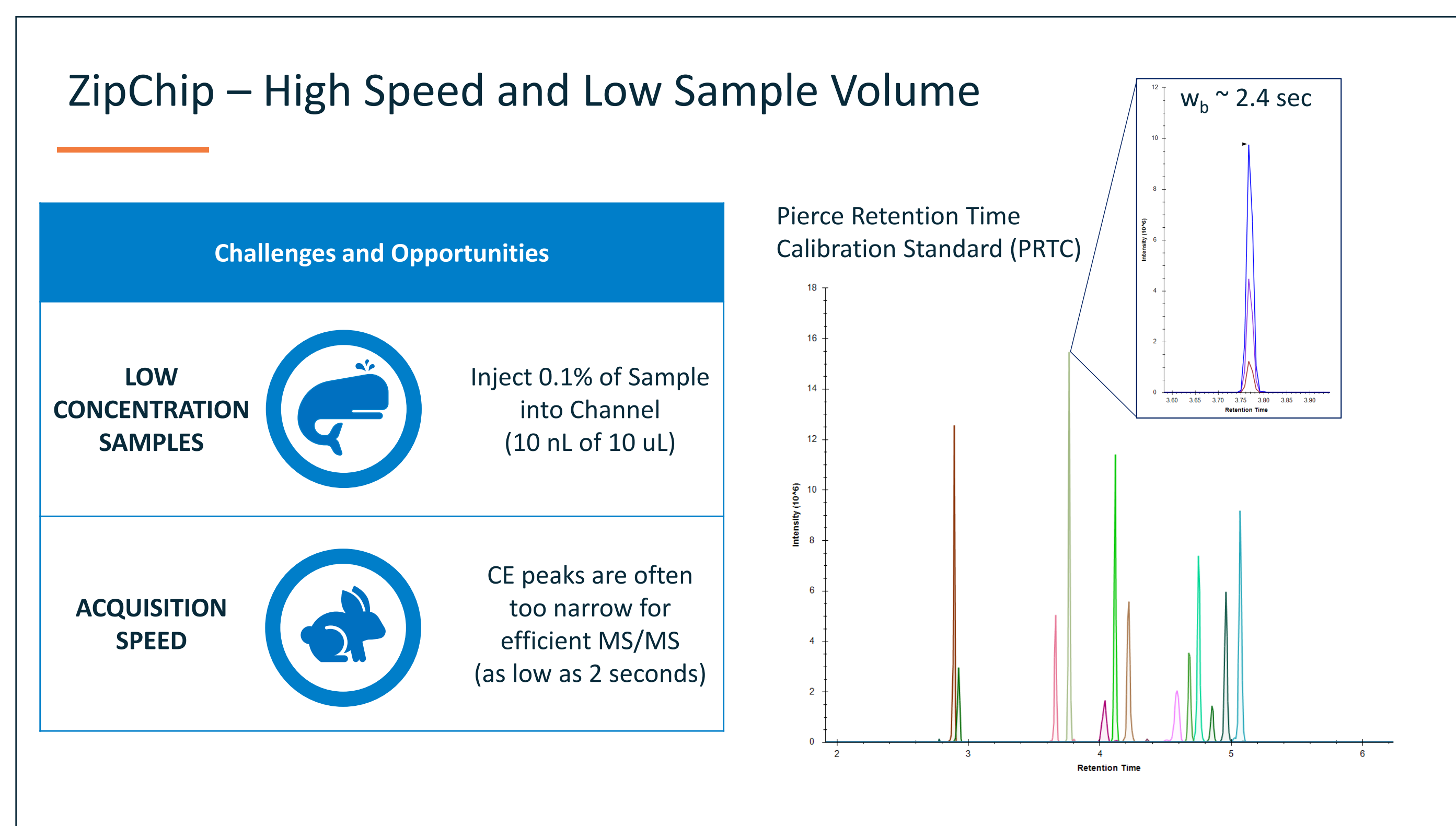


# Pushing the Boundaries of Speed and Sensitivity in Proteomics: Coupling SPE-Enabled Microfluidic Capillary Electrophoresis with Ultrafast Tandem Mass Spectrometry

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### 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