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CAPRION HistoGeneX

INTRODUCTION

- Precision oncology and the shift towards biomarker-driven trial designs
- Biomarker profiling of individual patients may be useful in guiding patient selection
- Identification of patients with the target biomarker profile may serve as an enrichment strategy for clinical trials
- Antibody-based assays for biomarker measurement may not be suitable or available
- Lack of specific antibodies, insufficient characterization, false +/- signals, limited multiplexing, etc.
- Mass spectrometry MRM assays for precise accurate quantitation of biomarkers, proteins of interest and novel markers can be quickly developed and validated
- Assay development based on knowledge of the target protein sequence(s)
- Reliability of MRM biomarker measurements demonstrated through CPTAC analytical validation
- Feasibility of adopting MRM biomarker assays in clinical trials
- Clinician-researchers require ad-hoc, 'sample analysis ready' biomarker panels, often within a short timeframe
- Sample analysis must be performed in a GCLP environment

GOALS / OBJECTIVES

- Demonstrate rapid assay development and analytical validation of up to 12-plex cancer protein biomarker panels in FFPE tissue
- Generate robust sample analysis protocols for accurate and precise MRM analysis of limiting amounts of clinical FFPE tissue
- Perform clinical sample analysis in a GCLP compliant environments

Sequential section(s)

• Dissection of tumor areas

Desalting

Deparaffinization

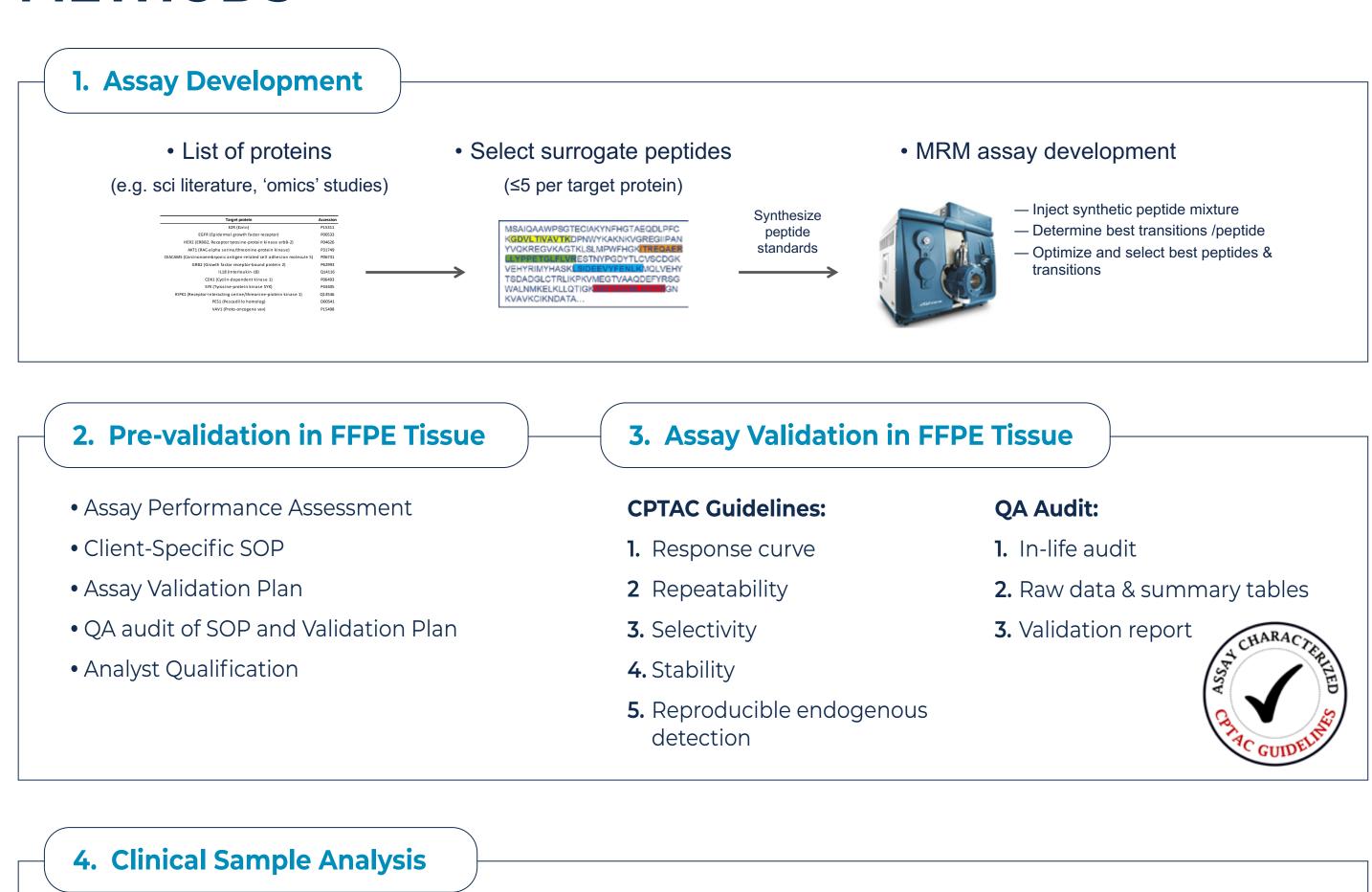
METHODS

Reference slide

Marking of tumor area

Mass Spectrometry

H&E evaluation



Removal of cros-links

High temperature cleavage of

Digestion to peptides

(Trypsin enzyme)

methylene bridges and protein

Homogenization

Total protein yield

• 4 μ m \longrightarrow ~1 to 2 μ g/mm² • 10 μ m \longrightarrow ~2 to 5 μ g/mm²

Rapigest buffer

Probe sonicator

RESULTS

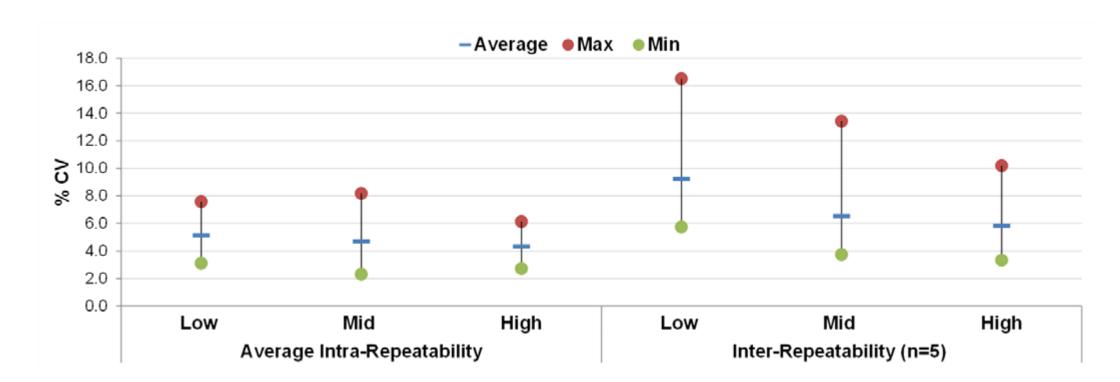
ANALYTICAL VALIDATION OF A 12-PLEX MRM ASSAY

CPTAC Experiment 1: Response Curves

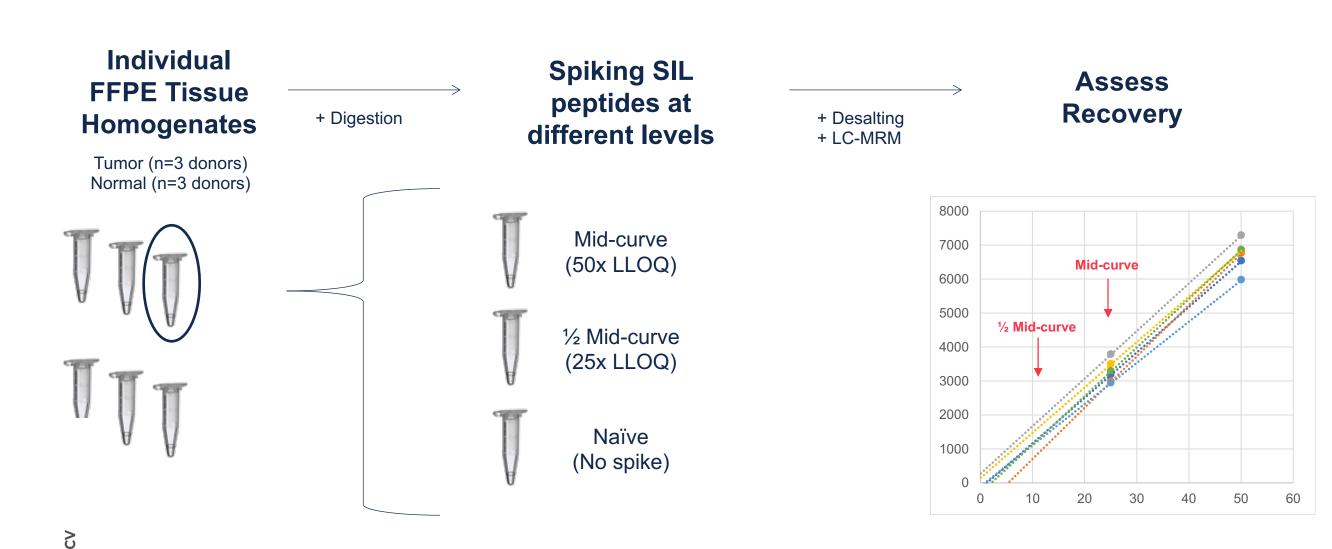
- Sensitivity: LOQ = 0.132 to 1.013 fmol/µg FFPE total protein
- Linearity: r-score > 0.99 (for all curves); Median = 0.9988

CPTAC Experiment 2: Repeatability, 5 Different Days

Total variability = 20 % criteria met for all peptides



CPTAC Experiment 3: Selectivity



Difference between mid-curve/2 and ½ mid curve: ≤ 11.4%

Difference in slope: ≤ 10.9%. Exception: SDLVNEEATGQFR (CEACAM5) in 1 donor was 23.5%

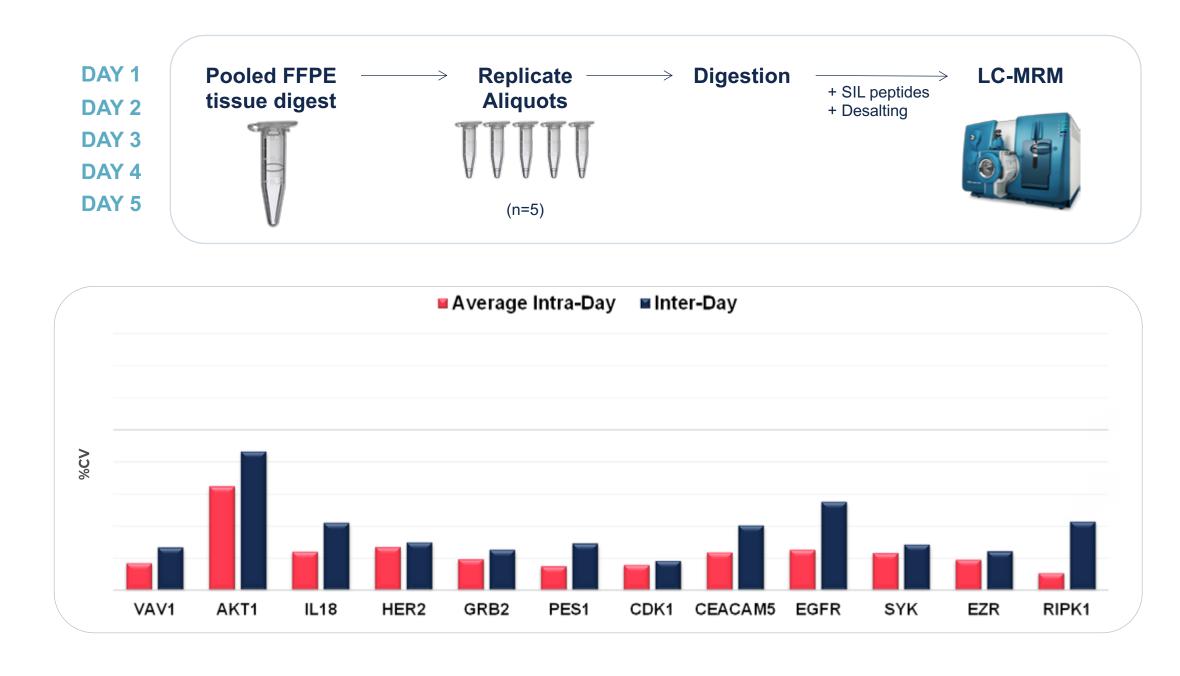
Illustration adapted from CPTAC guidelines. https://proteomics.cancer.gov/sites/default/files/assay-characterization-guidance-document.pdf

CPTAC Experiment 4: Stability

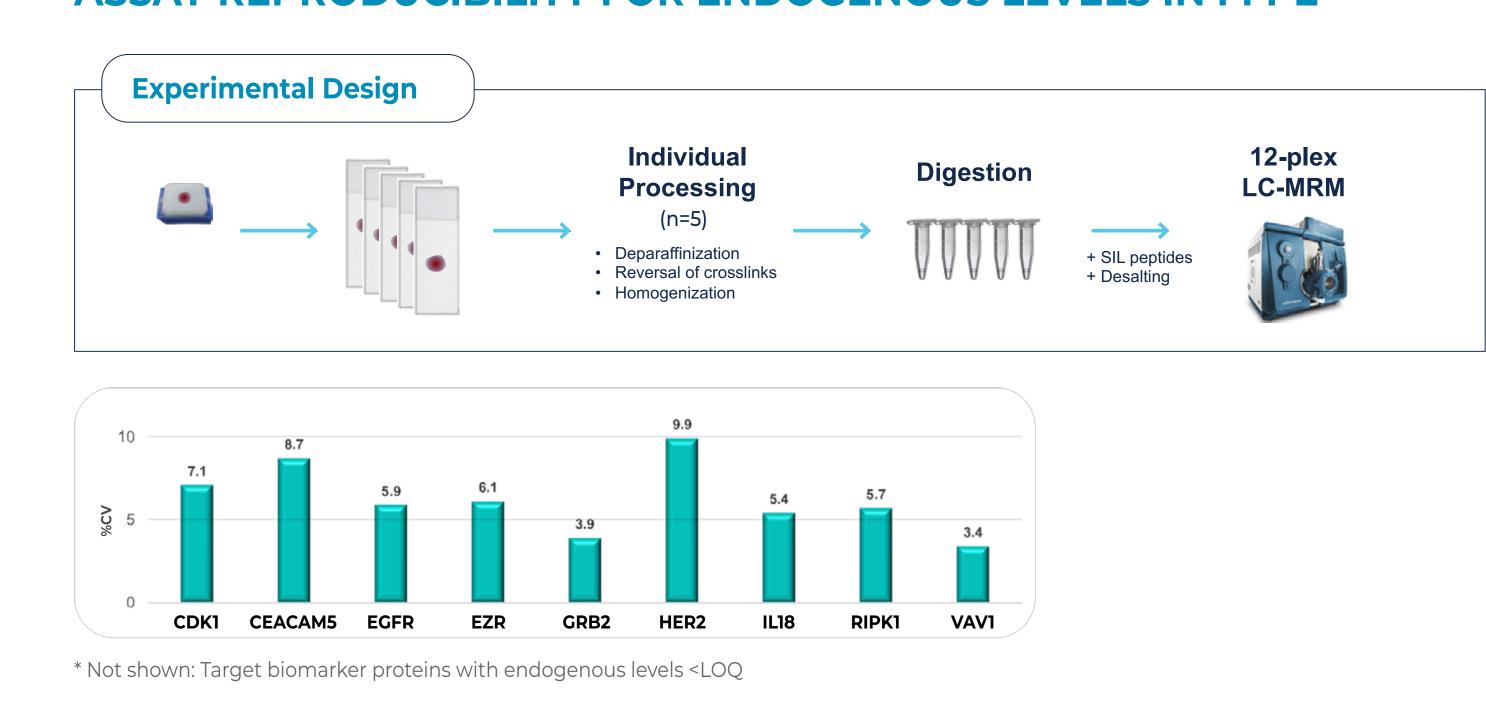
All peptides were stable (Wet for 48 h; Dry extract: 2X freeze-thaw, 14 d at -20 °C)

CPTAC Experiment 5: Reproducibility of Endogenous Detection

Median Intra-Day CV 6.5 %; Inter-Day CV: 12.8 %

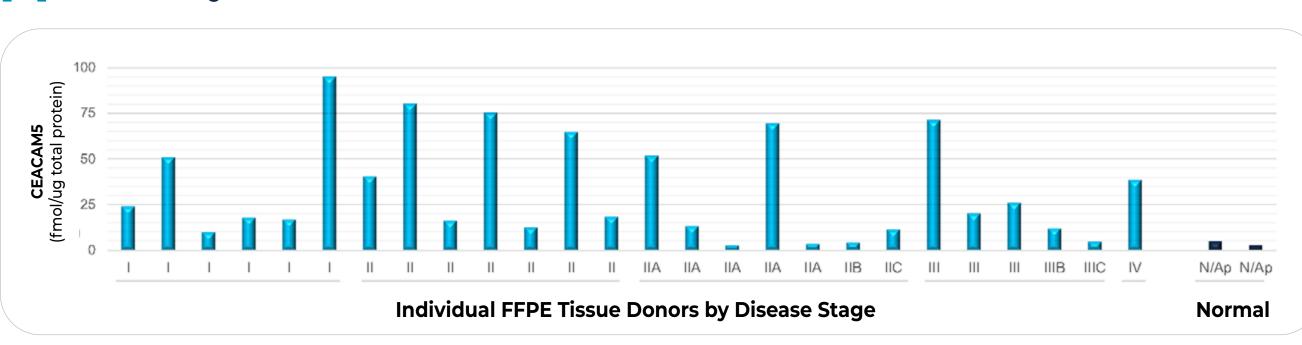


ASSAY REPRODUCIBILITY FOR ENDOGENOUS LEVELS IN FFPE

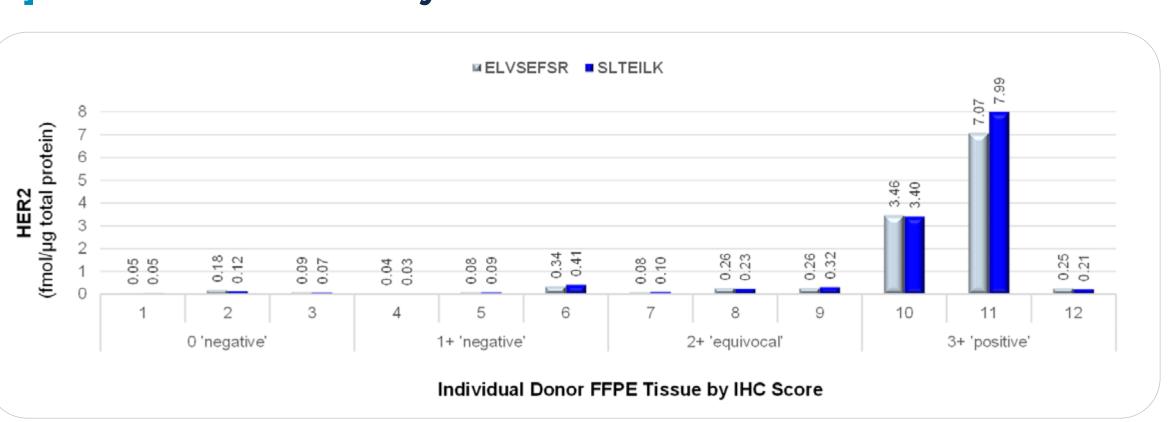


MRM BIOMARKER MEASUREMENTS VS DISEASE STAGE

[A] Variability of CEACAM5 in CRC I to IV

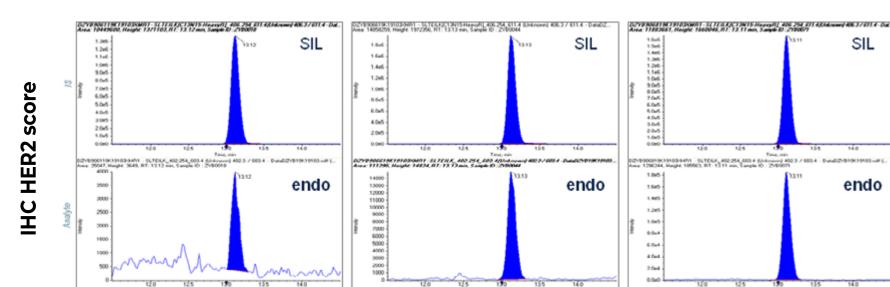


[B] HER2 Concentration by MRM vs IHC Score



 * HER2 was detected using both peptides in all 12 study samples with a S/N > 5

Representative MRM signal quality in FFPE tissues, peptide SLTEIK



CONCLUSION

- Precise accurate multiplexed quantitation of clinically relevant biomarkers in limiting amounts of FFPE tissue was demonstrated using a custom 12-plex biomarker panel validated to CPTAC guidelines
- GCLP-compliant quantitative multiplexed clinical analysis of protein biomarkers by MRM-MS in FFPE tissue is feasible
- Approach can be used for patient stratification, optimization of treatment outcomes, drug resistance prediction, and to support clinical development of novel therapies

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