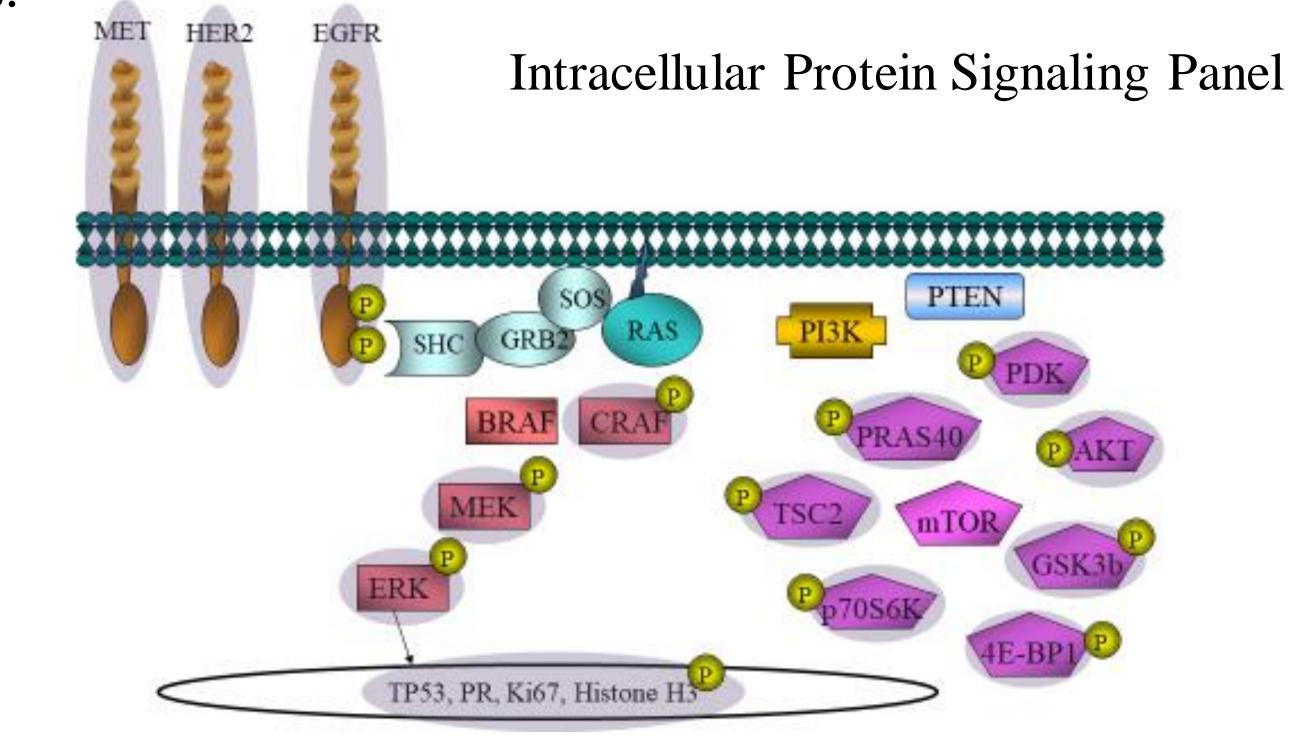




KNIGHT CANCER Institute

Introduction

Measuring protein expression by immunohistochemistry (IHC) in formalin-fixed, paraffin-embedded (FFPE) tissue is routine in clinical labs. However, current assays are limited to just 1 to 3 biomarkers per slide and histochemical signals are only semi-quantitative. Recently, a multiplexed panel of oligonucleotide-tagged antibodies has been developed (Nanostring 3D Vantage Solid Tumor Panel), comprised of antibodies, including 13 phosphorylated protein targets, specifically designed to interrogate the MAPK and PI3K/mTOR signaling pathways (ref.1). The panel uses the Nanostring nCounter system to quantitate oligonucleotides that are released by UV light after antibody binding. We undertook a validation of this panel with the goal of creating a new clinical assay for core biopsies of solid tumors.



Methods

Four micron sections of formalin-fixed paraffin-embedded (FFPE) cancer cell lines (controls) or 18-21 gauge cores of solid tumors (fixed within 3 minutes of biopsy) were subjected to citrate-based antigen retrieval and incubated overnight the cocktail of oligo-tagged with antibodies. After washing, the oligo-tags were released by UV light and quantitated on the Nanostring nCounter system. A set of 6 FFPE cancer cell lines were selected as positive controls and included on every run to assess antibody performance and inter-run normalizations. 28 support metastatic breast cancer core biopsies were analyzed to serve as a comparative cohort.

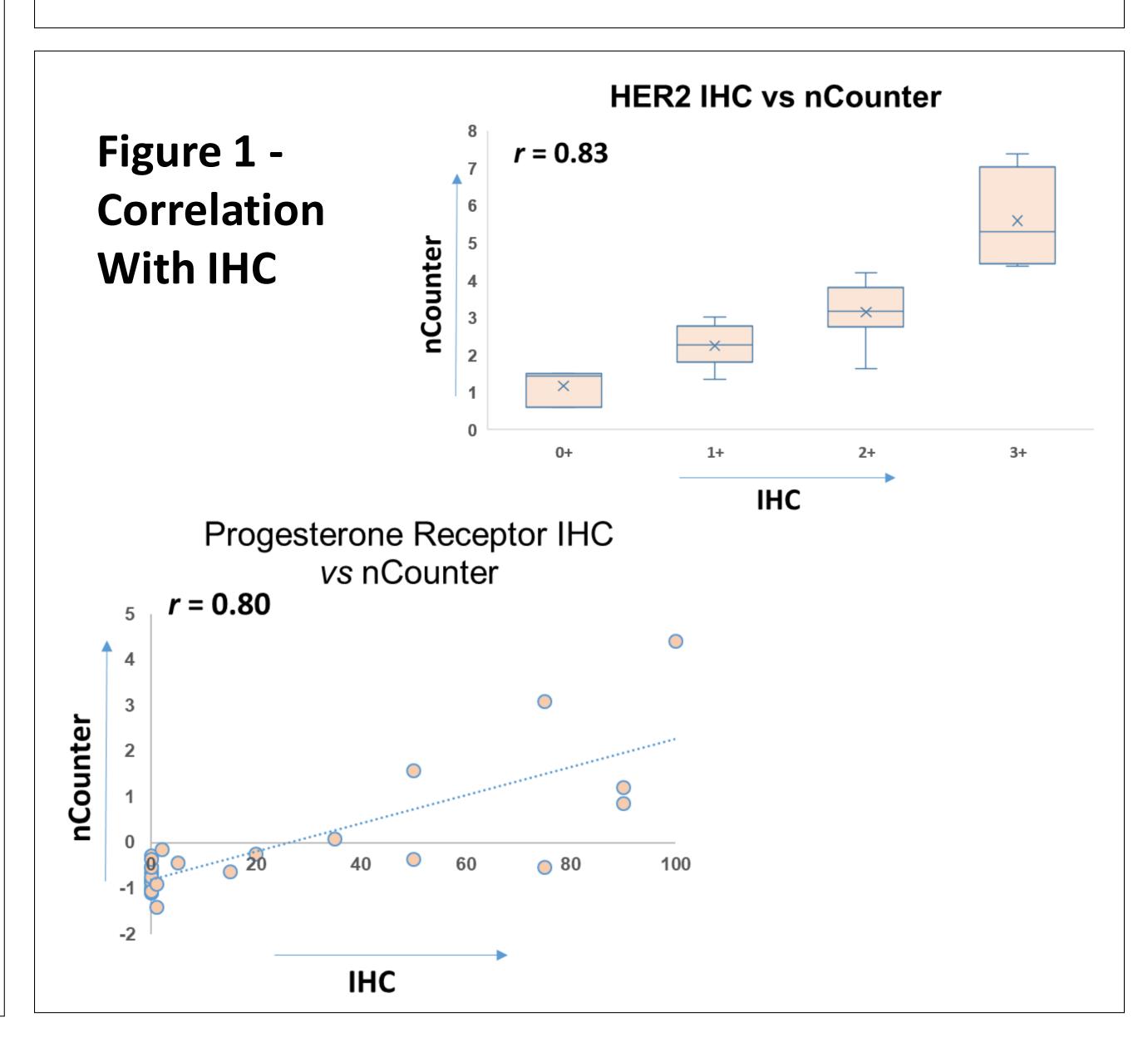
Analytical Validation of a Quantitative Intracellular Protein Signaling Panel for the Analysis of FFPE Breast Cancer Biopsies Jinho Lee, Todd Camp, Janice Patterson, Gordon B. Mills and Christopher L. Corless Knight Diagnostic Laboratories and Knight Cancer Institute, Oregon Health & Science University, Portland, OR





Results

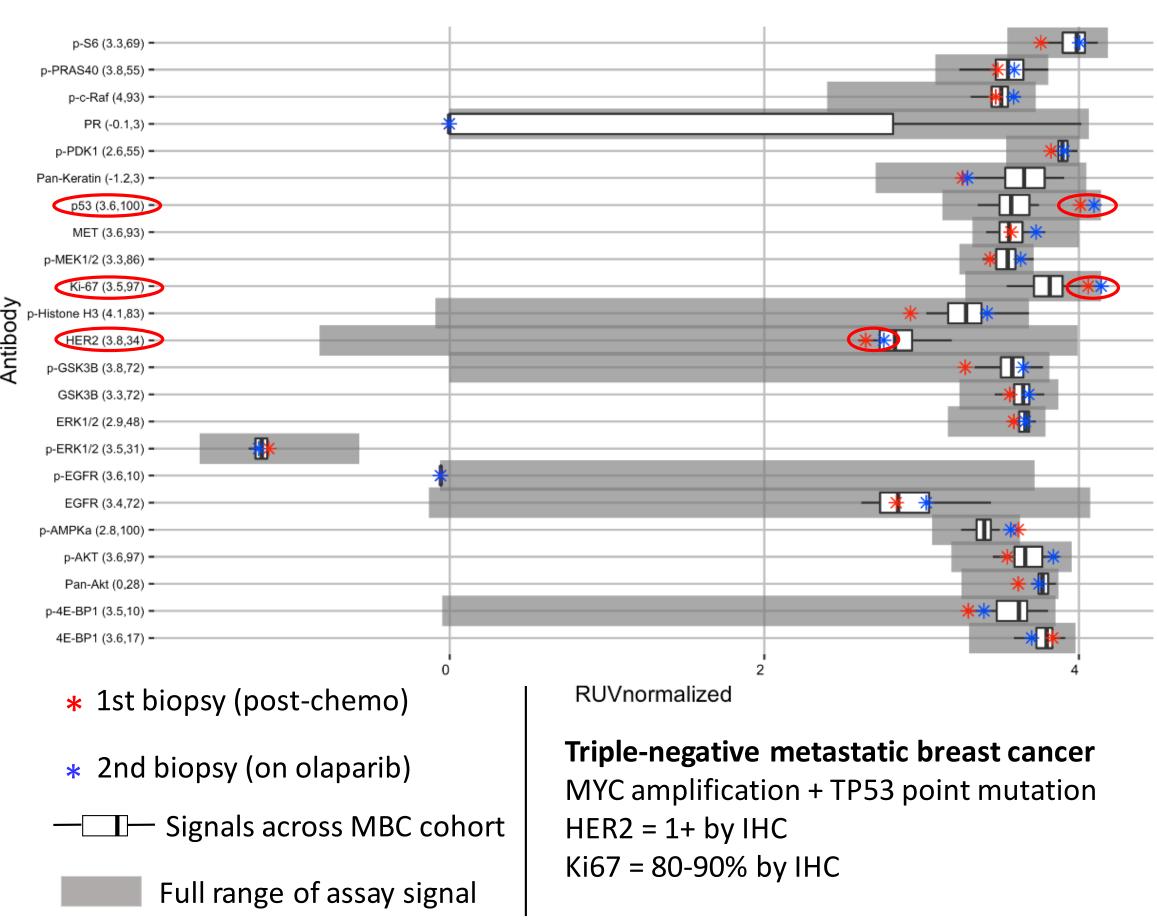
- In FFPE cell lines cancer progesterone receptor (high in MCF-7, BT474, T47D) and HER2 (high in HCC1954, SKBr3, BT474) matched reverse-phase protein array data. Pre-incubation of MDA-MB-468 with EGF led to expected increases in p-EGFR, p-MEK1/2, p-ERK1/2, p-AKT and p-S6.
- Among 10 rapidly-fixed FFPE solid tumors, signals for EFGR, p-EGFR, HER2, TP53, TSC2 and p-S6 were all consistent with known genomic alterations.
- There was good correlation with IHC results for PR and HER2 on sections of FFPE breast cancer core biopsies (Fig.1).
- Slide pre-treatment with lambda phosphatase eliminated phospho-protein signals (Fig.2).
- A bioinformatics strategy was developed to allow comparison of samples between runs (Fig 3).
- Analysis of 6 FFPE cancer cell lines selected as positive controls showed excellent inter-run reproducibility ($r \ge 0.92$).
- Data from 28 metastatic breast carcinoma core biopsies were generated to serve as a reference cohort (Fig.4).



detection of

Figure 2 – Specificity of Phosphoprotein Abs Melanoma Colon ca Breast ca Melanoma Colon ca Breast ca)1 (a Figure 3 – Bioinformatics Steps Normalize with Geometric Mean Loading Controls Subtract IgG Background lgG lgG Loading Controls Normalized Data Removal of Unwanted Variation Batch correction for inter-run comparisons (ref.4)

Figure 4 – Comparison of 2 serial biopsies to cohort of 28 metastatic breast cancers



No treatment

 λ -Phosphatase



Conclusions

The 3D Vantage Solid Tumor Panel provides a robust, quantitative approach to measuring 27 cell signaling biomarkers from a single section of FFPE tissue in <48 hours. The panel is useful for investigating treatment-induced changes in tumor cell signaling, but there are some limitations: 1) specimens must be fixed within minutes of biopsy to avoid protein de-phosphorylation (ref.2); 2) the assay requires a minimum of 40% tumor fraction; 3) any normal tissue should be excluded. The excellent performance of this slidebased approach suggests that it can be adapted to the new GeoMx Digital Spatial Pathology system (Nanostring), which uses micromirrors to focus UV light and release tags only from selected interest. With the cells of appropriate controls and bioinformatics steps, quantitative profiling oligoprotein using holds antibodies tagged great promise for future assays.

References

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