Measurement of the dynamic range of PD-L1 expression across different cores also revealed the improved sensitivity in PD-L1 detection provided by unmixing.

Conclusions The end-to-end Phenoptics staining, imaging, unmixing, and spatial analysis workflow described here provides a robust and sensitive platform for exploring the immune landscape within the tumor microenvironment.

Disclosure Information V. Goubert: None.

P03.05 DEEP SPATIAL PROFILING OF THE IMMUNE LANDSCAPE OF MSI AND MSS COLORECTAL TUMORS

SE Church, J Reeves, DR Zollinger, J McKay-Fleisch, AJ Bahrami, M Holpert*, AM White, MD Bailey, CR Merritt, M Hoang, S Warren, JM Beechem. NanString Technologies, Seattle, WA, USA

10.1136/jitc-2020-ITOC7.45

Introduction In colorectal cancer (CRC) there have been many recent advances in immune related biomarkers that are both prognostic and predictive of response to immunotherapy. Microsatellite instability (MSI)/mismatch repair deficiency dMMR is present in 15–20% of CRCs and correlates with increased immunogenic mutations that often augment lymphocyte infiltration into the tumor microenvironment (TME). Additionally, location of tumor infiltrating T cells in two areas of the TME, the tumor center (CT) and invasive margin (IM) has also been shown to be prognostic and predictive of response to immunotherapy. Here we use multiplexed protein and RNA digital spatial profiling to elicit the immune landscape of MSI-MSS characterized CRC tumors.

Methods Forty-eight CRC tumors were analyzed for gene expression using the NanoString® nCounter® PanCancer IO 360™ Research Use Only (RUO) Gene Expression Panel and assessed for 48 cell typing and biological signatures, including MMR loss/MSI predictor and the Tumor Inflammation Signature (TIS). A subset of 18 CRC tumors (6 MSI-TIS-hi, 6 MSS-TIS-hi, 6 MSS-TIS-lo) was selected for analysis with the RUO GeoMx™ Digital Spatial Profiler (DSP) using 40 antibodies (human IO protein panel), or 84 RNA probes (human IO RNA panel). Selection of regions of interest (ROIs) in two locations, CT and IM were guided by staining with fluorescent markers (CD45, CD3, pan-CK, DNA). 300–600 μM diameter circle ROIs were selected, and in some cases segmented by pan-CK+/pan-CK-. For 2 immune hot samples contour profiling at the IM into stromal and tumor regions was performed using 1400+ RNA probes with NGS readout.

Summary Using whole tissue gene expression analysis, we determined the TIS and IO 360 signature scores for 48 CRC tumors using PanCancer IO 360 assay. 18 tumors within this cohort were selected based on TIS status to further dissect the location-dependent immune contexture of the TME. Protein DSP confirmed loss of dMMR markers (MSSH2/MLH1) and identified an increased amount of potentially suppressive macrophages (CD163+PD-L1+) in MSI-TIS-hi versus MSS-TIS-hi tumors. Segmentation of ROIs based on tumor versus stroma (pan-CK2+) identified samples with high proportions of tumor-invading TILs. Two MSI-TIS-hi profiled using probes against 1400+ mRNA targets confirmed protein results (CD163 in IM) and identified tumor-related signatures corresponding to the inside of the tumor (Cytokereitins, HER2/ERBB2, MET).

Conclusions Here we show the use of novel high-plex spatial profiling to profile location and pathways in the TME of MSI and MSS CRC tumors. These findings elicit unique biology related to the location and signaling of immune cells, which have the potential to unveil targets for therapeutic combinations.