USING ADDITIONAL MORPHOLOGY MARKERS IN
NANOSTRING® GEOMX® WHOLE TRANSCRIPTOME
ATLAS ASSAY TO ASSESS NSCLC TUMOR SUBTYPE

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Background Recent publications have discussed techniques to identify tumor subtypes and a potential correlation with tumor immunity and immunotherapy success. Several techniques have been used for tumor subtype identification including RNA Seq, NanoString® nCounter®, and newer multi-omics approaches. NanoString’s GeoMx® DSP platform provides spatial context about cells and their interactions within a tumor while also producing high-plex gene expression data. Expansion of existing morphology markers used with GeoMx DSP enables more precise segmentation of tumors based on key characteristics and provides a better understanding of the tumor’s interaction with surrounding tissue. The subsequent transcriptomic profile from the Whole Transcriptome Atlas (WTA) panel may help identify characteristics that impact immunotherapies and the development of treatment screening tests. Lung cancer is still the leading cause of cancer death in the United States.1 As classified by the WHO/International Association for the Study of Lung Cancer (IASLC),2 there are three main subtypes of malignant NSCLS including squamous cell carcinoma (25% of lung cancers) and adenocarcinoma (40% of lung cancers).

Methods To evaluate the capability of this technology to selectively enrich specific cell types, we stained sections of non-small-cell lung cancer tumor (NSCLS) subtypes. Since molecular subtyping of NSCLC tumors is critical for targeted therapy and IHC biomarkers play a key role in the diagnosis and subclassification of lung cancer, we investigated if a histological approach combined with molecular profiling could assess both subtypes while identifying unique markers to each tumor subtype. NSCLC tissue was stained with P40 and TTF-1 antibodies to differentiate between squamous cell carcinoma and adenocarcinoma subtypes.3, 4 For all experiments, transcriptional profiles were assessed with the WTA panel for GeoMx DSP, covering over 18,000 genes and enabling oncology pathway analysis to profile the tumor, tumor microenvironment, and immune response. Analysis of this data set was performed using the GeoMx DSP Analysis Suite software.

Results The transcriptional profiles of these samples were then compared, and significant differences were revealed between these two tumor cell types.

Conclusions The findings support the notion that custom morphology markers enable better tumor stratification providing more meaningful gene expression analysis data. This gene expression data can then be integrated with gene signatures which are being developed for key targets of IO treatments to predict the utility of various immunotherapies for individual patient tumors. Studies with additional tumor types and markers are ongoing to further explore the utility of this technology for analyzing gene expression in different tumor types.

REFERENCES