**Introduction**

The success of immunotherapy for the treatment of metastatic cancers relies on the prediction and identification of potential neo-antigens. In recent years expression levels of these neo-antigens along with other immune system related genes have been evaluated in an effort to better understand response rates for immunotherapy in various cancers. Gene expression levels can be assessed by numerous techniques including hybridization-based or direct sequencing technologies. Two platforms-HTG Molecular and NanoString nCounter have been utilized to profile changes in gene expression and offer unique advantages for analyzing challenging specimens such as formalin-fixed paraffin embedded (FFPE) tissues. The NanoString nCounter platform utilizes hybridized fluorescent probes targeted against genes of interest for a non- amplified measurement of gene expression. Several studies have shown that the NanoString platform has good sensitivity, specificity and reproducibility for the assessment of gene expression levels from FFPE samples. The HTG platform is relatively new and also uses a hybridization based method to enrich genes of interest without first isolating RNA. To determine the robustness of the HTG platform, we profiled a set of 30 metastatic prostate cancer samples using the HTG Molecular EdgeSeq Immuno-Oncology Assay. In these experiments, we found that expression data obtained by using both extracted RNA and lysate from FFPE slides was highly reproducible (Spearman coefficient > 0.85). In addition, the expression profile of targeted genes obtained by using different slides from the same blocks was also highly correlated (Spearman coefficient > 0.90). Our experiments also showed a high correlation between gene expressions profiles obtained by HTG, the NanoString PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples. Further analysis to evaluate and compare the sensitivity of PanCancer Immune Profiling panel and RNA-Seq from the same set of 30 metastatic prostate cancer samples.