Introduction

Background:
- Link between the immune infiltrate and several human carcinoma types and prognosis and/or response to therapy
- Increasing evidence suggests that the number, type, and location of tumor-infiltrating lymphocytes in primary tumors harbor prognostic value, and this has led to the development of a “tumor immunoscore”

Aims:
- Develop comprehensive expression assay for analysis of cellular composition
- Molecular profiling of key immune-related genes, including drug targets, known biomarkers, and immune mechanisms
- Unbiased discovery of most informative biomarkers that can be analyzed by conventional IHC/FACS assays

What is ImmuneNet?
- Detect cellular composition of immune / stromal / cancer cells in tumor microenvironment
- Identify immunity status and immunoeediting mechanisms
- Discover novel biomarkers for immunotherapy
- Profiling of immunotherapy targets and all FDA-approved drug targets

ImmuneNet Assay Gene Composition

The ImmuneNet 2500 panel includes a comprehensive set of 2500 genes specific for detection and profiling of different types of immune cells, including T cells, B cells, fibroblasts, stromal and endothelial cells in the tumor microenvironment, activated immune cells suggestive of adaptive and innate immunity, immunity-related genes from 16 predictive and prognostic core gene signatures that have been validated in recent chemo- and immunotherapy clinical trials across several tumor types, including melanoma, colorectal, breast, and lung cancers.

Conclusions

We present the novel Cancer ImmuneNet 2500 assay panel, a quantitative, multiplexed, high throughput targeted RNASeq approach that leverages the power of multiplex PCR technologies and NGS and allows you to obtain the transcriptome profile of the tumor microenvironment.

The ImmuneNet Panel includes 2,500 immunity-related genes. In order to develop cell-type specific gene signatures, we developed a non-parametric, binary linear classifier algorithm to infer the level of infiltrating immune cells in tumor tissues. Our panel can distinguish hematopoietic cell phenotypes from bulk tissues and tumor cells and offers a unique approach to identify tumor-infiltrating cells.

In this study, we present the design and algorithms of our panel that can accurately resolve relative fractions of diverse immune cell types from complex tissues.

Intended Applications:
- The platform is applicable for novel predictive and prognostic biomarker discovery
- Comprehensive profiling of tumor-associated immune cell composition will provide important insights into cancer immunomodulating mechanisms
- Has the potential to provide a new molecular stratification approach to cancer immunotherapy. Currently, a portfolio (DriverMap®) of such assays are in development to address specific disease areas.