

OncoPeptTUME™

Assess the tumor microenvironment utilizing NGS data

OncoPeptTUME™ provides immune phenotyping of the tumor microenvironment and analyses potential biomarkers of response to enable success of checkpoint inhibitors.

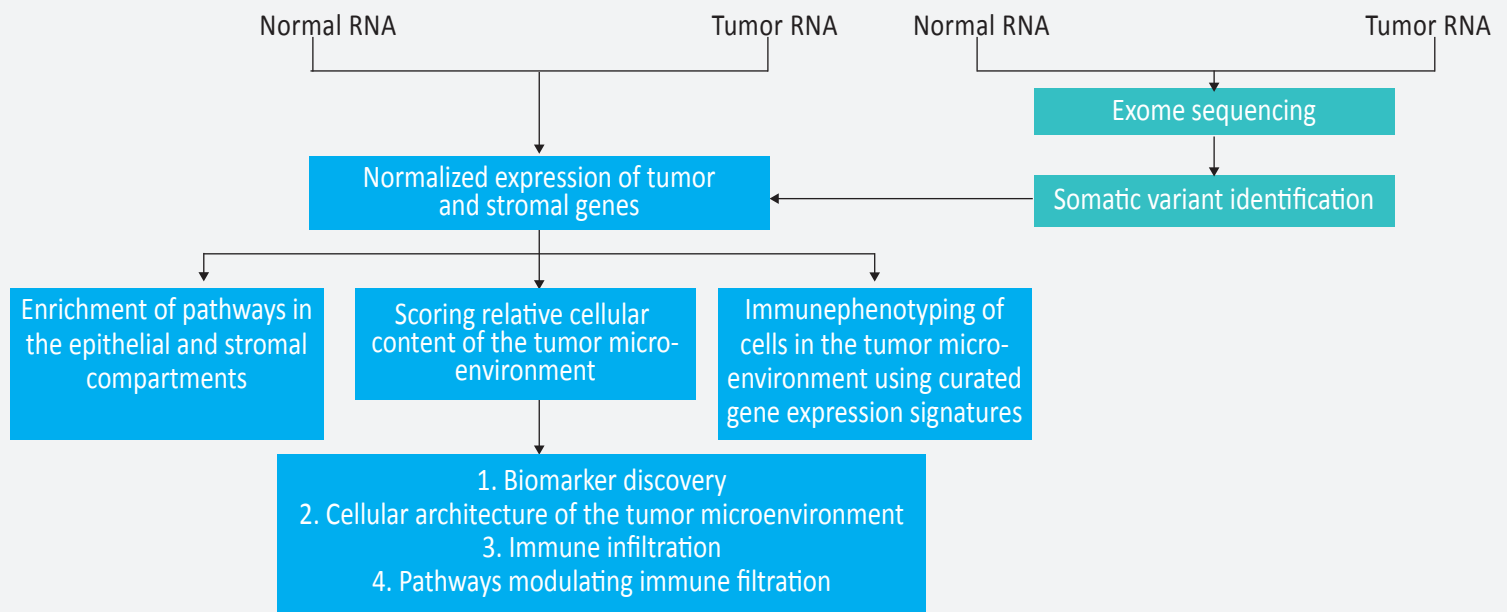
Highlights

- Optimized extraction methods to generate good quality material for NGS from poor quality FFPE samples
- Curated data of tumor-specific mutations by cancer bioinformatics experts which enables separation of epithelial-specific genes from stromal genes
- Proprietary analysis algorithms to identify bona-fide genetic alterations that are expressed in the samples
- Powerful computational methods to evaluate differentially expressed genes and pathways
- Analysis of relative composition of tumor, epithelial and stromal cells
- Evaluation of cytokine network within the tumor microenvironment
- Quick turnaround time

Key Benefits

Benefits	Features
Enables Patient stratification for single agent or combination therapies	<ul style="list-style-type: none">• Robust pipeline for RNA sequencing and analysis• Curated database of relevant cancer immunotherapy target genes• Relative expression of target genes normalized to cell types present in the tumor microenvironment• A refined scoring method to assess relative expression of genes for specific immune cell types
Enhances therapeutic benefit of checkpoint control inhibitors	<ul style="list-style-type: none">• Combination with cancer vaccines using OncoPeptVAC™ analysis• Combination with other therapies to modulate T-cell infiltration in T-cell depleted tumors.
Increases durability of response and Patient outcome and aids in predicting adverse reaction to the drug	<ul style="list-style-type: none">• Characterization of the mutational burden and density of T-cell neo-epitopes by applying OncoPeptVAC™ analysis• Gene Signature Expression Analysis (GSEA) provides the composition of the infiltrated immune cells• Immune cell scoring to enhance GSEA (scoring epithelial content, stromal content and immune content) to derive the gross composition of the tumor.• Relevant cell type analysis in the tumor microenvironment: T-cells and their subtypes, Macrophages, Myeloid derived suppressor cells, NK cells, B cells

Workflow



Key Deliverables

- ✓ Normalized gene expression data
- ✓ Differential expression of genes and pathways
- ✓ All data files
- ✓ Assessment of cell types present in the tumor microenvironment

Key Metrics

Sequencing Method	• Illumina Hi-Seq Platform
Bioinformatics	• Both Proprietary and Public tools
Depth	• DNA (150X); RNA (60-80 million reads)
Turn Around Time	• 4 weeks (Rapid TAT available at additional cost)
Sample Requirements	• Tumor only or tumor with matched normal
Sample Types	• Frozen tumor, FFPE, Blood
DNA Input Required	• 1µg-4µg
RNA Input Required	• 300ng-1µg
Blood Required	• 2-5 million blood cells
FFPE Required	• 3 X10 micron slides
Frozen tumor Required	• 300µg – 1mg

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