

# 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.

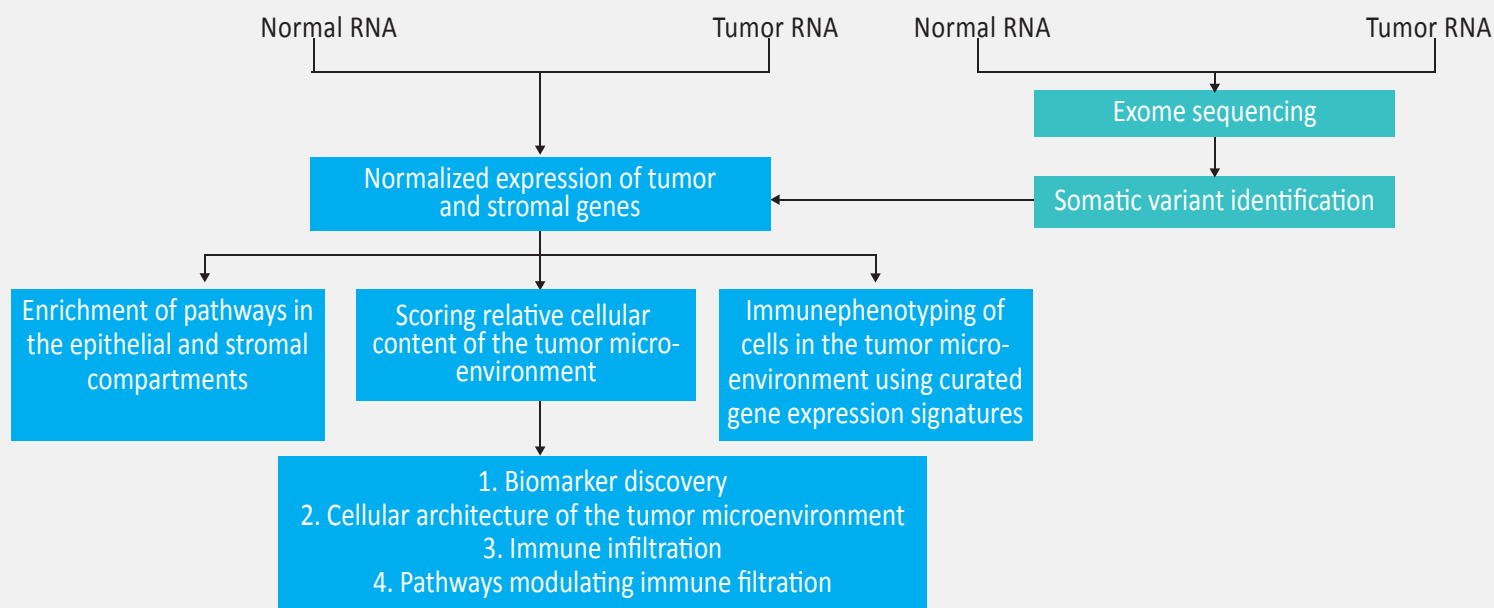
## Highlights

- 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"><li>• Robust pipeline for RNA sequencing and analysis</li><li>• Curated database of relevant cancer immunotherapy target genes</li><li>• Relative expression of target genes normalized to cell types present in the tumor microenvironment</li><li>• A refined scoring method to assess relative expression of genes for specific immune cell types</li></ul>
Enhances therapeutic benefit of checkpoint control inhibitors	<ul style="list-style-type: none"><li>• Combination with cancer vaccines using MedGenome's proprietary OncoPeptVAC™ analysis</li><li>• Combination with other therapies to modulate T-cell infiltration in T-cell depleted tumors.</li></ul>
Increases durability of response and Patient outcome and aids in predicting adverse reaction to the drug	<ul style="list-style-type: none"><li>• Characterization of the mutational burden and density of T-cell neo-epitopes by applying MedGenome's proprietary OncoPeptVAC™ analysis</li><li>• Gene Signature Expression Analysis (GSEA) provides the composition of the infiltrated immune cells</li><li>• Immune cell scoring to enhance GSEA (scoring epithelial content, stromal content and immune content) to derive the gross composition of the tumor.</li><li>• Relevant cell type analysis in the tumor microenvironment: T-cells and their subtypes, Macrophages, Myeloid derived suppressor cells, NK cells, B cells</li></ul>

# 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	• MedGenome 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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